

Daniel R Barnes

List of Publications by Year in descending order

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Version: 2024-02-01

46
papers

6,397
citations

201674

27
h-index

214800

47
g-index

54
all docs

54
docs citations

54
times ranked

13546
citing authors

#	ARTICLE	IF	CITATIONS
1	Breast and Prostate Cancer Risks for Male <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variant Carriers Using Polygenic Risk Scores. <i>Journal of the National Cancer Institute</i> , 2022, 114, 109-122.	6.3	19
2	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	2.8	23
3	A case-only study to identify genetic modifiers of breast cancer risk for <i>BRCA1/BRCA2</i> mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	12.8	19
4	<i>RNF168</i> regulates R-loop resolution and genomic stability in <i>BRCA1/2</i> -deficient tumors. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	38
5	The predictive ability of the 313 variant-based polygenic risk score for contralateral breast cancer risk prediction in women of European ancestry with a heterozygous <i>BRCA1</i> or <i>BRCA2</i> pathogenic variant. <i>Genetics in Medicine</i> , 2021, 23, 1726-1737.	2.4	16
6	Altered regulation of <i>BRCA1</i> exon 11 splicing is associated with breast cancer risk in carriers of <i>BRCA1</i> pathogenic variants. <i>Human Mutation</i> , 2021, 42, 1488-1502.	2.5	7
7	Association of Genomic Domains in <i>BRCA1</i> and <i>BRCA2</i> with Prostate Cancer Risk and Aggressiveness. <i>Cancer Research</i> , 2020, 80, 624-638.	0.9	39
8	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. <i>Molecular Psychiatry</i> , 2020, 25, 2392-2409.	7.9	83
9	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
10	Chromatin interactome mapping at 139 independent breast cancer risk signals. <i>Genome Biology</i> , 2020, 21, 8.	8.8	27
11	Polygenic risk scores and breast and epithelial ovarian cancer risks for carriers of <i>BRCA1</i> and <i>BRCA2</i> pathogenic variants. <i>Genetics in Medicine</i> , 2020, 22, 1653-1666.	2.4	82
12	Immune Cell Associations with Cancer Risk. <i>IScience</i> , 2020, 23, 101296.	4.1	6
13	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. <i>Nature Genetics</i> , 2020, 52, 572-581.	21.4	265
14	Characterization of the Cancer Spectrum in Men With Germline <i>BRCA1</i> and <i>BRCA2</i> Pathogenic Variants. <i>JAMA Oncology</i> , 2020, 6, 1218.	7.1	48
15	Transcriptome-wide association study of breast cancer risk by estrogen receptor status. <i>Genetic Epidemiology</i> , 2020, 44, 442-468.	1.3	32
16	Candidate Causal Variants at the 8p12 Breast Cancer Risk Locus Regulate <i>DUSP4</i> . <i>Cancers</i> , 2020, 12, 170.	3.7	6
17	Non-coding RNAs underlie genetic predisposition to breast cancer. <i>Genome Biology</i> , 2020, 21, 7.	8.8	21
18	The <i>FANCM</i> :p.Arg658* truncating variant is associated with risk of triple-negative breast cancer. <i>Npj Breast Cancer</i> , 2019, 5, 38.	5.2	28

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19	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	12.8	88
20	Genome-wide association and transcriptome studies identify target genes and risk loci for breast cancer. <i>Nature Communications</i> , 2019, 10, 1741.	12.8	90
21	Exome Chip Meta-analysis Fine Maps Causal Variants and Elucidates the Genetic Architecture of Rare Coding Variants in Smoking and Alcohol Use. <i>Biological Psychiatry</i> , 2019, 85, 946-955.	1.3	69
22	Tumour risks and genotype-phenotype correlations associated with germline variants in succinate dehydrogenase subunit genes <i>SDHB</i> , <i>SDHC</i> and <i>SDHD</i> . <i>Journal of Medical Genetics</i> , 2018, 55, 384-394.	3.2	177
23	Risks of breast or ovarian cancer in BRCA1 or BRCA2 predictive test negatives: findings from the EMBRACE study. <i>Genetics in Medicine</i> , 2018, 20, 1575-1582.	2.4	15
24	Exome array analysis identifies <i>ETFB</i> as a novel susceptibility gene for anthracycline-induced cardiotoxicity in cancer patients. <i>Breast Cancer Research and Treatment</i> , 2018, 167, 249-256.	2.5	23
25	Epidemiology of ATTRV30M neuropathy in Cyprus and the modifier effect of complement C1q on the age of disease onset. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2018, 25, 220-226.	3.0	12
26	A Transcriptome-Wide Association Study Among 97,898 Women to Identify Candidate Susceptibility Genes for Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2018, 78, 5419-5430.	0.9	54
27	Risks of Breast, Ovarian, and Contralateral Breast Cancer for <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers. <i>JAMA - Journal of the American Medical Association</i> , 2017, 317, 2402.	7.4	1,898
28	Fifteen new risk loci for coronary artery disease highlight arterial-wall-specific mechanisms. <i>Nature Genetics</i> , 2017, 49, 1113-1119.	21.4	260
29	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
30	Exome array analysis identifies <i>GPR35</i> as a novel susceptibility gene for anthracycline-induced cardiotoxicity in childhood cancer. <i>Pharmacogenetics and Genomics</i> , 2017, 27, 445-453.	1.5	22
31	Risk of breast or ovarian cancer in family members who do not carry the BRCA1 or BRCA2 family mutation: Findings from the EMBRACE study. <i>Journal of Clinical Oncology</i> , 2017, 35, 1558-1558.	1.6	0
32	Meta-analysis of Genome Wide Association Studies Identifies Genetic Markers of Late Toxicity Following Radiotherapy for Prostate Cancer. <i>EBioMedicine</i> , 2016, 10, 150-163.	6.1	69
33	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	21.4	261
34	Attenuated familial adenomatous polyposis manifests as autosomal dominant late-onset colorectal cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 1330-1333.	2.8	20
35	Prediction of measured weight from self-reported weight was not improved after stratification by body mass index. <i>Obesity</i> , 2013, 21, E137-42.	3.0	13
36	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. <i>American Journal of Human Genetics</i> , 2013, 92, 489-503.	6.2	201

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37	Exome Sequencing Identifies Rare Deleterious Mutations in DNA Repair Genes FANCC and BLM as Potential Breast Cancer Susceptibility Alleles. <i>PLoS Genetics</i> , 2012, 8, e1002894.	3.5	186
38	No Interactions Between Previously Associated 2-Hour Glucose Gene Variants and Physical Activity or BMI on 2-Hour Glucose Levels. <i>Diabetes</i> , 2012, 61, 1291-1296.	0.6	23
39	Impact of Common Variation in Bone-Related Genes on Type 2 Diabetes and Related Traits. <i>Diabetes</i> , 2012, 61, 2176-2186.	0.6	31
40	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycaemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	21.4	762
41	Evaluation of Association Methods for Analysing Modifiers of Disease Risk in Carriers of High-Risk Mutations. <i>Genetic Epidemiology</i> , 2012, 36, 274-291.	1.3	37
42	Unravelling modifiers of breast and ovarian cancer risk for <i>BRCA1</i> and <i>BRCA2</i> mutation carriers: update on genetic modifiers. <i>Journal of Internal Medicine</i> , 2012, 271, 331-343.	6.0	47
43	Genome-Wide Association Identifies Nine Common Variants Associated With Fasting Proinsulin Levels and Provides New Insights Into the Pathophysiology of Type 2 Diabetes. <i>Diabetes</i> , 2011, 60, 2624-2634.	0.6	335
44	No evidence for a causal link between uric acid and type 2 diabetes: a Mendelian randomisation approach. <i>Diabetologia</i> , 2011, 54, 2561-2569.	6.3	89
45	The rs2910164:G>C SNP in the MIR146A gene is not associated with breast cancer risk in <i>BRCA1</i> and <i>BRCA2</i> mutation carriers. <i>Human Mutation</i> , 2011, 32, 1004-1007.	2.5	39
46	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. <i>Diabetes</i> , 2010, 59, 3229-3239.	0.6	387