Karoline B Kuchenbaecker

List of Publications by Year
in descending order

50	8,850	159525 30	175177 52
papers	citations	h-index	g-index

64	64	64	15923
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Risks of Breast, Ovarian, and Contralateral Breast Cancer for BRCA1 and BRCA2 Mutation Carriers. JAMA - Journal of the American Medical Association, 2017, 317, 2402.	3.8	1,898
2	The interleukin-6 receptor as a target for prevention of coronary heart disease: a mendelian randomisation analysis. Lancet, The, 2012, 379, 1214-1224.	6.3	886
3	HMG-coenzyme A reductase inhibition, type 2 diabetes, and bodyweight: evidence from genetic analysis and randomised trials. Lancet, The, 2015, 385, 351-361.	6.3	562
4	Association between alcohol and cardiovascular disease: Mendelian randomisation analysis based on individual participant data. BMJ, The, 2014, 349, g4164-g4164.	3.0	528
5	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. Nature Genetics, 2013, 45, 371-384.	9.4	493
6	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
7	Genome-wide Association Studies in Ancestrally Diverse Populations: Opportunities, Methods, Pitfalls, and Recommendations. Cell, 2019, 179, 589-603.	13.5	428
8	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. Nature Genetics, 2017, 49, 680-691.	9.4	356
9	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	9.4	289
10	The OncoArray Consortium: A Network for Understanding the Genetic Architecture of Common Cancers. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 126-135.	1.1	278
11	Genome-Wide Association Study in BRCA1 Mutation Carriers Identifies Novel Loci Associated with Breast and Ovarian Cancer Risk. PLoS Genetics, 2013, 9, e1003212.	1.5	244
12	Evaluation of Polygenic Risk Scores for Breast and Ovarian Cancer Risk Prediction in BRCA1 and BRCA2 Mutation Carriers. Journal of the National Cancer Institute, 2017, 109, .	3.0	242
13	Selecting instruments for Mendelian randomization in the wake of genome-wide association studies. International Journal of Epidemiology, 2016, 45, 1600-1616.	0.9	232
14	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. Nature Genetics, 2015, 47, 164-171.	9.4	221
15	A roadmap to increase diversity in genomic studies. Nature Medicine, 2022, 28, 243-250.	15.2	195
16	Prediction of Breast and Prostate Cancer Risks in Male BRCA1 and BRCA2 Mutation Carriers Using Polygenic Risk Scores. Journal of Clinical Oncology, 2017, 35, 2240-2250.	0.8	152
17	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
18	Secretory Phospholipase A2-IIA and Cardiovascular Disease. Journal of the American College of Cardiology, 2013, 62, 1966-1976.	1.2	115

#	Article	IF	Citations
19	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	1.5	105
20	Identification of four novel susceptibility loci for oestrogen receptor negative breast cancer. Nature Communications, 2016, 7, 11375.	5.8	93
21	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008.	1.6	88
22	Shared heritability and functional enrichment across six solid cancers. Nature Communications, 2019, 10, 431.	5.8	88
23	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. JAMA Psychiatry, 2021, 78, 1258.	6.0	88
24	The transferability of lipid loci across African, Asian and European cohorts. Nature Communications, 2019, 10, 4330.	5.8	75
25	Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561.	1.8	68
26	Common Variants at the 19p13.1 and ZNF365 Loci Are Associated with ER Subtypes of Breast Cancer and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 645-657.	1.1	47
27	DNA Glycosylases Involved in Base Excision Repair May Be Associated with Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS Genetics, 2014, 10, e1004256.	1.5	47
28	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. Human Molecular Genetics, 2015, 24, 3595-3607.	1.4	40
29	Rate of Cognitive Decline in Alzheimerâ€™s Disease Stratified by Age. Journal of Alzheimer's Disease, 2019, 69, 1153-1160.	1.2	35
30	Ovarian cancer susceptibility alleles and risk of ovarian cancer inBRCA1andBRCA2mutation carriers. Human Mutation, 2012, 33, 690-702.	1.1	34
31	Assessing Associations between the AURKA-HMMR-TPX2-TUBG1 Functional Module and Breast Cancer Risk in BRCA1/2 Mutation Carriers. PLoS ONE, 2015, 10, e0120020.	1.1	34
32	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	5.8	33
33	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.	2.2	31
34	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.	2.2	26
35	Integrating polygenic risk scores in the prediction of type 2 diabetes risk and subtypes in British Pakistanis and Bangladeshis: A population-based cohort study. PLoS Medicine, 2022, 19, e1003981.	3.9	24
36	Candidate Genetic Modifiers for Breast and Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 308-316.	1.1	22

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37	Performance of Breast Cancer Polygenic Risk Scores in 760 FemaleCHEK2Germline Mutation Carriers. Journal of the National Cancer Institute, 2021, 113, 893-899.	3.0	21
38	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	0.6	18
39	Genetic copy number variants, cognition and psychosis: a meta-analysis and a family study. Molecular Psychiatry, 2021, 26, 5307-5319.	4.1	18
40	The genomics of heart failure: design and rationale of the HERMES consortium. ESC Heart Failure, 2021, 8, 5531-5541.	1.4	11
41	Fine-Scale Mapping at 9p22.2 Identifies Candidate Causal Variants That Modify Ovarian Cancer Risk in BRCA1 and BRCA2 Mutation Carriers. PLoS ONE, 2016, 11, e0158801.	1.1	10
42	The KL-VS sequence variant of Klotho and cancer risk in BRCA1 and BRCA2 mutation carriers. Breast Cancer Research and Treatment, 2012, 132, 1119-1126.	1.1	8
43	Transcriptome-wide association study reveals two genes that influence mismatch negativity. Cell Reports, 2021, 34, 108868.	2.9	8
44	The Influence of CYP2D6 and CYP2C19 Genetic Variation on Diabetes Mellitus Risk in People Taking Antidepressants and Antipsychotics. Genes, 2021, 12, 1758.	1.0	8
45	Type 2 diabetes risks and determinants in second-generation migrants and mixed ethnicity people of South Asian and African Caribbean descent in the UK. Diabetologia, 2022, 65, 113-127.	2.9	7
46	Mendelian randomization analyses implicate biogenesis of translation machinery in human aging. Genome Research, 2022, 32, 258-265.	2.4	7
47	Polygenic risk scores indicate extreme ages at onset of breast cancer in female BRCA1/2 pathogenic variant carriers. BMC Cancer, 2022, 22, .	1.1	6
48	Assessing Rare Variation in Complex Traits. Methods in Molecular Biology, 2018, 1793, 51-71.	0.4	4
49	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations. Scientific Reports, 2022, 12, 1131.	1.6	2
50	Editorial: Genetics of Complex Traits and Diseases From Under-Represented Populations. Frontiers in Genetics, 2021, 12, 817683.	1.1	0