

Taru Annika Muranen

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

5,765
citations

134610

34
h-index

145109

60
g-index

64
all docs

64
docs citations

64
times ranked

10239
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 1 | Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361. | 9.4 | 960 |
| 2 | Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380. | 9.4 | 513 |
| 3 | Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384. | 9.4 | 493 |
| 4 | Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, . | 3.0 | 428 |
| 5 | Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398. | 9.4 | 374 |
| 6 | Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581. | 9.4 | 265 |
| 7 | Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003212. | 1.5 | 244 |
| 8 | <i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811. | 1.5 | 174 |
| 9 | <i>CHEK2</i> *1100delC Heterozygosity in Women With Breast Cancer Associated With Early Death, Breast Cancer-specific Death, and Increased Risk of a Second Breast Cancer. <i>Journal of Clinical Oncology</i> , 2012, 30, 4308-4316. | 0.8 | 162 |
| 10 | Age- and Tumor Subtype-specific Breast Cancer Risk Estimates for <i>CH</i> <i>EK</i> <i>2</i> *1100delC Carriers. <i>Journal of Clinical Oncology</i> , 2016, 34, 2750-2760. | 0.8 | 152 |
| 11 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73. | 9.4 | 120 |
| 12 | Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999. | 5.8 | 105 |
| 13 | Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114. | 0.4 | 100 |
| 14 | Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219. | 3.0 | 99 |
| 15 | Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060. | 2.6 | 98 |
| 16 | Refined histopathological predictors of BRCA1 and BRCA2 mutation status: a large-scale analysis of breast cancer characteristics from the BCAC, CIMBA, and ENIGMA consortia. <i>Breast Cancer Research</i> , 2014, 16, 3419. | 2.2 | 97 |
| 17 | Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. <i>Nature Communications</i> , 2016, 7, 11375. | 5.8 | 93 |
| 18 | Common variants at 12p11, 12q24, 9p21, 9q31.2 and in ZNF365 are associated with breast cancer risk for BRCA1 and/or BRCA2 mutation carriers. <i>Breast Cancer Research</i> , 2012, 14, R33. | 2.2 | 78 |

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|----|--|-----|-----------|
| 19 | Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating MAP3K1. <i>American Journal of Human Genetics</i> , 2015, 96, 5-20. | 2.6 | 76 |
| 20 | Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. <i>Genetics in Medicine</i> , 2017, 19, 599-603. | 1.1 | 67 |
| 21 | Cell cycle-dependent nucleocytoplasmic shuttling of the neurofibromatosis 2 tumour suppressor merlin. <i>Oncogene</i> , 2005, 24, 1150-1158. | 2.6 | 59 |
| 22 | Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, . | 3.0 | 56 |
| 23 | Breast tumors from CHEK2 1100delC- mutation carriers: genomic landscape and clinical implications. <i>Breast Cancer Research</i> , 2011, 13, R90. | 2.2 | 55 |
| 24 | Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111. | 1.4 | 53 |
| 25 | E-cadherin breast tumor expression, risk factors and survival: Pooled analysis of 5,933 cases from 12 studies in the Breast Cancer Association Consortium. <i>Scientific Reports</i> , 2018, 8, 6574. | 1.6 | 51 |
| 26 | Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. <i>JAMA Oncology</i> , 2022, 8, e216744. | 3.4 | 51 |
| 27 | MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973. | 1.1 | 49 |
| 28 | Common Variants at the 19p13.1 and <i>ZNF365</i> Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 645-657. | 1.1 | 47 |
| 29 | Body mass index and breast cancer survival: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2017, 46, 1814-1822. | 0.9 | 45 |
| 30 | Genetic Predisposition to In Situ and Invasive Lobular Carcinoma of the Breast. <i>PLoS Genetics</i> , 2014, 10, e1004285. | 1.5 | 39 |
| 31 | Patient survival and tumor characteristics associated with CHEK2:p.1157T → findings from the Breast Cancer Association Consortium. <i>Breast Cancer Research</i> , 2016, 18, 98. | 2.2 | 39 |
| 32 | Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. <i>American Journal of Human Genetics</i> , 2020, 107, 837-848. | 2.6 | 39 |
| 33 | Identification and characterization of novel associations in the <i>CASP8/ALS2CR12</i> region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298. | 1.4 | 38 |
| 34 | Alcohol Consumption and Survival after a Breast Cancer Diagnosis: A Literature-Based Meta-analysis and Collaborative Analysis of Data for 29,239 Cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 934-945. | 1.1 | 37 |
| 35 | 11q13 is a susceptibility locus for hormone receptor positive breast cancer. <i>Human Mutation</i> , 2012, 33, 1123-1132. | 1.1 | 35 |
| 36 | A large-scale assessment of two-way SNP interactions in breast cancer susceptibility using 46 450 cases and 42 461 controls from the breast cancer association consortium. <i>Human Molecular Genetics</i> , 2014, 23, 1934-1946. | 1.4 | 32 |

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|----|--|-----|-----------|
| 37 | Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468. | 0.6 | 32 |
| 38 | The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38. | 2.3 | 28 |
| 39 | Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58. | 2.2 | 26 |
| 40 | Polygenic risk score is associated with increased disease risk in 52 Finnish breast cancer families. <i>Breast Cancer Research and Treatment</i> , 2016, 158, 463-469. | 1.1 | 24 |
| 41 | Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with prognosis of estrogen receptor-negative breast cancer after chemotherapy. <i>Breast Cancer Research</i> , 2015, 17, 18. | 2.2 | 20 |
| 42 | Recurrent moderate-risk mutations in Finnish breast and ovarian cancer patients. <i>International Journal of Cancer</i> , 2019, 145, 2692-2700. | 2.3 | 19 |
| 43 | Breast and Prostate Cancer Risks for Male BRCA1 and BRCA2 Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122. | 3.0 | 19 |
| 44 | Breast Cancer Risk Factors and Survival by Tumor Subtype: Pooled Analyses from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 623-642. | 1.1 | 19 |
| 45 | No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401. | 0.6 | 18 |
| 46 | 9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1783-1791. | 1.1 | 17 |
| 47 | 2q36.3 is associated with prognosis for oestrogen receptor-negative breast cancer patients treated with chemotherapy. <i>Nature Communications</i> , 2014, 5, 4051. | 5.8 | 16 |
| 48 | The SNP rs6500843 in 16p13.3 is associated with survival specifically among chemotherapy-treated breast cancer patients. <i>Oncotarget</i> , 2015, 6, 7390-7407. | 0.8 | 15 |
| 49 | Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51. | 2.2 | 14 |
| 50 | Inherited variants in the inner centromere protein (INCENP) gene of the chromosomal passenger complex contribute to the susceptibility of ER-negative breast cancer. <i>Carcinogenesis</i> , 2015, 36, 256-271. | 1.3 | 14 |
| 51 | The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. <i>Cancers</i> , 2020, 12, 292. | 1.7 | 11 |
| 52 | Mendelian randomisation study of smoking exposure in relation to breast cancer risk. <i>British Journal of Cancer</i> , 2021, 125, 1135-1145. | 2.9 | 9 |
| 53 | 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. <i>Breast Cancer Research</i> , 2021, 23, 86. | 2.2 | 7 |
| 54 | Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 2021, 108, 1190-1203. | 2.6 | 6 |

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|----|---|-----|-----------|
| 55 | Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65. | 2.0 | 6 |
| 56 | Germ-line variation at a functional p53 binding site increases susceptibility to breast cancer development. <i>The HUGO Journal</i> , 2009, 3, 31-40. | 4.1 | 5 |
| 57 | Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. <i>Npj Breast Cancer</i> , 2020, 6, 44. | 2.3 | 5 |
| 58 | High miR-30 Expression Associates with Improved Breast Cancer Patient Survival and Treatment Outcome. <i>Cancers</i> , 2021, 13, 2907. | 1.7 | 3 |
| 59 | A search for modifying genetic factors in CHEK2:c.1100delC breast cancer patients. <i>Scientific Reports</i> , 2021, 11, 14763. | 1.6 | 3 |
| 60 | Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. <i>Scientific Reports</i> , 2021, 11, 19787. | 1.6 | 2 |
| 61 | Abstract 758: The clinical utility of BRCA1/2 pathogenic variants in breast cancer patient prognosis. , 2021, , . | | 0 |