# Annika Lindblom

List of Publications by Year
in descending order

| 170 papers | 20,106 citations | 28274 55 h-index | 12272 133 g-index |
|---|---|---|---|
| 176 all docs | 176 docs citations | 176 times ranked | 19944 citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Mutation in the DNA mismatch repair gene homologue hMLH 1 is associated with hereditary non-polyposis colon cancer. Nature, 1994, 368, 258-261. | 27.8 | 2,001 |
| 2 | Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94. | 27.8 | 1,099 |
| 3 | Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361. | 21.4 | 960 |
| 4 | Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34. | 6.2 | 711 |
| 5 | Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97. | 27.8 | 548 |
| 6 | Breast Cancer Risk Genes â€" Association Analysis in More than 113,000 Women. New England Journal of Medicine, 2021, 384, 428-439. | 27.0 | 532 |
| 7 | Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. Nature Genetics, 2015, 47, 373-380. | 21.4 | 513 |
| 8 | The Clinical Phenotype of Lynch Syndrome Due to Germ-Line PMS2 Mutations. Gastroenterology, 2008, 135, 419-428.e1. | 1.3 | 480 |
| 9 | Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, . | 6.3 | 428 |
| 10 | 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. | 12.1 | 411 |
| 11 | Cancer risk and survival in <i>path_MMR</i> carriers by gene and gender up to 75 years of age: a report from the Prospective Lynch Syndrome Database. Gut, 2018, 67, 1306-1316. | 12.1 | 410 |
| 12 | Genetic mapping of a second locus predisposing to hereditary nonâ€"polyposis colon cancer. Nature Genetics, 1993, 5, 279-282. | 21.4 | 408 |
| 13 | Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87. | 21.4 | 377 |
| 14 | Genome-wide association studies identify four ER negativeâ€"specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398. | 21.4 | 374 |
| 15 | 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. | 2.4 | 365 |
| 16 | Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778. | 21.4 | 289 |
| 17 | Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581. | 21.4 | 265 |
| 18 | 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. | 13.7 | 220 |

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|---|---------|-----|-----------|
| 19 | 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. | 6.2 | 201 |
| 20 | Physical activity and risks of breast and colorectal cancer: a Mendelian randomisation analysis. Nature Communications, 2020, 11, 597. | 12.8 | 193 |
| 21 | Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397. | 27.8 | 183 |
| 22 | Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166. | 12.8 | 178 |
| 23 | Lynch Syndrome Caused by Germline *PMS2* Mutations: Delineating the Cancer Risk. Journal of Clinical Oncology, 2015, 33, 319-325. | 1.6 | 177 |
| 24 | *PALB2*, *CHEK2* and *ATM* rare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811. | 3.2 | 174 |
| 25 | Molecular basis of HNPCC: Mutations of MMR genes. Human Mutation, 1997, 10, 89-99. | 2.5 | 166 |
| 26 | *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, 4308-4316. | 1.6 | 162 |
| 27 | 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. | 9.4 | 157 |
| 28 | Age- and Tumor Subtype–Specific Breast Cancer Risk Estimates for *CH**EK**2*\*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760. | 1.6 | 152 |
| 29 | Cancer Risks for *PMS2*-Associated Lynch Syndrome. Journal of Clinical Oncology, 2018, 36, 2961-2968. | 1.6 | 147 |
| 30 | Novel Common Genetic Susceptibility Loci for Colorectal Cancer. Journal of the National Cancer Institute, 2019, 111, 146-157. | 6.3 | 129 |
| 31 | Identification of susceptibility loci for colorectal cancer in a genome-wide meta-analysis. Human Molecular Genetics, 2014, 23, 4729-4737. | 2.9 | 128 |
| 32 | 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. | 12.1 | 127 |
| 33 | Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386. | 21.4 | 125 |
| 34 | Genome-wide Modeling of Polygenic Risk Score in Colorectal Cancer Risk. American Journal of Human Genetics, 2020, 107, 432-444. | 6.2 | 124 |
| 35 | 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. Genes Chromosomes and Cancer, 1998, 22, 26-36. | 2.8 | 121 |
| 36 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73. | 21.4 | 120 |

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|---|---------|----|-----------|
| 37 | Colorectal cancer with and without microsatellite instability involves different genes. , 1999, 26, 247-252. | | 118 |
| 38 | 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. | 8.4 | 118 |
| 39 | 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. | 1.3 | 110 |
| 40 | Combined genetic and splicing analysis of BRCA1 c.[594-2A&gt;C; 641A&gt;G] highlights the relevance of naturally occurring in-frame transcripts for developing disease gene variant classification algorithms. Human Molecular Genetics, 2016, 25, 2256-2268. | 2.9 | 106 |
| 41 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999. | 12.8 | 105 |
| 42 | Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219. | 6.3 | 99 |
| 43 | 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. | 6.2 | 98 |
| 44 | Microsatellite Instability and hMLH1 and hMSH2 Expression Analysis in Familial and Sporadic Colorectal Cancer. Laboratory Investigation, 2001, 81, 535-541. | 3.7 | 97 |
| 45 | No evidence that protein truncating variants in <i>BRIP1</i> are associated with breast cancer risk: implications for gene panel testing. Journal of Medical Genetics, 2016, 53, 298-309. | 3.2 | 94 |
| 46 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375. | 12.8 | 93 |
| 47 | 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. | 1.3 | 90 |
| 48 | Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431. | 12.8 | 88 |
| 49 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast–ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675. | 12.8 | 78 |
| 50 | Five endometrial cancer risk loci identified through genome-wide association analysis. Nature Genetics, 2016, 48, 667-674. | 21.4 | 77 |
| 51 | 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. | 6.2 | 76 |
| 52 | Adiposity, metabolites, and colorectal cancer risk: Mendelian randomization study. BMC Medicine, 2020, 18, 396. | 5.5 | 76 |
| 53 | <i>BRCA2</i> Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799. | 0.9 | 75 |
| 54 | Microsatellite instability as a predictor of a mutation in a DNA mismatch repair gene in familial colorectal cancer. , 2000, 27, 17-25. | | 74 |

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|---|---------|----|-----------| 
| 55 | Fine scale mapping of the breast cancer 16q12 locus. Human Molecular Genetics, 2010, 19, 2507-2515. | 2.9 | 68 |
| 56 | Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603. | 2.4 | 67 |
| 57 | 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. | 2.5 | 64 |
| 58 | CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. Endocrine-Related Cancer, 2016, 23, 77-91. | 3.1 | 62 |
| 59 | Genetic overlap between endometriosis and endometrial cancer: evidence from cross‐disease genetic correlation and GWAS meta‐analyses. Cancer Medicine, 2018, 7, 1978-1987. | 2.8 | 62 |
| 60 | 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. | 6.2 | 59 |
| 61 | Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657. | 6.4 | 52 |
| 62 | Fine‐scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317. | 5.1 | 51 |
| 63 | Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744. | 7.1 | 51 |
| 64 | MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973. | 2.5 | 49 |
| 65 | 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. | 1.5 | 49 |
| 66 | A human compound heterozygote for two MLH1 missense mutations. Nature Genetics, 1997, 17, 135-136. | 21.4 | 47 |
| 67 | Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. Human Molecular Genetics, 2014, 23, 5545-5557. | 2.9 | 46 |
| 68 | Body mass index and breast cancer survival: a Mendelian randomization analysis. International Journal of Epidemiology, 2017, 46, 1814-1822. | 1.9 | 45 |
| 69 | Genetic variant predictors of gene expression provide new insight into risk of colorectal cancer. Human Genetics, 2019, 138, 307-326. | 3.8 | 44 |
| 70 | Genetic architectures of proximal and distal colorectal cancer are partly distinct. Gut, 2021, 70, 1325-1334. | 12.1 | 44 |
| 71 | Mismatch repair gene mutation spectrum in the Swedish Lynch syndrome population. Oncology Reports, 2016, 36, 2823-2835. | 2.6 | 43 |
| 72 | Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22. | 5.0 | 43 |

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|---|---------|-----|-----------|
| 73 | Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119. | 5.0 | 43 |
| 74 | Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. PLoS Genetics, 2014, 10, e1004285. | 3.5 | 39 |
| 75 | Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. Cancer Research, 2020, 80, 624-638. | 0.9 | 39 |
| 76 | Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848. | 6.2 | 39 |
| 77 | 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. | 6.2 | 37 |
| 78 | Identifying Novel Susceptibility Genes for Colorectal Cancer Risk From a Transcriptome-Wide Association Study of 125,478 Subjects. Gastroenterology, 2021, 160, 1164-1178.e6. | 1.3 | 36 |
| 79 | 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. | 3.3 | 35 |
| 80 | Mendelian randomization analysis of C-reactive protein on colorectal cancer risk. International Journal of Epidemiology, 2019, 48, 767-780. | 1.9 | 35 |
| 81 | Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. International Journal of Cancer, 2021, 148, 307-319. | 5.1 | 35 |
| 82 | 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. | 2.9 | 33 |
| 83 | Regulator of Chromosome Condensation 2 Identifies High-Risk Patients within Both Major Phenotypes of Colorectal Cancer. Clinical Cancer Research, 2015, 21, 3759-3770. | 7.0 | 32 |
| 84 | 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. | 1.8 | 31 |
| 85 | 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. | 5.0 | 31 |
| 86 | Exome sequencing in one family with gastric- and rectal cancer. BMC Genetics, 2016, 17, 41. | 2.7 | 31 |
| 87 | A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312. | 12.8 | 30 |
| 88 | GermlineBRCA1 andHMLH1 mutations in a family with male and female breast carcinoma. , 2000, 85, 796-800. | | 29 |
| 89 | Germline mutation screening of the STK11/LKB1 gene in familial breast cancer with LOH on 19p. Clinical Genetics, 2000, 57, 394-397. | 2.0 | 28 |
| 90 | Circulating bilirubin levels and risk of colorectal cancer: serological and Mendelian randomization analyses. BMC Medicine, 2020, 18, 229. | 5.5 | 28 |

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|---|---------|----|-----------|
| 91 | Systematic meta-analyses, field synopsis and global assessment of the evidence of genetic association studies in colorectal cancer. Gut, 2020, 69, 1460-1471. | 12.1 | 27 |
| 92 | 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. | 4.7 | 27 |
| 93 | 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. | 5.0 | 26 |
| 94 | 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. | 2.8 | 26 |
| 95 | Mendelian Randomization of Circulating Polyunsaturated Fatty Acids and Colorectal Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 860-870. | 2.5 | 26 |
| 96 | RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788. | 2.5 | 26 |
| 97 | Four separate regions on chromosome 17 show loss of heterozygosity in familial breast carcinomas. Human Genetics, 1993, 91, 6-12. | 3.8 | 25 |
| 98 | Comprehensive genetic assessment of the ESR1 locus identifies a risk region for endometrial cancer. Endocrine-Related Cancer, 2015, 22, 851-861. | 3.1 | 25 |
| 99 | 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. | 2.5 | 25 |
| 100 | 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. | 2.5 | 24 |
| 101 | Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144. | 5.0 | 24 |
| 102 | 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 |
| 103 | Bioinformatics for Human Genetics: Promises and Challenges. Human Mutation, 2011, 32, 495-500. | 2.5 | 21 |
| 104 | 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. | 1.8 | 21 |
| 105 | Low frequency of hMSH2 mutations in Swedish HNPCC families. , 1997, 74, 134-137. | | 20 |
| 106 | BRCA2 germline mutations in Swedish breast cancer families. European Journal of Human Genetics, 1998, 6, 134-139. | 2.8 | 20 |
| 107 | The gynecological surveillance of women with Lynch syndrome in Sweden. Gynecologic Oncology, 2015, 138, 717-722. | 1.4 | 20 |
| 108 | DGGE screening of mutations in mismatch repair genes (hMSH2 and hMLH1) in 34 Swedish families with colorectal cancer. Clinical Genetics, 1998, 53, 131-135. | 2.0 | 19 |

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|---|---------|-----|-----------|
| 109 | 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. | 3.3 | 19 |
| 110 | The <i>BRCA2</i> c.68-7TÂ&gt;ÂA variant is not pathogenic: A model for clinical calibration of spliceogenicity. Human Mutation, 2018, 39, 729-741. | 2.5 | 19 |
| 111 | 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. | 2.5 | 19 |
| 112 | Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51. | 8.2 | 19 |
| 113 | No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401. | 1.4 | 18 |
| 114 | Exome sequencing in 51 early onset nonâ€familial CRC cases. Molecular Genetics &amp; Genomic Medicine, 2019, 7, e605. | 1.2 | 17 |
| 115 | 2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. Nature Communications, 2014, 5, 4051. | 12.8 | 16 |
| 116 | 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. | 6.4 | 16 |
| 117 | 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. | 2.4 | 15 |
| 118 | The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. Oncotarget, 2015, 6, 7390-7407. | 1.8 | 15 |
| 119 | Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2. | 5.0 | 15 |
| 120 | Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51. | 5.0 | 14 |
| 121 | Genetic anticipation in Swedish Lynch syndrome families. PLoS Genetics, 2017, 13, e1007012. | 3.5 | 14 |
| 122 | Prediction of contralateral breast cancer: external validation of risk calculators in 20 international cohorts. Breast Cancer Research and Treatment, 2020, 181, 423-434. | 2.5 | 14 |
| 123 | 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. | 1.8 | 14 |
| 124 | Hereditary breast cancer in sweden: a predominance of maternally inherited cases. Breast Cancer Research and Treatment, 1992, 24, 159-165. | 2.5 | 12 |
| 125 | Finnish mutations in Swedish HNPCC families. Nature Medicine, 1995, 1, 1104-1104. | 30.7 | 12 |
| 126 | Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316. | 2.5 | 12 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|----|-----------|
| 127 | Familial breast cancer and genes involved in breast carcinogenesis. Breast Cancer Research and Treatment, 1995, 34, 171-183. | 2.5 | 11 |
| 128 | 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. | 2.2 | 11 |
| 129 | Hereditary Cancer. Acta OncolÃ³gica, 1999, 38, 439-447. | 1.8 | 11 |
| 130 | Tumour spectrum in non-BRCA hereditary breast cancer families in Sweden. Hereditary Cancer in Clinical Practice, 2015, 13, 15. | 1.5 | 11 |
| 131 | A retrospective study of extracolonic, non-endometrial cancer in Swedish Lynch syndrome families. Hereditary Cancer in Clinical Practice, 2018, 16, 16. | 1.5 | 11 |
| 132 | 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. | 2.4 | 11 |
| 133 | Sublocalization of a locus at 3p21.3?23 predisposing to hereditary nonpolyposis colon cancer. Human Genetics, 1994, 94, 210-4. | 3.8 | 10 |
| 134 | Genome-wide scan of the effect of common nsSNPs on colorectal cancer survival outcome. British Journal of Cancer, 2018, 119, 988-993. | 6.4 | 10 |
| 135 | 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. | 2.5 | 10 |
| 136 | Recurrent, low-frequency coding variants contributing to colorectal cancer in the Swedish population. PLoS ONE, 2018, 13, e0193547. | 2.5 | 10 |
| 137 | Linkage Analysis in Familial Non-Lynch Syndrome Colorectal Cancer Families from Sweden. PLoS ONE, 2013, 8, e83936. | 2.5 | 9 |
| 138 | <i>PHIP</i>- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782. | 1.8 | 9 |
| 139 | Defining New Colorectal Cancer Syndromes in a Population-based Cohort of the Disease. Anticancer Research, 2017, 37, 1831-1835. | 1.1 | 9 |
| 140 | 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. | 5.0 | 7 |
| 141 | The MLH1 c.1852_1853delinsGC (p.K618A) Variant in Colorectal Cancer: Genetic Association Study in 18,723 Individuals. PLoS ONE, 2014, 9, e95022. | 2.5 | 7 |
| 142 | Cancer risk susceptibility loci in a Swedish population. Oncotarget, 2017, 8, 110300-110310. | 1.8 | 7 |
| 143 | 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. | 2.4 | 6 |
| 144 | Familial cancer among consecutive uterine cancer patients in Sweden. Hereditary Cancer in Clinical Practice, 2014, 12, 14. | 1.5 | 6 |

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|---|---------|-----|-----------|
| 145 | Genetic analyses supporting colorectal, gastric, and prostate cancer syndromes. Genes Chromosomes and Cancer, 2019, 58, 775-782. | 2.8 | 6 |
| 146 | Response to Li and Hopper. American Journal of Human Genetics, 2021, 108, 527-529. | 6.2 | 5 |
| 147 | Variants of the PPARD Gene and Their Clinicopathological Significance in Colorectal Cancer. PLoS ONE, 2013, 8, e83952. | 2.5 | 5 |
| 148 | Predicting Outcome in Colonoscopic High-risk Surveillance. Anticancer Research, 2015, 35, 4813-9. | 1.1 | 5 |
| 149 | Testing strategies to reduce morbidity and mortality from Lynch syndrome. Scandinavian Journal of Gastroenterology, 2018, 53, 1535-1540. | 1.5 | 4 |
| 150 | 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. | 2.8 | 4 |
| 151 | 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. | 3.7 | 4 |
| 152 | Two novel colorectal cancer risk loci in the region on chromosome 9q22.32. Oncotarget, 2018, 9, 11170-11179. | 1.8 | 4 |
| 153 | Whole-genome Linkage Analysis and Sequence Analysis of Candidate Loci in Familial Breast Cancer. Anticancer Research, 2015, 35, 3155-65. | 1.1 | 4 |
| 154 | Enhanced detection of mutations in BRCA1 exon 11 using restriction endonuclease fingerprinting-single-strand conformation polymorphism. Journal of Molecular Medicine, 2000, 78, 580-587. | 3.9 | 3 |
| 155 | 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. | 1.8 | 3 |
| 156 | Haplotype analysis suggest that the MLH1 c.2059Câ‰&gt;â‰T mutation is a Swedish founder mutation. Familial Cancer, 2018, 17, 531-537. | 1.9 | 3 |
| 157 | Hemochromatosis risk genotype is not associated with colorectal cancer or age at its diagnosis. Human Genetics and Genomics Advances, 2020, 1, 100010. | 1.7 | 3 |
| 158 | Massive parallel sequencing in a family with rectal cancer. Hereditary Cancer in Clinical Practice, 2021, 19, 23. | 1.5 | 3 |
| 159 | A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. Scientific Reports, 2021, 11, 14763. | 3.3 | 3 |
| 160 | Salicylic Acid and Risk of Colorectal Cancer: A Two-Sample Mendelian Randomization Study. Nutrients, 2021, 13, 4164. | 4.1 | 3 |
| 161 | Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688. | 3.3 | 2 |
| 162 | Sequencing for germline mutations in Swedish breast cancer families reveals novel breast cancer risk genes. Scientific Reports, 2021, 11, 14737. | 3.3 | 2 |

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|---|---------|----|-----------|
| 163 | Molecular basis of HNPCC: Mutations of MMR genes. , 0, . | | 2 |
| 164 | Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787. | 3.3 | 2 |
| 165 | Colorectal cancer risk susceptibility loci in a Swedish population. Molecular Carcinogenesis, 2021, , . | 2.7 | 2 |
| 166 | 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 |
| 167 | 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. | 3.7 | 1 |
| 168 | Increased risk for uterine cancer among first-degree relatives to Swedish gastric cancer patients. Hereditary Cancer in Clinical Practice, 2020, 18, 12. | 1.5 | 0 |
| 169 | Identification of known and novel familial cancer genes in Swedish colorectal cancer families. International Journal of Cancer, 2021, 149, 627-634. | 5.1 | 0 |
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