

Nick Orr

List of Publications by Year in descending order

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Version: 2024-02-01

92
papers

14,439
citations

44069

48
h-index

42399

92
g-index

98
all docs

98
docs citations

98
times ranked

17219
citing authors

#	ARTICLE	IF	CITATIONS
1	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. <i>International Journal of Epidemiology</i> , 2022, 50, 1897-1911.	1.9	43
2	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. <i>Breast Cancer Research</i> , 2022, 24, 2.	5.0	15
3	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. <i>Scientific Reports</i> , 2022, 12, 6199.	3.3	2
4	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2021, 113, 329-337.	6.3	45
5	Common Susceptibility Loci for Male Breast Cancer. <i>Journal of the National Cancer Institute</i> , 2021, 113, 453-461.	6.3	12
6	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. <i>British Journal of Cancer</i> , 2021, 124, 842-854.	6.4	5
7	Functional annotation of the 2q35 breast cancer risk locus implicates a structural variant in influencing activity of a long-range enhancer element. <i>American Journal of Human Genetics</i> , 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. <i>Breast Cancer Research</i> , 2021, 23, 86.	5.0	7
9	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. <i>Journal of the National Cancer Institute</i> , 2020, 112, 278-285.	6.3	61
10	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	21.4	120
11	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
12	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. <i>Scientific Reports</i> , 2020, 10, 9688.	3.3	2
13	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. <i>Nature Communications</i> , 2020, 11, 312.	12.8	30
14	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. <i>Clinical Epigenetics</i> , 2019, 11, 66.	4.1	21
15	Genome-wide association study of germline variants and breast cancer-specific mortality. <i>British Journal of Cancer</i> , 2019, 120, 647-657.	6.4	52
16	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	6.2	711
17	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. <i>Blood</i> , 2019, 133, 1130-1139.	1.4	29
18	Associations of obesity and circulating insulin and glucose with breast cancer risk: a Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2019, 48, 795-806.	1.9	81

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19	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. <i>International Journal of Epidemiology</i> , 2018, 47, 526-536.	1.9	88
20	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. <i>Nature Communications</i> , 2018, 9, 1028.	12.8	98
21	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. <i>European Urology</i> , 2018, 74, 248-252.	1.9	20
22	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. <i>Oncotarget</i> , 2018, 9, 12630-12638.	1.8	8
23	Genetic Determinants of Breast Cancer Risk in Childhood Cancer Survivors. <i>Journal of the National Cancer Institute</i> , 2017, 109, .	6.3	0
24	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. <i>Nature Genetics</i> , 2017, 49, 1133-1140.	21.4	120
25	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	27.8	1,099
26	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	21.4	289
27	Prediction of Breast and Prostate Cancer Risks in Male <i>BRCA1</i> and <i>BRCA2</i> Mutation Carriers Using Polygenic Risk Scores. <i>Journal of Clinical Oncology</i> , 2017, 35, 2240-2250.	1.6	152
28	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. <i>PLoS ONE</i> , 2016, 11, e0160316.	2.5	12
29	Fine-scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. <i>International Journal of Cancer</i> , 2016, 139, 1303-1317.	5.1	51
30	<i>PALB2</i> , <i>CHEK2</i> and <i>ATM</i> rare variants and cancer risk: data from COGS. <i>Journal of Medical Genetics</i> , 2016, 53, 800-811.	3.2	174
31	Genetic predisposition to ductal carcinoma in situ of the breast. <i>Breast Cancer Research</i> , 2016, 18, 22.	5.0	43
32	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating <i>IGFBP5</i> expression. <i>Human Molecular Genetics</i> , 2016, 25, 3863-3876.	2.9	33
33	rs2735383, located at a microRNA binding site in the 3'UTR of <i>NBS1</i> , is not associated with breast cancer risk. <i>Scientific Reports</i> , 2016, 6, 36874.	3.3	2
34	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. <i>Cancer Discovery</i> , 2016, 6, 1052-1067.	9.4	157
35	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	12.8	78
36	Fine scale mapping of the 17q22 breast cancer locus using dense SNPs, genotyped within the Collaborative Oncological Gene-Environment Study (COGs). <i>Scientific Reports</i> , 2016, 6, 32512.	3.3	19

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37	Prognostic value of automated Ki67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. <i>Breast Cancer Research</i> , 2016, 18, 104.	5.0	56
38	High-throughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. <i>Journal of Pathology: Clinical Research</i> , 2016, 2, 138-153.	3.0	19
39	Cytochrome P450 Allele <i>CYP3A7*1C</i> Associates with Adverse Outcomes in Chronic Lymphocytic Leukemia, Breast, and Lung Cancer. <i>Cancer Research</i> , 2016, 76, 1485-1493.	0.9	28
40	Breast cancer risk variants at 6q25 display different phenotype associations and regulate <i>ESR1</i> , <i>RMND1</i> and <i>CCDC170</i> . <i>Nature Genetics</i> , 2016, 48, 374-386.	21.4	125
41	No clinical utility of <i>KRAS</i> variant rs61764370 for ovarian or breast cancer. <i>Gynecologic Oncology</i> , 2016, 141, 386-401.	1.4	18
42	<i>RAD51B</i> in Familial Breast Cancer. <i>PLoS ONE</i> , 2016, 11, e0153788.	2.5	26
43	Investigation of gene-environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. <i>International Journal of Cancer</i> , 2015, 136, E685-96.	5.1	34
44	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	6.3	428
45	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. <i>Human Molecular Genetics</i> , 2015, 24, 2966-2984.	2.9	40
46	Fine-Scale Mapping of the 5q11.2 Breast Cancer Locus Reveals at Least Three Independent Risk Variants Regulating <i>MAP3K1</i> . <i>American Journal of Human Genetics</i> , 2015, 96, 5-20.	6.2	76
47	Genome-wide association analysis of more than 120,000 individuals identifies 15 new susceptibility loci for breast cancer. <i>Nature Genetics</i> , 2015, 47, 373-380.	21.4	513
48	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. <i>Nature Genetics</i> , 2015, 47, 987-995.	21.4	218
49	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. <i>Journal of the National Cancer Institute</i> , 2015, 107, djv219.	6.3	99
50	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1680-1691.	2.5	24
51	Identification and characterization of novel associations in the <i>CASP8/ALS2CR12</i> region on chromosome 2 with breast cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 285-298.	2.9	38
52	Temporal Stability and Determinants of White Blood Cell DNA Methylation in the Breakthrough Generations Study. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 221-229.	2.5	60
53	MicroRNA Related Polymorphisms and Breast Cancer Risk. <i>PLoS ONE</i> , 2014, 9, e109973.	2.5	49
54	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the <i>TERT-CLPTM1L</i> region on chromosome 5p15.33. <i>Human Molecular Genetics</i> , 2014, 23, 6616-6633.	2.9	90

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55	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2014, 23, 6096-6111.	2.9	53
56	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. <i>Genome Research</i> , 2014, 24, 1854-1868.	5.5	219
57	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. <i>Nature Communications</i> , 2014, 5, 4999.	12.8	105
58	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. <i>Human Molecular Genetics</i> , 2014, 23, 6034-6046.	2.9	12
59	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. <i>Breast Cancer Research</i> , 2014, 16, R51.	5.0	14
60	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	6.2	98
61	Multiple independent variants at the TERT locus are associated with telomere length and risks of breast and ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 371-384.	21.4	493
62	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
63	Genome-wide association studies identify four ER negative-specific breast cancer risk loci. <i>Nature Genetics</i> , 2013, 45, 392-398.	21.4	374
64	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. <i>Nature Genetics</i> , 2013, 45, 353-361.	21.4	960
65	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. <i>PLoS Genetics</i> , 2013, 9, e1003173.	3.5	105
66	Intragenic ATM Methylation in Peripheral Blood DNA as a Biomarker of Breast Cancer Risk. <i>Cancer Research</i> , 2012, 72, 2304-2313.	0.9	142
67	Estimating Causal Effects of Genetic Risk Variants for Breast Cancer Using Marker Data from Bilateral and Familial Cases. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 262-272.	2.5	6
68	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. <i>Nature Genetics</i> , 2012, 44, 1182-1184.	21.4	99
69	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2012, 21, 1783-1791.	2.5	17
70	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. <i>Journal of the National Cancer Institute</i> , 2012, 104, 657-669.	6.3	30
71	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). <i>PLoS ONE</i> , 2012, 7, e42380.	2.5	51
72	Multidrug resistance gene expression and ABCB1 SNPs in plasma cell myeloma. <i>Leukemia Research</i> , 2011, 35, 1457-1463.	0.8	17

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73	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. <i>Human Molecular Genetics</i> , 2011, 20, 2869-2878.	2.9	43
74	Associations of common variants at 1p11.2 and 14q24.1 (RAD51L1) with breast cancer risk and heterogeneity by tumor subtype: findings from the Breast Cancer Association Consortium. <i>Human Molecular Genetics</i> , 2011, 20, 4693-4706.	2.9	71
75	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. <i>Human Molecular Genetics</i> , 2011, 20, 3322-3329.	2.9	28
76	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. <i>Journal of the National Cancer Institute</i> , 2011, 103, 425-435.	6.3	225
77	Genetic Variants at Chromosomes 2q35, 5p12, 6q25.1, 10q26.13, and 16q12.1 Influence the Risk of Breast Cancer in Men. <i>PLoS Genetics</i> , 2011, 7, e1002290.	3.5	43
78	Reply to "Associations of CFHR1 and CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independent". <i>Nature Genetics</i> , 2010, 42, 555-556.	21.4	18
79	A Sequence Polymorphism in MSTN Predicts Sprinting Ability and Racing Stamina in Thoroughbred Horses. <i>PLoS ONE</i> , 2010, 5, e8645.	2.5	154
80	Missense Variants in <i>ATM</i> in 26,101 Breast Cancer Cases and 29,842 Controls. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010, 19, 2143-2151.	2.5	33
81	Fine mapping and functional analysis of a common variant in <i>MSMB</i> on chromosome 10q11.2 associated with prostate cancer susceptibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 7933-7938.	7.1	96
82	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). <i>Nature Genetics</i> , 2009, 41, 579-584.	21.4	487
83	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. <i>Nature Genetics</i> , 2009, 41, 1055-1057.	21.4	218
84	<i>ABC B1 (MDR1)</i> rs1045642 is associated with increased overall survival in plasma cell myeloma. <i>Leukemia and Lymphoma</i> , 2009, 50, 566-570.	1.3	23
85	A Genome Scan for Positive Selection in Thoroughbred Horses. <i>PLoS ONE</i> , 2009, 4, e5767.	2.5	123
86	Comprehensive resequence analysis of a 136 kb region of human chromosome 8q24 associated with prostate and colon cancers. <i>Human Genetics</i> , 2008, 124, 161-170.	3.8	104
87	Multiple loci identified in a genome-wide association study of prostate cancer. <i>Nature Genetics</i> , 2008, 40, 310-315.	21.4	871
88	Chapter 1 Common Genetic Variation and Human Disease. <i>Advances in Genetics</i> , 2008, 62, 1-32.	1.8	55
89	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. <i>Nature Genetics</i> , 2007, 39, 645-649.	21.4	1,059
90	A genome-wide association study identifies alleles in <i>FGFR2</i> associated with risk of sporadic postmenopausal breast cancer. <i>Nature Genetics</i> , 2007, 39, 870-874.	21.4	1,370

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91	Neovascular Age-Related Macular Degeneration Risk Based on CFH, LOC387715/HTRA1, and Smoking. PLoS Medicine, 2007, 4, e355.	8.4	101
92	A common CFH haplotype, with deletion of CFHR1 and CFHR3, is associated with lower risk of age-related macular degeneration. Nature Genetics, 2006, 38, 1173-1177.	21.4	421