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List of Publications by Year
in descending order

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50 papers	4,419 citations	236925 25 h-index	197818 49 g-index
51 all docs	51 docs citations	51 times ranked	8320 citing authors

#	Article	IF	Citations
1	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
2	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
3	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
4	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
5	A transcriptome-wide association study of 229,000 women identifies new candidate susceptibility genes for breast cancer. Nature Genetics, 2018, 50, 968-978.	21.4	184
6	Age- and Tumor Subtypeâ€"Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
7	Plasma DNA integrity as a biomarker for primary and metastatic breast cancer and potential marker for early diagnosis. Breast Cancer Research and Treatment, 2014, 146, 163-174.	2.5	142
8	Blood-based DNA methylation as biomarker for breast cancer: a systematic review. Clinical Epigenetics, 2016, 8, 115.	4.1	121
9	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.	2.9	106
10	Plasma miRâ€122 and miRâ€200 family are prognostic markers in colorectal cancer. International Journal of Cancer, 2017, 140, 176-187.	5.1	104
11	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
12	Exploring the genetics of irritable bowel syndrome: a GWA study in the general population and replication in multinational case-control cohorts. Gut, 2015, 64, 1774-1782.	12.1	97
13	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.	3.2	94
14	FANCMc.5791C>T nonsense mutation (rs144567652) induces exon skipping, affects DNA repair activity and is a familial breast cancer risk factor. Human Molecular Genetics, 2015, 24, 5345-5355.	2.9	91
15	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. International Journal of Epidemiology, 2019, 48, 795-806.	1.9	81
16	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
17	Capture and Amplification by Tailing and Switching (CATS). RNA Biology, 2014, 11, 817-828.	3.1	68
18	Heterozygosity for ARID2 loss-of-function mutations in individuals with a Coffinâ€"Siris syndrome-like phenotype. Human Genetics, 2017, 136, 297-305.	3.8	53

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19	Predisposition for TMPRSS2-ERG Fusion in Prostate Cancer by Variants in DNA Repair Genes. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3030-3035.	2.5	51
20	Circulating free DNA integrity and concentration as independent prognostic markers in metastatic breast cancer. Breast Cancer Research and Treatment, 2018, 169, 69-82.	2.5	50
21	Identification of new TRIP12 variants and detailed clinical evaluation of individuals with non-syndromic intellectual disability with or without autism. Human Genetics, 2017, 136, 179-192.	3.8	43
22	Identification and characterization of novel associations in the CASP8/ALS2CR12 region on chromosome 2 with breast cancer risk. Human Molecular Genetics, 2015, 24, 285-298.	2.9	38
23	Heritability of baseline and induced micronucleus frequencies. Mutagenesis, 2011, 26, 111-117.	2.6	37
24	Cell-free circulating DNA integrity is an independent predictor of impending breast cancer recurrence. Oncotarget, 2017, 8, 54537-54547.	1.8	34
25	DNA methylation array analysis identifies breast cancer associated RPTOR, MGRN1 and RAPSN hypomethylation in peripheral blood DNA. Oncotarget, 2016, 7, 64191-64202.	1.8	33
26	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
27	Germline mutations of theMSR1 gene in prostate cancer families from Germany. Human Mutation, 2006, 27, 98-102.	2.5	22
28	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
29	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
30	MCM3APandPOMPMutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. Human Mutation, 2016, 37, 257-268.	2.5	18
31	Profound inhibition of CD73-dependent formation of anti-inflammatory adenosine in B cells of SLE patients. EBioMedicine, 2021, 73, 103616.	6.1	14
32	C2orf69 mutations disrupt mitochondrial function and cause a multisystem human disorder with recurring autoinflammation. Journal of Clinical Investigation, 2021, 131, .	8.2	13
33	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. Cancer Gene Therapy, 2022, 29, 697-708.	4.6	10
34	The Macrophage Migration Inhibitory Factor (MIF) Promoter Polymorphisms (rs3063368, rs755622) Predict Acute Kidney Injury and Death after Cardiac Surgery. Journal of Clinical Medicine, 2020, 9, 2936.	2.4	9
35	Increased Radiosensitivity as an Indicator of Genes Conferring Breast Cancer Susceptibility. Strahlentherapie Und Onkologie, 2007, 183, 655-660.	2.0	8
36	Clinical and molecular characterization of the BRCA2 p.Asn3124Ile variant reveals substantial evidence for pathogenic significance. Breast Cancer Research and Treatment, 2014, 145, 451-460.	2.5	8

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37	Circulating cell-free DNA variables as marker of ovarian cancer patients: A pilot study. Cancer Biomarkers, 2020, 28, 159-167.	1.7	7
38	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
39	A lowâ€frequency haplotype spanning SLX4/FANCP constitutes a new risk locus for earlyâ€onset breast cancer (<60 years) and is associated with reduced DNA repair capacity. International Journal of Cancer, 2018, 142, 757-768.	5.1	6
40	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.	6.2	6
41	High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. British Journal of Dermatology, 2021, , .	1.5	6
42	Acute myeloid leukemia-induced functional inhibition of healthy CD34+ hematopoietic stem and progenitor cells. Stem Cells, 2021, 39, 1270-1284.	3.2	6
43	Reduced DNA repair in BRCA1 mutation carriers undetectable before onset of breast cancer?. British Journal of Cancer, 2007, 97, 1184-1186.	6.4	5
44	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
45	<scp>QRICH1</scp> variants in <scp>Ververiâ€Brady</scp> syndromeâ€”delineation of the genotypic and phenotypic spectrum. Clinical Genetics, 2021, 99, 199-207.	2.0	5
46	The prostate cancer risk locus at 10q11 is associated with DNA repair capacity. DNA Repair, 2012, 11, 693-701.	2.8	4
47	The recurrent missense mutation p.(Arg367Trp) in YARS1 causes a distinct neurodevelopmental phenotype. Journal of Molecular Medicine, 2021, 99, 1755-1768.	3.9	3
48	The GPRC5A frameshift variant c.183del is not associated with increased breast cancer risk in BRCA1 mutation carriers. International Journal of Cancer, 2019, 144, 1761-1763.	5.1	2
49	Adenoma and colorectal cancer risks in Lynch syndrome, Lynchâ€like syndrome and familial colorectal cancer type X. International Journal of Cancer, 2022, 150, 56-66.	5.1	2
50	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2