Melissa C. Southey

List of Publications by Year in Descending Order

562 papers	34,229 citations	88 h-index	168 g-index
603 ext. papers	41,318 ext. citations	8.7 avg, IF	5.77 L-index

#	Paper	IF	Citations
562	Cancer Risks Associated With and Pathogenic Variants.. *Journal of Clinical Oncology*, **2022**, JCO2102112	2.2	7
561	Rare germline copy number variants (CNVs) and breast cancer risk.. *Communications Biology*, **2022**, 5, 65	6.7	0
560	Value of the loss of heterozygosity to BRCA1 variant classification.. *Npj Breast Cancer*, **2022**, 8, 9	7.8	
559	Common variants in breast cancer risk loci predispose to distinct tumor subtypes.. *Breast Cancer Research*, **2022**, 24, 2	8.3	3
558	Pathology of Tumors Associated With Pathogenic Germline Variants in 9 Breast Cancer Susceptibility Genes.. *JAMA Oncology*, **2022**,	13.4	4
557	Familial Aspects of Mammographic Density Measures Associated with Breast Cancer Risk.. *Cancers*, **2022**, 14,	6.6	2
556	Early life affects late-life health through determining DNA methylation across the lifespan: A twin study.. *EBioMedicine*, **2022**, 77, 103927	8.8	1
555	Population-based estimates of age-specific cumulative risk of breast cancer for pathogenic variants in ATM.. *Breast Cancer Research*, **2022**, 24, 24	8.3	0
554	A Genome-Wide Gene-Based GeneEnvironment Interaction Study of Breast Cancer in More than 90,000 Women. *Cancer Research Communications*, **2022**, 2, 211-219		0
553	Improving breast cancer risk prediction with epigenetic risk factors.. *Nature Reviews Clinical Oncology*, **2022**,	19.4	1
552	Genome-wide and transcriptome-wide association studies of mammographic density phenotypes reveal novel loci.. *Breast Cancer Research*, **2022**, 24, 27	8.3	1
551	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women.. *Scientific Reports*, **2022**, 12, 6199	4.9	
550	Within-sibship genome-wide association analyses decrease bias in estimates of direct genetic effects.. *Nature Genetics*, **2022**, 54, 581-592	36.3	6
549	Breast cancer risks associated with missense variants in breast cancer susceptibility genes.. *Genome Medicine*, **2022**, 14, 51	14.4	0
548	Genetic Aspects of Mammographic Density Measures Associated with Breast Cancer Risk. *Cancers*, **2022**, 14, 2767	6.6	
547	Risks of breast and ovarian cancer for women harboring pathogenic missense variants in BRCA1 and BRCA2 compared with those harboring protein truncating variants.. *Genetics in Medicine*, **2021**,	8.1	2
546	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. *Scientific Reports*, **2021**, 11, 19787	4.9	0

545	Repeatability of methylation measures using a QIAseq targeted methyl panel and comparison with the Illumina HumanMethylation450 assay. *BMC Research Notes*, **2021**, 14, 394	2.3	0
544	Biological Aging Measures Based on Blood DNA Methylation and Risk of Cancer: A Prospective Study. *JNCI Cancer Spectrum*, **2021**, 5, pkaa109	4.6	11
543	Prognostic Impact of Total Plasma Cell-free DNA Concentration in Androgen Receptor Pathway Inhibitor-treated Metastatic Castration-resistant Prostate Cancer. *European Urology Focus*, **2021**, 7, 1287-1291	5.1	3
542	Prospective Evaluation of the Addition of Polygenic Risk Scores to Breast Cancer Risk Models. *JNCI Cancer Spectrum*, **2021**, 5, pkab021	4.6	3
541	: Genetic Variation, Heritable Methylation and Disease Association. *International Journal of Molecular Sciences*, **2021**, 22,	6.3	3
540	Population-Based Estimates of the Age-Specific Cumulative Risk of Breast Cancer for Pathogenic Variants in : Findings from the Australian Breast Cancer Family Registry. *Cancers*, **2021**, 13,	6.6	2
539	Rare Germline Pathogenic Variants Identified by Multigene Panel Testing and the Risk of Aggressive Prostate Cancer. *Cancers*, **2021**, 13,	6.6	1
538	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. *International Journal of Epidemiology*, **2021**,	7.8	6
537	Epigenetic Drift Association with Cancer Risk and Survival, and Modification by Sex. *Cancers*, **2021**, 13,	6.6	4
536	Evaluation of the association of heterozygous germline variants in NTHL1 with breast cancer predisposition: an international multi-center study of 47,180 subjects. *Npj Breast Cancer*, **2021**, 7, 52	7.8	2
535	DNA Methylation Signatures and the Contribution of Age-Associated Methylomic Drift to Carcinogenesis in Early-Onset Colorectal Cancer. *Cancers*, **2021**, 13,	6.6	3
534	First international workshop of the ATM and cancer risk group (4-5 December 2019). *Familial Cancer* , **2021**, 1	3	5
533	Association of markers of inflammation, the kynurenine pathway and B vitamins with age and mortality, and a signature of inflammaging. *Journals of Gerontology - Series A Biological Sciences and Medical Sciences*, **2021**,	6.4	7
532	Genomic Risk Prediction for Breast Cancer in Older Women. *Cancers*, **2021**, 13,	6.6	1
531	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	11	1
530	Transcriptomic changes in peripheral blood mononuclear cells with weight loss: systematic literature review and primary data synthesis. *Genes and Nutrition*, **2021**, 16, 12	4.3	2
529	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	9.7	14
528	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	10.2	9

527	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
526	Novel mammogram-based measures improve breast cancer risk prediction beyond an established mammographic density measure. *International Journal of Cancer*, **2021**, 148, 2193-2202	7.5	8
525	Methylation marks of prenatal exposure to maternal smoking and risk of cancer in adulthood. *International Journal of Epidemiology*, **2021**, 50, 105-115	7.8	2
524	Comparing 5-Year and Lifetime Risks of Breast Cancer using the Prospective Family Study Cohort. *Journal of the National Cancer Institute*, **2021**, 113, 785-791	9.7	5
523	DNA Methylation in Peripheral Blood and Risk of Gastric Cancer: A Prospective Nested Case-control Study. *Cancer Prevention Research*, **2021**, 14, 233-240	3.2	2
522	Germline Sequencing DNA Repair Genes in 5545 Men With Aggressive and Nonaggressive Prostate Cancer. *Journal of the National Cancer Institute*, **2021**, 113, 616-625	9.7	14
521	Alcohol consumption is associated with widespread changes in blood DNA methylation: Analysis of cross-sectional and longitudinal data. *Addiction Biology*, **2021**, 26, e12855	4.6	13
520	DNA methylation and breast cancer risk: value of twin and family studies **2021**, 67-83		1
519	The EUS molecular evaluation of pancreatic cancer: A prospective multicenter cohort trial. *Endoscopic Ultrasound*, **2021**, 10, 335-343	3.6	1
518	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	8.7	2
517	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	36.3	62
516	Association of variably methylated tumour DNA regions with overall survival for invasive lobular breast cancer. *Clinical Epigenetics*, **2021**, 13, 11	7.7	2
515	Genome-wide homozygosity and risk of four non-Hodgkin lymphoma subtypes. *Journal of Translational Genetics and Genomics*, **2021**, 5, 200-217	1.7	
514	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. *Nature Communications*, **2021**, 12, 1078	17.4	4
513	Breast Cancer Risk Genes - Association Analysis in More than 113,000 Women. *New England Journal of Medicine*, **2021**, 384, 428-439	59.2	143
512	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. *Human Genetics*, **2021**, 140, 1353-1365	6.3	5
511	Independent prognostic impact of plasma NCOA2 alterations in metastatic castration-resistant prostate cancer. *Prostate*, **2021**, 81, 992-1001	4.2	1
510	Inflammation-Related Marker Profiling of Dietary Patterns and All-cause Mortality in the Melbourne Collaborative Cohort Study. *Journal of Nutrition*, **2021**, 151, 2908-2916	4.1	2

509	Surrounding Greenness and Biological Aging Based on DNA Methylation: A Twin and Family Study in Australia. *Environmental Health Perspectives*, **2021**, 129, 87007	8.4	2
508	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
507	Androgens alter the heterogeneity of small extracellular vesicles and the small RNA cargo in prostate cancer. *Journal of Extracellular Vesicles*, **2021**, 10, e12136	16.4	2
506	Mendelian randomisation study of smoking exposure in relation to breast cancer risk. *British Journal of Cancer*, **2021**, 125, 1135-1145	8.7	0
505	Genetic insights into biological mechanisms governing human ovarian ageing. *Nature*, **2021**, 596, 393-397	50.4	28
504	Rare Germline Variants in ATM Predispose to Prostate Cancer: A PRACTICAL Consortium Study. *European Urology Oncology*, **2021**, 4, 570-579	6.7	12
503	Ambient temperature and genome-wide DNA methylation: A twin and family study in Australia. *Environmental Pollution*, **2021**, 285, 117700	9.3	1
502	Residential surrounding greenness and DNA methylation: An epigenome-wide association study. *Environment International*, **2021**, 154, 106556	12.9	6
501	Smoking Methylation Marks for Prediction of Urothelial Cancer Risk. *Cancer Epidemiology Biomarkers and Prevention*, **2021**, 30, 2197-2206	4	1
500	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
499	Independent evaluation of melanoma polygenic risk scores in UK and Australian prospective cohorts.. *British Journal of Dermatology*, **2021**,	4	1
498	Recreational Physical Activity and Outcomes After Breast Cancer in Women at High Familial Risk.. *JNCI Cancer Spectrum*, **2021**, 5, pkab090	4.6	0
497	Population-based estimates of breast cancer risk for carriers of pathogenic variants identified by gene-panel testing. *Npj Breast Cancer*, **2021**, 7, 153	7.8	1
496	The Variant C.349A>G Is Associated with Prostate Cancer Risk and Carriers Share a Common Ancestor. *Cancers*, **2020**, 12,	6.6	4
495	Genetic and environmental causes of variation in epigenetic aging across the lifespan. *Clinical Epigenetics*, **2020**, 12, 158	7.7	15
494	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
493	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. *Scientific Reports*, **2020**, 10, 9688	4.9	2
492	PALB2 Genetic Variants: Can Functional Assays Assist Translation?. *Trends in Cancer*, **2020**, 6, 263-265	12.5	3

491	Characterization of the Cancer Spectrum in Men With Germline BRCA1 and BRCA2 Pathogenic Variants: Results From the Consortium of Investigators of Modifiers of BRCA1/2 (CIMBA). *JAMA Oncology*, **2020**, 6, 1218-1230	13.4	25
490	The MLH1 polymorphism rs1800734 and risk of endometrial cancer with microsatellite instability. *Clinical Epigenetics*, **2020**, 12, 102	7.7	2
489	Integrating DNA methylation measures to improve clinical risk assessment: are we there yet? The case of BRCA1 methylation marks to improve clinical risk assessment of breast cancer. *British Journal of Cancer*, **2020**, 122, 1133-1140	8.7	11
488	Transcriptome-wide association study of breast cancer risk by estrogen-receptor status. *Genetic Epidemiology*, **2020**, 44, 442-468	2.6	9
487	Mismatch repair gene pathogenic germline variants in a population-based cohort of breast cancer. *Familial Cancer*, **2020**, 19, 197-202	3	3
486	Palm reading and water divining: A cross-sectional study of the accuracy of palmar hyperlinearity and transepidermal water loss to identify individuals with a filaggrin gene null mutation. *Journal of the American Academy of Dermatology*, **2020**, 83, 1186-1188	4.5	1
485	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. *Nature Communications*, **2020**, 11, 312	17.4	20
484	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
483	Rare germline genetic variants and risk of aggressive prostate cancer. *International Journal of Cancer*, **2020**, 147, 2142-2149	7.5	7
482	Association of Genomic Domains in and with Prostate Cancer Risk and Aggressiveness. *Cancer Research*, **2020**, 80, 624-638	10.1	22
481	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. *Nature Genetics*, **2020**, 52, 56-73	36.3	56
480	Overall lack of replication of associations between dietary intake of folate and vitamin B-12 and DNA methylation in peripheral blood. *American Journal of Clinical Nutrition*, **2020**, 111, 228-230	7	2
479	Dysfunctional epigenetic aging of the normal colon and colorectal cancer risk. *Clinical Epigenetics*, **2020**, 12, 5	7.7	27
478	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
477	Cancer Risks Associated With Germline Pathogenic Variants: An International Study of 524 Families. *Journal of Clinical Oncology*, **2020**, 38, 674-685	2.2	133
476	Postmenopausal Hormone Therapy and Colorectal Cancer Risk by Molecularly Defined Subtypes and Tumor Location. *JNCI Cancer Spectrum*, **2020**, 4, pkaa042	4.6	2
475	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	8.1	34
474	Analytical validation of an error-corrected ultra-sensitive ctDNA next-generation sequencing assay. *BioTechniques*, **2020**, 69, 133-140	2.5	3

473	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	4	6
472	Breast Cancer Polygenic Risk Score and Contralateral Breast Cancer Risk. *American Journal of Human Genetics*, **2020**, 107, 837-848	11	12
471	Association of germline variation with the survival of women with pathogenic variants and breast cancer. *Npj Breast Cancer*, **2020**, 6, 44	7.8	3
470	Genetic testing in Poland and Ukraine: should comprehensive germline testing of and be recommended for women with breast and ovarian cancer?. *Genetical Research*, **2020**, 102, e6	1.1	0
469	Considerations When Using Breast Cancer Risk Models for Women with Negative BRCA1/BRCA2 Mutation Results. *Journal of the National Cancer Institute*, **2020**, 112, 418-422	9.7	1
468	Recreational Physical Activity Is Associated with Reduced Breast Cancer Risk in Adult Women at High Risk for Breast Cancer: A Cohort Study of Women Selected for Familial and Genetic Risk. *Cancer Research*, **2020**, 80, 116-125	10.1	15
467	Smoking and blood DNA methylation: an epigenome-wide association study and assessment of reversibility. *Epigenetics*, **2020**, 15, 358-368	5.7	22
466	Interval breast cancer risk associations with breast density, family history and breast tissue aging. *International Journal of Cancer*, **2020**, 147, 375-382	7.5	10
465	Evaluation of associations between genetically predicted circulating protein biomarkers and breast cancer risk. *International Journal of Cancer*, **2020**, 146, 2130-2138	7.5	9
464	Hi-Plex2: a simple and robust approach to targeted sequencing-based genetic screening. *BioTechniques*, **2019**, 67, 118-122	2.5	6
463	Methylation alteration of as a predictive, diagnostic and prognostic biomarker for chronic lymphocytic leukemia. *Oncotarget*, **2019**, 10, 4987-5002	3.3	8
462	Two truncating variants in FANCC and breast cancer risk. *Scientific Reports*, **2019**, 9, 12524	4.9	2
461	A Cost-effectiveness Analysis of Multigene Testing for All Patients With Breast Cancer. *JAMA Oncology*, **2019**,	13.4	46
460	Body size and dietary risk factors for aggressive prostate cancer: a case-control study. *Cancer Causes and Control*, **2019**, 30, 1301-1312	2.8	2
459	Shared heritability and functional enrichment across six solid cancers. *Nature Communications*, **2019** , 10, 431	17.4	45
458	Genome-wide association study of peripheral blood DNA methylation and conventional mammographic density measures. *International Journal of Cancer*, **2019**, 145, 1768-1773	7.5	13
457	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	8.3	18
456	Blood DNA methylation and breast cancer risk: a meta-analysis of four prospective cohort studies. *Breast Cancer Research*, **2019**, 21, 62	8.3	20

455	Regular use of aspirin and other non-steroidal anti-inflammatory drugs and breast cancer risk for women at familial or genetic risk: a cohort study. *Breast Cancer Research*, **2019**, 21, 52	8.3	29
454	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. *Clinical Epigenetics*, **2019**, 11, 66	7.7	12
453	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. *Nature Communications*, **2019**, 10, 1741	17.4	47
452	Dietary Intake of Nutrients Involved in One-Carbon Metabolism and Risk of Gastric Cancer: A Prospective Study. *Nutrition and Cancer*, **2019**, 71, 605-614	2.8	13
451	Alternative splicing and ACMG-AMP-2015-based classification of PALB2 genetic variants: an ENIGMA report. *Journal of Medical Genetics*, **2019**, 56, 453-460	5.8	10
450	Autologous platelet-rich plasma for healing chronic venous leg ulcers: Clinical efficacy and potential mechanisms. *International Wound Journal*, **2019**, 16, 788-792	2.6	10
449	Genome-wide association study of germline variants and breast cancer-specific mortality. *British Journal of Cancer*, **2019**, 120, 647-657	8.7	28
448	Benign breast disease increases breast cancer risk independent of underlying familial risk profile: Findings from a Prospective Family Study Cohort. *International Journal of Cancer*, **2019**, 145, 370-379	7.5	4
447	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	7.5	7
446	Genetically Determined Height and Risk of Non-hodgkin Lymphoma. *Frontiers in Oncology*, **2019**, 9, 1539	5.3	1
445	Novel Common Genetic Susceptibility Loci for Colorectal Cancer. *Journal of the National Cancer Institute*, **2019**, 111, 146-157	9.7	67
444	Inference about causation between body mass index and DNA methylation in blood from a twin family study. *International Journal of Obesity*, **2019**, 43, 243-252	5.5	29
443	Homologous recombination DNA repair defects in associated breast cancers. *Npj Breast Cancer*, **2019**, 5, 23	7.8	20
442	Genetic overlap between autoimmune diseases and non-Hodgkin lymphoma subtypes. *Genetic Epidemiology*, **2019**, 43, 844-863	2.6	15
441	The :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. *Npj Breast Cancer*, **2019**, 5, 38	7.8	12
440	DNA methylation-based biological age, genome-wide average DNA methylation, and conventional breast cancer risk factors. *Scientific Reports*, **2019**, 9, 15055	4.9	6
439	Accuracy of Risk Estimates from the iPrevent Breast Cancer Risk Assessment and Management Tool. *JNCI Cancer Spectrum*, **2019**, 3, pkz066	4.6	7
438	Socioeconomic position, lifestyle habits and biomarkers of epigenetic aging: a multi-cohort analysis. *Aging*, **2019**, 11, 2045-2070	5.6	67

437	10-year performance of four models of breast cancer risk: a validation study. *Lancet Oncology, The*, **2019**, 20, 504-517	21.7	73
436	Physical Activity, Television Viewing Time, and DNA Methylation in Peripheral Blood. *Medicine and Science in Sports and Exercise*, **2019**, 51, 490-498	1.2	9
435	Prediction and clinical utility of a contralateral breast cancer risk model. *Breast Cancer Research*, **2019**, 21, 144	8.3	11
434	Alcohol consumption, cigarette smoking, and familial breast cancer risk: findings from the Prospective Family Study Cohort (ProF-SC). *Breast Cancer Research*, **2019**, 21, 128	8.3	8
433	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. *American Journal of Human Genetics*, **2019**, 104, 21-34	11	363
432	Circulating concentrations of B group vitamins and urothelial cell carcinoma. *International Journal of Cancer*, **2019**, 144, 1909-1917	7.5	6
431	Discovery of common and rare genetic risk variants for colorectal cancer. *Nature Genetics*, **2019**, 51, 76-87	36.3	177
430	Risk-Reducing Oophorectomy and Breast Cancer Risk Across the Spectrum of Familial Risk. *Journal of the National Cancer Institute*, **2019**, 111, 331-334	9.7	22
429	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. *International Journal of Epidemiology*, **2019**, 48, 795-806	7.8	52
428	Assessing the ProMCol classifier as a prognostic marker for non-metastatic colorectal cancer within the Melbourne Collaborative Cohort Study. *Gut*, **2019**, 68, 761-762	19.2	
427	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
426	Cohort Profile: The Colon Cancer Family Registry Cohort (CCFRC). *International Journal of Epidemiology*, **2018**, 47, 387-388i	7.8	23
425	Heritable DNA methylation marks associated with susceptibility to breast cancer. *Nature Communications*, **2018**, 9, 867	17.4	52
424	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. *British Journal of Cancer*, **2018**, 118, 1123-1129	8.7	10
423	Mutational spectrum in a worldwide study of 29,700 families with BRCA1 or BRCA2 mutations. *Human Mutation*, **2018**, 39, 593-620	4.7	138
422	Dietary intake of nutrients involved in one-carbon metabolism and risk of urothelial cell carcinoma: A prospective cohort study. *International Journal of Cancer*, **2018**, 143, 298-306	7.5	11
421	Obtaining high quality transcriptome data from formalin-fixed, paraffin-embedded diagnostic prostate tumor specimens. *Laboratory Investigation*, **2018**, 98, 537-550	5.9	7
420	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	7.8	53

419	Is RNASEL:p.Glu265* a modifier of early-onset breast cancer risk for carriers of high-risk mutations?. *BMC Cancer*, **2018**, 18, 165	4.8	3
418	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	3	11
417	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	3	6
416	Association of DNA Methylation-Based Biological Age With Health Risk Factors and Overall and Cause-Specific Mortality. *American Journal of Epidemiology*, **2018**, 187, 529-538	3.8	61
415	Associations of alcohol intake, smoking, physical activity and obesity with survival following colorectal cancer diagnosis by stage, anatomic site and tumor molecular subtype. *International Journal of Cancer*, **2018**, 142, 238-250	7.5	53
414	Heritable methylation marks associated with breast and prostate cancer risk. *Prostate*, **2018**, 78, 962-969	4.2	9
413	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	10.1	32
412	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. *PLoS ONE*, **2018**, 13, e0197561	3.7	9
411	HLA Class I and II Diversity Contributes to the Etiologic Heterogeneity of Non-Hodgkin Lymphoma Subtypes. *Cancer Research*, **2018**, 78, 4086-4096	10.1	18
410	FANCM and RECQL genetic variants and breast cancer susceptibility: relevance to South Poland and West Ukraine. *BMC Medical Genetics*, **2018**, 19, 12	2.1	13
409	The utility of DNA extracted from saliva for genome-wide molecular research platforms. *BMC Research Notes*, **2018**, 11, 8	2.3	16
408	Causal effect of smoking on DNA methylation in peripheral blood: a twin and family study. *Clinical Epigenetics*, **2018**, 10, 18	7.7	50
407	Epigenetic supersimilarity of monozygotic twin pairs. *Genome Biology*, **2018**, 19, 2	18.3	52
406	Identification of nine new susceptibility loci for endometrial cancer. *Nature Communications*, **2018**, 9, 3166	17.4	70
405	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	3
404	Dietary intake of one-carbon metabolism nutrients and DNA methylation in peripheral blood. *American Journal of Clinical Nutrition*, **2018**, 108, 611-621	7	24
403	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. *Nature Genetics*, **2018**, 50, 928-936	36.3	340
402	Fine-mapping of prostate cancer susceptibility loci in a large meta-analysis identifies candidate causal variants. *Nature Communications*, **2018**, 9, 2256	17.4	57

401	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. *Nature Genetics*, **2018**, 50, 968-978	36.3	101
400	DNA methylation-based biological aging and cancer risk and survival: Pooled analysis of seven prospective studies. *International Journal of Cancer*, **2018**, 142, 1611-1619	7.5	83
399	Risk of colorectal cancer for carriers of a germ-line mutation in POLE or POLD1. *Genetics in Medicine* , **2018**, 20, 890-895	8.1	34
398	Cirrus: An Automated Mammography-Based Measure of Breast Cancer Risk Based on Textural Features. *JNCI Cancer Spectrum*, **2018**, 2, pky057	4.6	15
397	Genome-wide DNA methylation assessment of BRCA1-like early-onset breast cancer: Data from the Australian Breast Cancer Family Registry. *Experimental and Molecular Pathology*, **2018**, 105, 404-410	4.4	12
396	Age-specific breast cancer risk by body mass index and familial risk: prospective family study cohort (ProF-SC). *Breast Cancer Research*, **2018**, 20, 132	8.3	24
395	Predicting interval and screen-detected breast cancers from mammographic density defined by different brightness thresholds. *Breast Cancer Research*, **2018**, 20, 152	8.3	13
394	Oral Contraceptive Use and Breast Cancer Risk: Retrospective and Prospective Analyses From a BRCA1 and BRCA2 Mutation Carrier Cohort Study. *JNCI Cancer Spectrum*, **2018**, 2, pky023	4.6	13
393	sEst: Accurate Sex-Estimation and Abnormality Detection in Methylation Microarray Data. *International Journal of Molecular Sciences*, **2018**, 19,	6.3	2
392	Genome-wide average DNA methylation is determined in utero. *International Journal of Epidemiology*, **2018**, 47, 908-916	7.8	26
391	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	8.1	31
390	Tumor testing to identify lynch syndrome in two Australian colorectal cancer cohorts. *Journal of Gastroenterology and Hepatology (Australia)*, **2017**, 32, 427-438	4	27
389	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. *British Journal of Cancer*, **2017**, 116, 524-535	8.7	18
388	Mutation screening of ACKR3 and COPS8 in kidney cancer cases from the CONFIRM study. *Familial Cancer*, **2017**, 16, 411-416	3	4
387	Genome-Wide Measures of Peripheral Blood Dna Methylation and Prostate Cancer Risk in a Prospective Nested Case-Control Study. *Prostate*, **2017**, 77, 471-478	4.2	24
386	Hypomorphic Missense Variants Confer Moderate Risks of Breast Cancer. *Cancer Research*, **2017**, 77, 2789-2799	10.1	49
385	Genome-wide association analysis implicates dysregulation of immunity genes in chronic lymphocytic leukaemia. *Nature Communications*, **2017**, 8, 14175	17.4	54
384	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	36.3	257

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4	Prospective Evaluation of a Breast Cancer Risk Model Integrating Classical Risk Factors and Polygenic Risk in 15 Cohorts from Six Countries	2
3	Biological aging measures based on blood DNA methylation and risk of cancer: a prospective study	1
2	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses	2
1	Segregation analysis of 17,425 population-based breast cancer families: evidence for genetic susceptibility and risk prediction	1