Annika Lindblom

List of Publications by Citations

167 papers	13,955 citations	49 h-index	117 g-index
176 ext. papers	17,405 ext. citations	10.5 avg, IF	4.79 L-index

#	Paper	IF	Citations
167	Mutation in the DNA mismatch repair gene homologue hMLH1 is associated with hereditary non-polyposis colon cancer. *Nature*, **1994**, 368, 258-61	50.4	1788
166	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. *Nature Genetics*, **2013**, 45, 353-61, 361e1-2	36.3	813
165	Association analysis identifies 65 new breast cancer risk loci. *Nature*, **2017**, 551, 92-94	50.4	643
164	The clinical phenotype of Lynch syndrome due to germ-line PMS2 mutations. *Gastroenterology*, **2008**, 135, 419-28	13.3	411
163	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. *Nature Genetics*, **2015**, 47, 373-80	36.3	406
162	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
161	Genetic mapping of a second locus predisposing to hereditary non-polyposis colon cancer. *Nature Genetics*, **1993**, 5, 279-82	36.3	375
160	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
159	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. *Nature Genetics*, **2013**, 45, 392-8, 398e1-2	36.3	327
158	Prediction of breast cancer risk based on profiling with common genetic variants. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	324
157	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	19.2	291
156	Cancer risk and survival in carriers by gene and gender up to 75 years of age: a report from the Prospective Lynch Syndrome Database. *Gut*, **2018**, 67, 1306-1316	19.2	259
155	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. *Nature Genetics*, **2017**, 49, 1767-1778	36.3	186
154	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
153	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	11	167
152	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	8.1	164
151	Molecular basis of HNPCC: mutations of MMR genes. *Human Mutation*, **1997**, 10, 89-99	4.7	145

150	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
149	Lynch syndrome caused by germline PMS2 mutations: delineating the cancer risk. *Journal of Clinical Oncology*, **2015**, 33, 319-25	2.2	137
148	CHEK2*1100delC heterozygosity in women with breast cancer associated with early death, breast cancer-specific death, and increased risk of a second breast cancer. *Journal of Clinical Oncology*, **2012**, 30, 4308-16	2.2	134
147	PALB2, CHEK2 and ATM rare variants and cancer risk: data from COGS. *Journal of Medical Genetics*, **2016**, 53, 800-811	5.8	121
146	Age- and Tumor Subtype-Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. *Journal of Clinical Oncology*, **2016**, 34, 2750-60	2.2	107
145	Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. *Human Molecular Genetics*, **2014**, 23, 4729-37	5.6	107
144	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, 1052-67	24.4	104
143	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		103
142	Cancer Risks for PMS2-Associated Lynch Syndrome. *Journal of Clinical Oncology*, **2018**, 36, 2961-2968	2.2	102
141	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
140	Microsatellite Instability and hMLH1 and hMSH2 expression analysis in familial and sporadic colorectal cancer. *Laboratory Investigation*, **2001**, 81, 535-41	5.9	91
139	Colorectal cancer with and without microsatellite instability involves different genes **1999**, 26, 247-252		90
138	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	40	88
137	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	19.2	87
136	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. *Nature Communications*, **2014**, 4, 4999	17.4	87
135	No evidence that protein truncating variants in BRIP1 are associated with breast cancer risk: implications for gene panel testing. *Journal of Medical Genetics*, **2016**, 53, 298-309	5.8	83
134	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, 1046-60	11	80
133	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	11.6	80

132	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
131	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. *Journal of the National Cancer Institute*, **2015**, 107,	9.7	74
130	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
129	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
128	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. *Nature Communications*, **2016**, 7, 11375	17.4	64
127	Microsatellite instability as a predictor of a mutation in a DNA mismatch repair gene in familial colorectal cancer. *Genes Chromosomes and Cancer*, **2000**, 27, 17-25	5	63
126	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	11	59
125	Fine scale mapping of the breast cancer 16q12 locus. *Human Molecular Genetics*, **2010**, 19, 2507-15	5.6	57
124	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
123	Five endometrial cancer risk loci identified through genome-wide association analysis. *Nature Genetics*, **2016**, 48, 667-674	36.3	56
122	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	5.6	55
121	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. *Nature Communications*, **2016**, 7, 12675	17.4	53
120	Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. *Genetics in Medicine*, **2017**, 19, 599-603	8.1	51
119	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
118	Cumulative Burden of Colorectal Cancer-Associated Genetic Variants Is More Strongly Associated With Early-Onset vs Late-Onset Cancer. *Gastroenterology*, **2020**, 158, 1274-1286.e12	13.3	47
117	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019**, 10, 431	17.4	45
116	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	13.3	45
115	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	11	43

114	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	4	42
113	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. *Endocrine-Related Cancer*, **2016**, 23, 77-91	5.7	41
112	A human compound heterozygote for two MLH1 missense mutations. *Nature Genetics*, **1997**, 17, 135-6	36.3	41
111	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. *Cancer Medicine*, **2018**, 7, 1978-1987	4.8	40
110	Genetic predisposition to in situ and invasive lobular carcinoma of the breast. *PLoS Genetics*, **2014**, 10, e1004285	6	38
109	MicroRNA related polymorphisms and breast cancer risk. *PLoS ONE*, **2014**, 9, e109973	3.7	37
108	Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. *Nature Communications*, **2020**, 11, 597	17.4	36
107	Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 432-444	11	31
106	Genetic predisposition to ductal carcinoma in situ of the breast. *Breast Cancer Research*, **2016**, 18, 22	8.3	31
105	Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. *Human Molecular Genetics*, **2014**, 23, 5545-57	5.6	29
104	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
103	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
102	Colorectal cancer incidence in carriers subjected to different follow-up protocols: a Prospective Lynch Syndrome Database report. *Hereditary Cancer in Clinical Practice*, **2017**, 15, 18	2.3	27
101	Body mass index and breast cancer survival: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2017**, 46, 1814-1822	7.8	27
100	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	4.9	27
99	Regulator of Chromosome Condensation 2 Identifies High-Risk Patients within Both Major Phenotypes of Colorectal Cancer. *Clinical Cancer Research*, **2015**, 21, 3759-70	12.9	27
98	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	11	26
97	Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. *Breast Cancer Research*, **2017**, 19, 119	8.3	26

96	Exome sequencing in one family with gastric- and rectal cancer. *BMC Genetics*, **2016**, 17, 41	2.6	26
95	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. *International Journal of Cancer*, **2016**, 139, 1303-1317	7.5	26
94	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	8.3	25
93	Mismatch repair gene mutation spectrum in the Swedish Lynch syndrome population. *Oncology Reports*, **2016**, 36, 2823-2835	3.5	25
92	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	5.6	24
91	Germline mutation screening of the STK11/LKB1 gene in familial breast cancer with LOH on 19p. *Clinical Genetics*, **2000**, 57, 394-7	4	23
90	Four separate regions on chromosome 17 show loss of heterozygosity in familial breast carcinomas. *Human Genetics*, **1993**, 91, 6-12	6.3	23
89	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
88	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
87	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	3.3	21
86	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
85	BRCA2 germline mutations in Swedish breast cancer families. *European Journal of Human Genetics*, **1998**, 6, 134-9	5.3	20
84	Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. *Endocrine-Related Cancer*, **2015**, 22, 851-61	5.7	19
83	BRCA1 mutations in a population-based study of breast cancer in Stockholm County. *Genetic Testing and Molecular Biomarkers*, **2004**, 8, 127-32		19
82	Bioinformatics for human genetics: promises and challenges. *Human Mutation*, **2011**, 32, 495-500	4.7	18
81	RAD51B in Familial Breast Cancer. *PLoS ONE*, **2016**, 11, e0153788	3.7	18
80	Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. *International Journal of Epidemiology*, **2019**, 48, 767-780	7.8	18
79	Fine-scale mapping of the 4q24 locus identifies two independent loci associated with breast cancer risk. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 1680-91	4	17

78	Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. *BMC Medicine*, **2020**, 18, 396	11.4	17
77	Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. *Human Genetics*, **2019**, 138, 307-326	6.3	17
76	The BRCA2 c.68-7T>A variant is not pathogenic: A model for clinical calibration of spliceogenicity. *Human Mutation*, **2018**, 39, 729-741	4.7	16
75	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	4.9	16
74	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	8.3	16
73	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. *Gynecologic Oncology*, **2016**, 141, 386-401	4.9	15
72	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	5.3	15
71	The gynecological surveillance of women with Lynch syndrome in Sweden. *Gynecologic Oncology*, **2015**, 138, 717-22	4.9	15
70	Low frequency of hMSH2 mutations in Swedish HNPCC families. *International Journal of Cancer*, **1997**, 74, 134-7	7.5	15
69	DGGE screening of mutations in mismatch repair genes (hMSH2 and hMLH1) in 34 Swedish families with colorectal cancer. *Clinical Genetics*, **1998**, 53, 131-5	4	15
68	Association of genetic susceptibility variants for type 2 diabetes with breast cancer risk in women of European ancestry. *Cancer Causes and Control*, **2016**, 27, 679-93	2.8	15
67	Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. *Gastroenterology*, **2021**, 160, 1164-1178.e6	13.3	15
66	The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. *Oncotarget*, **2015**, 6, 7390-407	3.3	14
65	2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. *Nature Communications*, **2014**, 5, 4051	17.4	13
64	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. *International Journal of Cancer*, **2021**, 148, 307-319	7.5	13
63	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, 405-9	8.1	12
62	Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 860-870	4	12
61	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. *Breast Cancer Research*, **2014**, 16, R51	8.3	12

60	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
59	Systematic meta-analyses, field synopsis and global assessment of the evidence of genetic association studies in colorectal cancer. *Gut*, **2020**, 69, 1460-1471	19.2	11
58	Familial breast cancer and genes involved in breast carcinogenesis. *Breast Cancer Research and Treatment*, **1995**, 34, 171-83	4.4	11
57	Finnish mutations in Swedish HNPCC families. *Nature Medicine*, **1995**, 1, 1104	50.5	11
56	Hereditary breast cancer in Sweden: a predominance of maternally inherited cases. *Breast Cancer Research and Treatment*, **1992**, 24, 159-65	4.4	11
55	Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. *BMC Medicine*, **2020**, 18, 229	11.4	11
54	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. *PLoS ONE*, **2016**, 11, e0160316	3.7	11
53	Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Research*, **2019**, 21, 144	8.3	11
52	Tumour spectrum in non-BRCA hereditary breast cancer families in Sweden. *Hereditary Cancer in Clinical Practice*, **2015**, 13, 15	2.3	10
51	Hereditary cancer. *Acta Oncologica*, **1999**, 38, 439-47	3.2	10
50	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 3p22-p21 tumour-suppressor region by two-colour fluorescence in situ hybridization. *Chromosome Research*, **1996**, 4, 310-3	4.4	10
49	Exome sequencing in 51 early onset non-familial CRC cases. *Molecular Genetics & Genomic Medicine*, **2019**, 7, e605	2.3	10
48	Genetic anticipation in Swedish Lynch syndrome families. *PLoS Genetics*, **2017**, 13, e1007012	6	9
47	Linkage analysis in familial non-Lynch syndrome colorectal cancer families from Sweden. *PLoS ONE*, **2013**, 8, e83936	3.7	9
46	Sublocalization of a locus at 3p21.3-23 predisposing to hereditary nonpolyposis colon cancer. *Human Genetics*, **1994**, 94, 210-4	6.3	8
45	A retrospective study of extracolonic, non-endometrial cancer in Swedish Lynch syndrome families. *Hereditary Cancer in Clinical Practice*, **2018**, 16, 16	2.3	8
44	Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. *Breast Cancer Research and Treatment*, **2020**, 181, 423-434	4.4	7
43	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	3.3	7

42	Genetic architectures of proximal and distal colorectal cancer are partly distinct. *Gut*, **2021**, 70, 1325-1334	19.2	7
41	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	8.7	7
40	Colorectal cancer as a complex disease: defining at-risk subjects in the general population - a preventive strategy. *Expert Review of Anticancer Therapy*, **2004**, 4, 377-85	3.5	6
39	The MLH1 c.1852_1853delinsGC (p.K618A) variant in colorectal cancer: genetic association study in 18,723 individuals. *PLoS ONE*, **2014**, 9, e95022	3.7	6
38	Defining New Colorectal Cancer Syndromes in a Population-based Cohort of the Disease. *Anticancer Research*, **2017**, 37, 1831-1835	2.3	6
37	Familial cancer among consecutive uterine cancer patients in Sweden. *Hereditary Cancer in Clinical Practice*, **2014**, 12, 14	2.3	5
36	Cancer risk susceptibility loci in a Swedish population. *Oncotarget*, **2017**, 8, 110300-110310	3.3	5
35	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	7	5
34	Genome-wide scan of the effect of common nsSNPs on colorectal cancer survival outcome. *British Journal of Cancer*, **2018**, 119, 988-993	8.7	4
33	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
32	Variants of the PPARD gene and their clinicopathological significance in colorectal cancer. *PLoS ONE*, **2013**, 8, e83952	3.7	4
31	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	4	4
30	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	4	4
29	Whole-genome Linkage Analysis and Sequence Analysis of Candidate Loci in Familial Breast Cancer. *Anticancer Research*, **2015**, 35, 3155-65	2.3	4
28	Predicting Outcome in Colonoscopic High-risk Surveillance. *Anticancer Research*, **2015**, 35, 4813-9	2.3	4
27	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	2.6	3
26	Genetic analyses supporting colorectal, gastric, and prostate cancer syndromes. *Genes Chromosomes and Cancer*, **2019**, 58, 775-782	5	3
25	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3

24	Recurrent, low-frequency coding variants contributing to colorectal cancer in the Swedish population. *PLoS ONE*, **2018**, 13, e0193547	3.7	3
23	- a novel candidate breast cancer susceptibility locus on 6q14.1. *Oncotarget*, **2017**, 8, 102769-102782	3.3	3
22	Testing strategies to reduce morbidity and mortality from Lynch syndrome. *Scandinavian Journal of Gastroenterology*, **2018**, 53, 1535-1540	2.4	3
21	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
20	Haplotype analysis suggest that the MLH1 c.2059C > T mutation is a Swedish founder mutation. *Familial Cancer*, **2018**, 17, 531-537	3	2
19	Enhanced detection of mutations in BRCA1 exon 11 using restriction endonuclease fingerprinting-single-strand conformation polymorphism. *Journal of Molecular Medicine*, **2000**, 78, 580-7	5.5	2
18	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	4	2
17	Two novel colorectal cancer risk loci in the region on chromosome 9q22.32. *Oncotarget*, **2018**, 9, 11170-11179	5.3	2
16	Massive parallel sequencing in a family with rectal cancer. *Hereditary Cancer in Clinical Practice*, **2021**, 19, 23	2.3	2
15	Molecular basis of HNPCC: Mutations of MMR genes		2
14	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	5.3	1
13	Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis.. *Human Genetics and Genomics Advances*, **2020**, 1, 100010	0.8	1
12	Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. *Nutrients*, **2021**, 13,	6.7	1
11	Response to Li and Hopper. *American Journal of Human Genetics*, **2021**, 108, 527-529	11	1
10	No Difference in Penetrance between Truncating and Missense/Aberrant Splicing Pathogenic Variants in and : A Prospective Lynch Syndrome Database Study. *Journal of Clinical Medicine*, **2021**, 10,	5.1	1
9	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	8.3	1
8	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		1
7	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0

6	A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. *Scientific Reports*, **2021**, 11, 14763	4.9	0
5	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
4	Increased risk for uterine cancer among first-degree relatives to Swedish gastric cancer patients. *Hereditary Cancer in Clinical Practice*, **2020**, 18, 12	2.3	
3	Parent of Origin and Prognosis in Familial Breast Cancer in Sweden. *Anticancer Research*, **2017**, 37, 1257-1262	1.5	
2	Sequencing for germline mutations in Swedish breast cancer families reveals novel breast cancer risk genes. *Scientific Reports*, **2021**, 11, 14737	4.9	
1	Identification of known and novel familial cancer genes in Swedish colorectal cancer families. *International Journal of Cancer*, **2021**, 149, 627-634	7.5	