# Melissa C Southey

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/10411299/publications.pdf

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|---|---|---|---|
| 339 papers | 31,787 citations | 4831 87 h-index | 6512 162 g-index |
| 351 all docs | 351 docs citations | 351 times ranked | 31209 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | First international workshop of the ATM and cancer risk group (4-5 December 2019). Familial Cancer, 2022, 21, 211-227. | 0.9 | 10 |
| 2 | Cancer Risks Associated With BRCA1 and BRCA2 Pathogenic Variants. Journal of Clinical Oncology, 2022, 40, 1529-1541. | 0.8 | 90 |
| 3 | Rare germline copy number variants (CNVs) and breast cancer risk. Communications Biology, 2022, 5, 65. | 2.0 | 6 |
| 4 | Polygenic risk modeling for prediction of epithelial ovarian cancer risk. European Journal of Human Genetics, 2022, 30, 349-362. | 1.4 | 23 |
| 5 | Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2. | 2.2 | 15 |
| 6 | Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes. JAMA Oncology, 2022, 8, e216744. | 3.4 | 51 |
| 7 | Familial Aspects of Mammographic Density Measures Associated with Breast Cancer Risk. Cancers, 2022, 14, 1483. | 1.7 | 6 |
| 8 | Population-based estimates of age-specific cumulative risk of breast cancer for pathogenic variants in ATM. Breast Cancer Research, 2022, 24, 24. | 2.2 | 3 |
| 9 | Improving breast cancer risk prediction with epigenetic risk factors. Nature Reviews Clinical Oncology, 2022, , . | 12.5 | 2 |
| 10 | Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci. Breast Cancer Research, 2022, 24, 27. | 2.2 | 15 |
| 11 | Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199. | 1.6 | 2 |
| 12 | Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51. | 3.6 | 19 |
| 13 | Genetic Aspects of Mammographic Density Measures Associated with Breast Cancer Risk. Cancers, 2022, 14, 2767. | 1.7 | 5 |
| 14 | Does genetic predisposition modify the effect of lifestyle-related factors on DNA methylation?. Epigenetics, 2022, 17, 1838-1847. | 1.3 | 2 |
| 15 | Adherence to the 2020 American Cancer Society Guideline for Cancer Prevention and risk of breast cancer for women at increased familial and genetic risk in the Breast Cancer Family Registry: an evaluation of the weight, physical activity, and alcohol consumption recommendations. Breast Cancer Research and Treatment, 2022, 194, 673-682. | 1.1 | 1 |
| 16 | Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337. | 3.0 | 45 |
| 17 | Two-stage Study of Familial Prostate Cancer by Whole-exome Sequencing and Custom Capture Identifies 10 Novel Genes Associated with the Risk of Prostate Cancer. European Urology, 2021, 79, 353-361. | 0.9 | 28 |
| 18 | Novel mammogramâ€based measures improve breast cancer risk prediction beyond an established mammographic density measure. International Journal of Cancer, 2021, 148, 2193-2202. | 2.3 | 18 |

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|---|---|---|---|
| 19 | Germline Sequencing DNA Repair Genes in 5545 Men With Aggressive and Nonaggressive Prostate Cancer. Journal of the National Cancer Institute, 2021, 113, 616-625. | 3.0 | 40 |
| 20 | DNA methylation and breast cancer risk: value of twin and family studies. , 2021, , 67-83. | | 1 |
| 21 | CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854. | 2.9 | 5 |
| 22 | Trans-ancestry genome-wide association meta-analysis of prostate cancer identifies new susceptibility loci and informs genetic risk prediction. Nature Genetics, 2021, 53, 65-75. | 9.4 | 264 |
| 23 | Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. , 2021, 5, 200-217. | | 0 |
| 24 | A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. Nature Communications, 2021, 12, 1078. | 5.8 | 19 |
| 25 | 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 |
| 26 | Prospective Evaluation of the Addition of Polygenic Risk Scores to Breast Cancer Risk Models. JNCI Cancer Spectrum, 2021, 5, pkab021. | 1.4 | 19 |
| 27 | VTRNA2-1: Genetic Variation, Heritable Methylation and Disease Association. International Journal of Molecular Sciences, 2021, 22, 2535. | 1.8 | 15 |
| 28 | Population-Based Estimates of the Age-Specific Cumulative Risk of Breast Cancer for Pathogenic Variants in CHEK2: Findings from the Australian Breast Cancer Family Registry. Cancers, 2021, 13, 1378. | 1.7 | 5 |
| 29 | Rare Germline Pathogenic Variants Identified by Multigene Panel Testing and the Risk of Aggressive Prostate Cancer. Cancers, 2021, 13, 1495. | 1.7 | 12 |
| 30 | 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 |
| 31 | Genomic Risk Prediction for Breast Cancer in Older Women. Cancers, 2021, 13, 3533. | 1.7 | 6 |
| 32 | Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. American Journal of Human Genetics, 2021, 108, 1190-1203. | 2.6 | 6 |
| 33 | 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 |
| 34 | Mendelian randomisation study of smoking exposure in relation to breast cancer risk. British Journal of Cancer, 2021, 125, 1135-1145. | 2.9 | 9 |
| 35 | Genetic insights into biological mechanisms governing human ovarian ageing. Nature, 2021, 596, 393-397. | 13.7 | 183 |
| 36 | Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. European Urology Oncology, 2021, 4, 570-579. | 2.6 | 38 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787. | 1.6 | 2 |
| 38 | A Polygenic Risk Score Predicts Incident Prostate Cancer Risk in Older Men but Does Not Select for Clinically Significant Disease. Cancers, 2021, 13, 5815. | 1.7 | 7 |
| 39 | Association of FOXO3 Blood DNA Methylation with Cancer Risk, Cancer Survival, and Mortality. Cells, 2021, 10, 3384. | 1.8 | 6 |
| 40 | Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. Npj Breast Cancer, 2021, 7, 153. | 2.3 | 10 |
| 41 | Interval breast cancer risk associations with breast density, family history and breast tissue aging. International Journal of Cancer, 2020, 147, 375-382. | 2.3 | 22 |
| 42 | Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. International Journal of Cancer, 2020, 146, 2130-2138. | 2.3 | 13 |
| 43 | Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73. | 9.4 | 120 |
| 44 | 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 |
| 45 | Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of BRCA1 and BRCA2 pathogenic variants. Genetics in Medicine, 2020, 22, 1653-1666. | 1.1 | 82 |
| 46 | Stochastic Epigenetic Mutations Are Associated with Risk of Breast Cancer, Lung Cancer, and Mature B-cell Neoplasms. Cancer Epidemiology Biomarkers and Prevention, 2020, 29, 2026-2037. | 1.1 | 18 |
| 47 | Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. American Journal of Human Genetics, 2020, 107, 837-848. | 2.6 | 39 |
| 48 | Association of germline variation with the survival of women with BRCA1/2 pathogenic variants and breast cancer. Npj Breast Cancer, 2020, 6, 44. | 2.3 | 5 |
| 49 | The CHEK2 Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. Cancers, 2020, 12, 3254. | 1.7 | 16 |
| 50 | 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 |
| 51 | Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688. | 1.6 | 2 |
| 52 | PALB2 Genetic Variants: Can Functional Assays Assist Translation?. Trends in Cancer, 2020, 6, 263-265. | 3.8 | 3 |
| 53 | Integrating DNA methylation measures to improve clinical risk assessment: are we there yet? The case of BRCA1Âmethylation marks to improve clinical risk assessment of breast cancer. British Journal of Cancer, 2020, 122, 1133-1140. | 2.9 | 18 |
| 54 | Transcriptomeâ€wide association study of breast cancer risk by estrogenâ€receptor status. Genetic Epidemiology, 2020, 44, 442-468. | 0.6 | 32 |

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|---|---|---|---|
| 55 | Mismatch repair gene pathogenic germline variants in a population-based cohort of breast cancer. Familial Cancer, 2020, 19, 197-202. | 0.9 | 6 |
| 56 | A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312. | 5.8 | 30 |
| 57 | The Spectrum of FANCM Protein Truncating Variants in European Breast Cancer Cases. Cancers, 2020, 12, 292. | 1.7 | 11 |
| 58 | 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 |
| 59 | Rare germline genetic variants and risk of aggressive prostate cancer. International Journal of Cancer, 2020, 147, 2142-2149. | 2.3 | 12 |
| 60 | Homologous recombination DNA repair defects in PALB2-associated breast cancers. Npj Breast Cancer, 2019, 5, 23. | 2.3 | 39 |
| 61 | Genetic overlap between autoimmune diseases and nonâ€Hodgkin lymphoma subtypes. Genetic Epidemiology, 2019, 43, 844-863. | 0.6 | 28 |
| 62 | The FANCM:p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. Npj Breast Cancer, 2019, 5, 38. | 2.3 | 28 |
| 63 | DNA methylation-based biological age, genome-wide average DNA methylation, and conventional breast cancer risk factors. Scientific Reports, 2019, 9, 15055. | 1.6 | 18 |
| 64 | Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524. | 1.6 | 5 |
| 65 | Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431. | 5.8 | 88 |
| 66 | Genomeâ€wide association study of peripheral blood DNA methylation and conventional mammographic density measures. International Journal of Cancer, 2019, 145, 1768-1773. | 2.3 | 17 |
| 67 | Joint association of mammographic density adjusted for age and body mass index and polygenic risk score with breast cancer risk. Breast Cancer Research, 2019, 21, 68. | 2.2 | 31 |
| 68 | Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. Breast Cancer Research, 2019, 21, 62. | 2.2 | 34 |
| 69 | Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. Nature Communications, 2019, 10, 1741. | 5.8 | 90 |
| 70 | Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657. | 2.9 | 52 |
| 71 | Mortality after breast cancer as a function of time since diagnosis by estrogen receptor status and age at diagnosis. International Journal of Cancer, 2019, 145, 3207-3217. | 2.3 | 14 |
| 72 | Prediction and clinical utility of a contralateral breast cancer risk model. Breast Cancer Research, 2019, 21, 144. | 2.2 | 24 |

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|---|---|---|---|
| 73 | Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34. | 2.6 | 711 |
| 74 | Discovery of common and rare genetic risk variants for colorectal cancer. Nature Genetics, 2019, 51, 76-87. | 9.4 | 377 |
| 75 | Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806. | 0.9 | 81 |
| 76 | Genetically Determined Height and Risk of Non-hodgkin Lymphoma. Frontiers in Oncology, 2019, 9, 1539. | 1.3 | 6 |
| 77 | 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 |
| 78 | Heritable DNA methylation marks associated with susceptibility to breast cancer. Nature Communications, 2018, 9, 867. | 5.8 | 76 |
| 79 | Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. British Journal of Cancer, 2018, 118, 1123-1129. | 2.9 | 15 |
| 80 | Obtaining high quality transcriptome data from formalin-fixed, paraffin-embedded diagnostic prostate tumor specimens. Laboratory Investigation, 2018, 98, 537-550. | 1.7 | 9 |
| 81 | Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536. | 0.9 | 88 |
| 82 | Is RNASEL:p.Glu265* a modifier of early-onset breast cancer risk for carriers of high-risk mutations?. BMC Cancer, 2018, 18, 165. | 1.1 | 6 |
| 83 | Somatic mutations of the coding microsatellites within the beta-2-microglobulin gene in mismatch repair-deficient colorectal cancers and adenomas. Familial Cancer, 2018, 17, 91-100. | 0.9 | 21 |
| 84 | Targeted massively parallel sequencing characterises the mutation spectrum of PALB2 in breast and ovarian cancer cases from Poland and Ukraine. Familial Cancer, 2018, 17, 345-349. | 0.9 | 7 |
| 85 | Cirrus: An Automated Mammography-Based Measure of Breast Cancer Risk Based on Textural Features. JNCI Cancer Spectrum, 2018, 2, pky057. | 1.4 | 24 |
| 86 | Genome-wide DNA methylation assessment of â€˜BRCA1-likeâ€™ early-onset breast cancer: Data from the Australian Breast Cancer Family Registry. Experimental and Molecular Pathology, 2018, 105, 404-410. | 0.9 | 26 |
| 87 | A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. Cancer Research, 2018, 78, 5419-5430. | 0.4 | 54 |
| 88 | Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. PLoS ONE, 2018, 13, e0197561. | 1.1 | 9 |
| 89 | HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. Cancer Research, 2018, 78, 4086-4096. | 0.4 | 34 |
| 90 | Causal effect of smoking on DNA methylation in peripheral blood: a twin and family study. Clinical Epigenetics, 2018, 10, 18. | 1.8 | 95 |

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|---|---|---|---|
| 91 | Identification of nine new susceptibility loci for endometrial cancer. Nature Communications, 2018, 9, 3166. | 5.8 | 178 |
| 92 | rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473. | 1.8 | 3 |
| 93 | Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. Nature Genetics, 2018, 50, 928-936. | 9.4 | 652 |
| 94 | Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. Nature Communications, 2018, 9, 2256. | 5.8 | 88 |
| 95 | A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978. | 9.4 | 184 |
| 96 | Mammographic density defined by higher than conventional brightness thresholds better predicts breast cancer risk. International Journal of Epidemiology, 2017, 46, dyw212. | 0.9 | 24 |
| 97 | Breast cancer risk prediction using a polygenic risk score in the familial setting: a prospective study from the Breast Cancer Family Registry and kConFab. Genetics in Medicine, 2017, 19, 30-35. | 1.1 | 53 |
| 98 | Tumor testing to identify lynch syndrome in two Australian colorectal cancer cohorts. Journal of Gastroenterology and Hepatology (Australia), 2017, 32, 427-438. | 1.4 | 47 |
| 99 | BRCA2 Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. Cancer Research, 2017, 77, 2789-2799. | 0.4 | 75 |
| 100 | Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841. | 9.4 | 426 |
| 101 | Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691. | 9.4 | 356 |
| 102 | Lifetime alcohol intake is associated with an increased risk of KRAS+ and BRAFâ€‘KRASâ€•but not BRAF+ colorectal cancer. International Journal of Cancer, 2017, 140, 1485-1493. | 2.3 | 27 |
| 103 | Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94. | 13.7 | 1,099 |
| 104 | Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778. | 9.4 | 289 |
| 105 | Geneâ€“environment interactions involving functional variants: Results from the Breast Cancer Association Consortium. International Journal of Cancer, 2017, 141, 1830-1840. | 2.3 | 20 |
| 106 | Height, selected genetic markers and prostate cancer risk: results from the PRACTICAL consortium. British Journal of Cancer, 2017, 117, 734-743. | 2.9 | 7 |
| 107 | Testing for Gene-Environment Interactions Using a Prospective Family Cohort Design: Body Mass Index in Early and Later Adulthood and Risk of Breast Cancer. American Journal of Epidemiology, 2017, 185, 487-500. | 1.6 | 5 |
| 108 | Increased genomic burden of germline copy number variants is associated with early onset breast cancer: Australian breast cancer family registry. Breast Cancer Research, 2017, 19, 30. | 2.2 | 14 |

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|---|---|---|---|
| 109 | Genetic modifiers of CHEK2*1100delC-associated breast cancer risk. Genetics in Medicine, 2017, 19, 599-603. | 1.1 | 67 |
| 110 | Reproductive profiles and risk of breast cancer subtypes: a multi-center case-only study. Breast Cancer Research, 2017, 19, 119. | 2.2 | 43 |
| 111 | Blood pressure and risk of breast cancer, overall and by subtypes. Journal of Hypertension, 2017, 35, 1371-1380. | 0.3 | 7 |
| 112 | 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 |
| 113 | PHIP- a novel candidate breast cancer susceptibility locus on 6q14.1. Oncotarget, 2017, 8, 102769-102782. | 0.8 | 9 |
| 114 | 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 |
| 115 | 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 |
| 116 | Gene panel testing for hereditary breast cancer. Medical Journal of Australia, 2016, 204, 188-190. | 0.8 | 12 |
| 117 | ABRAXAS (FAM175A) and Breast Cancer Susceptibility: No Evidence of Association in the Breast Cancer Family Registry. PLoS ONE, 2016, 11, e0156820. | 1.1 | 5 |
| 118 | Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316. | 1.1 | 12 |
| 119 | Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. International Journal of Epidemiology, 2016, 45, 884-895. | 0.9 | 71 |
| 120 | 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 |
| 121 | PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811. | 1.5 | 174 |
| 122 | Breast Cancer Risk From Modifiable and Nonmodifiable Risk Factors Among White Women in the United States. JAMA Oncology, 2016, 2, 1295. | 3.4 | 285 |
| 123 | Genes associated with histopathologic features of triple negative breast tumors predict molecular subtypes. Breast Cancer Research and Treatment, 2016, 157, 117-131. | 1.1 | 18 |
| 124 | Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22. | 2.2 | 43 |
| 125 | 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 |
| 126 | Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114. | 0.4 | 100 |

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|---|---|---|---|
| 127 | Analysis of the breast cancer methylome using formalin-fixed paraffin-embedded tumour. Breast Cancer Research and Treatment, 2016, 160, 173-180. | 1.1 | 6 |
| 128 | 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 |
| 129 | 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 |
| 130 | Use of a Novel Nonparametric Version of DEPTH to Identify Genomic Regions Associated with Prostate Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 1619-1624. | 1.1 | 7 |
| 131 | rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874. | 1.6 | 2 |
| 132 | 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 |
| 133 | Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675. | 5.8 | 78 |
| 134 | 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 |
| 135 | Atlas of prostate cancer heritability in European and African-American men pinpoints tissue-specific regulation. Nature Communications, 2016, 7, 10979. | 5.8 | 50 |
| 136 | The PALB2 p.Leu939Trp mutation is not associated with breast cancer risk. Breast Cancer Research, 2016, 18, 111. | 2.2 | 11 |
| 137 | Genome-wide association of familial prostate cancer cases identifies evidence for a rare segregating haplotype at 8q24.21. Human Genetics, 2016, 135, 923-938. | 1.8 | 37 |
| 138 | Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760. | 0.8 | 152 |
| 139 | PALB2: research reaching to clinical outcomes for women with breast cancer. Hereditary Cancer in Clinical Practice, 2016, 14, 9. | 0.6 | 27 |
| 140 | SNP rs16906252C>T Is an Expression and Methylation Quantitative Trait Locus Associated with an Increased Risk of Developing MGMT-Methylated Colorectal Cancer. Clinical Cancer Research, 2016, 22, 6266-6277. | 3.2 | 22 |
| 141 | Breast Cancer Risk Prediction Using Clinical Models and 77 Independent Risk-Associated SNPs for Women Aged Under 50 Years: Australian Breast Cancer Family Registry. Cancer Epidemiology Biomarkers and Prevention, 2016, 25, 359-365. | 1.1 | 96 |
| 142 | Genetically predicted longer telomere length is associated with increased risk of B-cell lymphoma subtypes. Human Molecular Genetics, 2016, 25, 1663-1676. | 1.4 | 52 |
| 143 | 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 |
| 144 | Germline mutations inPMS2andMLH1in individuals with solitary loss of PMS2 expression in colorectal carcinomas from the Colon Cancer Family Registry Cohort. BMJ Open, 2016, 6, e010293. | 0.8 | 33 |

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|---|---|---|---|
| 145 | 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 |
| 146 | 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 |
| 147 | Heterogeneity of luminal breast cancer characterised by immunohistochemical expression of basal markers. British Journal of Cancer, 2016, 114, 298-304. | 2.9 | 7 |
| 148 | Genetic variation in the immunosuppression pathway genes and breast cancer susceptibility: a pooled analysis of 42,510 cases and 40,577 controls from the Breast Cancer Association Consortium. Human Genetics, 2016, 135, 137-154. | 1.8 | 8 |
| 149 | BRCA2 Polymorphic Stop Codon K3326X and the Risk of Breast, Prostate, and Ovarian Cancers. Journal of the National Cancer Institute, 2016, 108, djv315. | 3.0 | 77 |
| 150 | Evidence of a genetic link between endometriosis and ovarian cancer. Fertility and Sterility, 2016, 105, 35-43.e10. | 0.5 | 37 |
| 151 | RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788. | 1.1 | 26 |
| 152 | Methylation of Breast Cancer Predisposition Genes in Early-Onset Breast Cancer: Australian Breast Cancer Family Registry. PLoS ONE, 2016, 11, e0165436. | 1.1 | 12 |
| 153 | Assessment of variation in immunosuppressive pathway genes reveals TGFBR2 to be associated with risk of clear cell ovarian cancer. Oncotarget, 2016, 7, 69097-69110. | 0.8 | 5 |
| 154 | Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96. | 2.3 | 34 |
| 155 | Genome wide association study identifies a novel putative mammographic density locus at 1q12â€q21. International Journal of Cancer, 2015, 136, 2427-2436. | 2.3 | 18 |
| 156 | Epithelialâ€Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. Genetic Epidemiology, 2015, 39, 689-697. | 0.6 | 22 |
| 157 | Common germline polymorphisms associated with breast cancer-specific survival. Breast Cancer Research, 2015, 17, 58. | 2.2 | 26 |
| 158 | A comprehensive evaluation of interaction between genetic variants and use of menopausal hormone therapy on mammographic density. Breast Cancer Research, 2015, 17, 110. | 2.2 | 19 |
| 159 | Tools for translational epigenetic studies involving formalin-fixed paraffin-embedded human tissue: applying the Infinium HumanMethyation450 Beadchip assay to large population-based studies. BMC Research Notes, 2015, 8, 543. | 0.6 | 15 |
| 160 | Prediction of individual genetic risk to prostate cancer using a polygenic score. Prostate, 2015, 75, 1467-1474. | 1.2 | 54 |
| 161 | Large-Scale Genomic Analyses Link Reproductive Aging to Hypothalamic Signaling, Breast Cancer Susceptibility, and BRCA1-Mediated DNA Repair. Obstetrical and Gynecological Survey, 2015, 70, 758-762. | 0.2 | 0 |
| 162 | Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. PLoS ONE, 2015, 10, e0128106. | 1.1 | 44 |

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|---|---|---|---|
| 163 | SNP-SNP interaction analysis of NF-Î³B signaling pathway on breast cancer survival. Oncotarget, 2015, 6, 37979-37994. | 0.8 | 20 |
| 164 | Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, . | 3.0 | 428 |
| 165 | Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607. | 1.4 | 40 |
| 166 | Association of breast cancer risk loci with breast cancer survival. International Journal of Cancer, 2015, 137, 2837-2845. | 2.3 | 33 |
| 167 | Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984. | 1.4 | 40 |
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