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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	Whole-exome sequencing in eccrine porocarcinoma indicates promising therapeutic strategies. Cancer Gene Therapy, 2022, 29, 697-708.	4.6	10
2	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
3	Breast cancer risks associated with missense variants in breast cancer susceptibility genes. Genome Medicine, 2022, 14, 51.	8.2	19
4	<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
5	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
6	C2orf69 mutations disrupt mitochondrial function and cause a multisystem human disorder with recurring autoinflammation. Journal of Clinical Investigation, 2021, 131, .	8.2	13
7	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
8	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
9	High tumour mutational burden and EGFR/MAPK pathway activation are therapeutic targets in metastatic porocarcinoma. British Journal of Dermatology, 2021, , .	1.5	6
10	The recurrent missense mutation p.(Arg367Trp) in YARS1 causes a distinct neurodevelopmental phenotype. Journal of Molecular Medicine, 2021, 99, 1755-1768.	3.9	3
11	Germline variants and breast cancer survival in patients with distant metastases at primary breast cancer diagnosis. Scientific Reports, 2021, 11, 19787.	3.3	2
12	Profound inhibition of CD73-dependent formation of anti-inflammatory adenosine in B cells of SLE patients. EBioMedicine, 2021, 73, 103616.	6.1	14
13	Acute myeloid leukemia-induced functional inhibition of healthy CD34+ hematopoietic stem and progenitor cells. Stem Cells, 2021, 39, 1270-1284.	3.2	6
14	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
15	Circulating cell-free DNA variables as marker of ovarian cancer patients: A pilot study. Cancer Biomarkers, 2020, 28, 159-167.	1.7	7
16	Two truncating variants in FANCC and breast cancer risk. Scientific Reports, 2019, 9, 12524.	3.3	5
17	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
18	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

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19	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
20	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
21	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
22	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
23	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
24	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
25	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
26	Plasma miRâ€122 and miRâ€200 family are prognostic markers in colorectal cancer. International Journal of Cancer, 2017, 140, 176-187.	5.1	104
27	Cell-free circulating DNA integrity is an independent predictor of impending breast cancer recurrence. Oncotarget, 2017, 8, 54537-54547.	1.8	34
28	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
29	Blood-based DNA methylation as biomarker for breast cancer: a systematic review. Clinical Epigenetics, 2016, 8, 115.	4.1	121
30	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
31	MCM3APandPOMPMutations Cause a DNA-Repair and DNA-Damage-Signaling Defect in an Immunodeficient Child. Human Mutation, 2016, 37, 257-268.	2.5	18
32	Age- and Tumor Subtypeâ€“Specific Breast Cancer Risk Estimates for CHEK2*1100delC Carriers. Journal of Clinical Oncology, 2016, 34, 2750-2760.	1.6	152
33	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
34	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
35	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
36	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

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37	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
38	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
39	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
40	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
41	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
42	Capture and Amplification by Tailing and Switching (CATS). RNA Biology, 2014, 11, 817-828.	3.1	68
43	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
44	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
45	The prostate cancer risk locus at 10q11 is associated with DNA repair capacity. DNA Repair, 2012, 11, 693-701.	2.8	4
46	Heritability of baseline and induced micronucleus frequencies. Mutagenesis, 2011, 26, 111-117.	2.6	37
47	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
48	Reduced DNA repair in BRCA1 mutation carriers undetectable before onset of breast cancer?. British Journal of Cancer, 2007, 97, 1184-1186.	6.4	5
49	Increased Radiosensitivity as an Indicator of Genes Conferring Breast Cancer Susceptibility. Strahlentherapie Und Onkologie, 2007, 183, 655-660.	2.0	8
50	Germline mutations of theMSR1 gene in prostate cancer families from Germany. Human Mutation, 2006, 27, 98-102.	2.5	22