Nick Orr

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11441570/publications.pdf

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	A genome-wide association study identifies alleles in FGFR2 associated with risk of sporadic postmenopausal breast cancer. Nature Genetics, 2007, 39, 870-874.	21.4	1,370
2	Association analysis identifies 65 new breast cancer risk loci. Nature, 2017, 551, 92-94.	27.8	1,099
3	Genome-wide association study of prostate cancer identifies a second risk locus at 8q24. Nature Genetics, 2007, 39, 645-649.	21.4	1,059
4	Large-scale genotyping identifies 41 new loci associated with breast cancer risk. Nature Genetics, 2013, 45, 353-361.	21.4	960
5	Multiple loci identified in a genome-wide association study of prostate cancer. Nature Genetics, 2008, 40, 310-315.	21.4	871
6	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. American Journal of Human Genetics, 2019, 104, 21-34.	6.2	711
7	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
8	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.	21.4	493
9	A multistage genome-wide association study in breast cancer identifies two new risk alleles at 1p11.2 and 14q24.1 (RAD51L1). Nature Genetics, 2009, 41, 579-584.	21.4	487
10	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. Journal of the National Cancer Institute, 2015, 107, .	6.3	428
11	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
12	Genome-wide association studies identify four ER negativeâ€“specific breast cancer risk loci. Nature Genetics, 2013, 45, 392-398.	21.4	374
13	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. Nature Genetics, 2017, 49, 1767-1778.	21.4	289
14	Genome-wide association study identifies 32 novel breast cancer susceptibility loci from overall and subtype-specific analyses. Nature Genetics, 2020, 52, 572-581.	21.4	265
15	Novel Breast Cancer Susceptibility Locus at 9q31.2: Results of a Genome-Wide Association Study. Journal of the National Cancer Institute, 2011, 103, 425-435.	6.3	225
16	Unbiased analysis of potential targets of breast cancer susceptibility loci by Capture Hi-C. Genome Research, 2014, 24, 1854-1868.	5.5	219
17	Identification of a new prostate cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2009, 41, 1055-1057.	21.4	218
18	Genome-wide meta-analysis identifies five new susceptibility loci for cutaneous malignant melanoma. Nature Genetics, 2015, 47, 987-995.	21.4	218

#	Article	IF	Citations
19	Functional Variants at the 11q13 Risk Locus for Breast Cancer Regulate Cyclin D1 Expression through Long-Range Enhancers. American Journal of Human Genetics, 2013, 92, 489-503.	6.2	201
20	PALB2,CHEK2andATMrare variants and cancer risk: data from COGS. Journal of Medical Genetics, 2016, 53, 800-811.	3.2	174
21	Genome-Wide Meta-Analyses of Breast, Ovarian, and Prostate Cancer Association Studies Identify Multiple New Susceptibility Loci Shared by at Least Two Cancer Types. Cancer Discovery, 2016, 6, 1052-1067.	9.4	157
22	A Sequence Polymorphism in MSTN Predicts Sprinting Ability and Racing Stamina in Thoroughbred Horses. PLoS ONE, 2010, 5, e8645.	2.5	154
23	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.	1.6	152
24	Intragenic ATM Methylation in Peripheral Blood DNA as a Biomarker of Breast Cancer Risk. Cancer Research, 2012, 72, 2304-2313.	0.9	142
25	Breast cancer risk variants at 6q25 display different phenotype associations and regulate ESR1, RMND1 and CCDC170. Nature Genetics, 2016, 48, 374-386.	21.4	125
26	A Genome Scan for Positive Selection in Thoroughbred Horses. PLoS ONE, 2009, 4, e5767.	2.5	123
27	Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. Nature Genetics, 2017, 49, 1133-1140.	21.4	120
28	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. Nature Genetics, 2020, 52, 56-73.	21.4	120
29	Identification of a BRCA2-Specific Modifier Locus at 6p24 Related to Breast Cancer Risk. PLoS Genetics, 2013, 9, e1003173.	3.5	105
30	Evidence that breast cancer risk at the 2q35 locus is mediated through IGFBP5 regulation. Nature Communications, 2014, 5, 4999.	12.8	105
31	Comprehensive resequence analysis of a 136Âkb region of human chromosome 8q24 associated with prostate and colon cancers. Human Genetics, 2008, 124, 161-170.	3.8	104
32	Neovascular Age-Related Macular Degeneration Risk Based on CFH, LOC387715/HTRA1, and Smoking. PLoS Medicine, 2007, 4, e355.	8.4	101
33	Genome-wide association study identifies a common variant in RAD51B associated with male breast cancer risk. Nature Genetics, 2012, 44, 1182-1184.	21.4	99
34	Height and Breast Cancer Risk: Evidence From Prospective Studies and Mendelian Randomization. Journal of the National Cancer Institute, 2015, 107, djv219.	6.3	99
35	Fine-Scale Mapping of the FGFR2 Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind FOXA1 and E2F1. American Journal of Human Genetics, 2013, 93, 1046-1060.	6.2	98
36	Capture Hi-C identifies putative target genes at 33 breast cancer risk loci. Nature Communications, 2018, 9, 1028.	12.8	98

#	Article	IF	Citations
37	Fine mapping and functional analysis of a common variant in MSMB on chromosome 10q11.2 associated with prostate cancer susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 7933-7938.	7.1	96
38	Imputation and subset-based association analysis across different cancer types identifies multiple independent risk loci in the TERT-CLPTM1L region on chromosome 5p15.33. Human Molecular Genetics, 2014, 23, 6616-6633.	2.9	90
39	Joint associations of a polygenic risk score and environmental risk factors for breast cancer in the Breast Cancer Association Consortium. International Journal of Epidemiology, 2018, 47, 526-536.	1.9	88
40	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
41	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breastâ€“ovarian cancer susceptibility locus. Nature Communications, 2016, 7, 12675.	12.8	78
42	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
43	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 Consortiumâ€. Human Molecular Genetics, 2011, 20, 4693-4706.	2.9	71
44	Comparative Validation of Breast Cancer Risk Prediction Models and Projections for Future Risk Stratification. Journal of the National Cancer Institute, 2020, 112, 278-285.	6.3	61
45	Temporal Stability and Determinants of White Blood Cell DNA Methylation in the Breakthrough Generations Study. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 221-229.	2.5	60
46	Prognostic value of automated KI67 scoring in breast cancer: a centralised evaluation of 8088 patients from 10 study groups. Breast Cancer Research, 2016, 18, 104.	5.0	56
47	Chapter 1 Common Genetic Variation and Human Disease. Advances in Genetics, 2008, 62, 1-32.	1.8	55
48	Common non-synonymous SNPs associated with breast cancer susceptibility: findings from the Breast Cancer Association Consortium. Human Molecular Genetics, 2014, 23, 6096-6111.	2.9	53
49	Genome-wide association study of germline variants and breast cancer-specific mortality. British Journal of Cancer, 2019, 120, 647-657.	6.4	52
50	Fineâ€scale mapping of 8q24 locus identifies multiple independent risk variants for breast cancer. International Journal of Cancer, 2016, 139, 1303-1317.	5.1	51
51	Comparison of 6q25 Breast Cancer Hits from Asian and European Genome Wide Association Studies in the Breast Cancer Association Consortium (BCAC). PLoS ONE, 2012, 7, e42380.	2.5	51
52	MicroRNA Related Polymorphisms and Breast Cancer Risk. PLoS ONE, 2014, 9, e109973.	2.5	49
53	Combined Associations of a Polygenic Risk Score and Classical Risk Factors With Breast Cancer Risk. Journal of the National Cancer Institute, 2021, 113, 329-337.	6.3	45
54	Fine mapping of a region of chromosome 11q13 reveals multiple independent loci associated with risk of prostate cancer. Human Molecular Genetics, 2011, 20, 2869-2878.	2.9	43

#	Article	IF	Citations
55	Genetic Variants at Chromosomes 2q35, 5p12, 6q25.1, 10q26.13, and 16q12.1 Influence the Risk of Breast Cancer in Men. PLoS Genetics, 2011, 7, e1002290.	3.5	43
56	Genetic predisposition to ductal carcinoma in situ of the breast. Breast Cancer Research, 2016, 18, 22.	5.0	43
57	Prospective evaluation of a breast-cancer risk model integrating classical risk factors and polygenic risk in 15 cohorts from six countries. International Journal of Epidemiology, 2022, 50, 1897-1911.	1.9	43
58	Fine-mapping identifies two additional breast cancer susceptibility loci at 9q31.2. Human Molecular Genetics, 2015, 24, 2966-2984.	2.9	40
59	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
60	Investigation of geneâ€environment interactions between 47 newly identified breast cancer susceptibility loci and environmental risk factors. International Journal of Cancer, 2015, 136, E685-96.	5.1	34
61	Missense Variants in ATM in 26,101 Breast Cancer Cases and 29,842 Controls. Cancer Epidemiology Biomarkers and Prevention, 2010, 19, 2143-2151.	2.5	33
62	An intergenic risk locus containing an enhancer deletion in 2q35 modulates breast cancer risk by deregulating IGFBP5 expression. Human Molecular Genetics, 2016, 25, 3863-3876.	2.9	33
63	CYP3A Variation, Premenopausal Estrone Levels, and Breast Cancer Risk. Journal of the National Cancer Institute, 2012, 104, 657-669.	6.3	30
64	A network analysis to identify mediators of germline-driven differences in breast cancer prognosis. Nature Communications, 2020, 11, 312.	12.8	30
65	Genetic susceptibility to radiation-induced breast cancer after Hodgkin lymphoma. Blood, 2019, 133, 1130-1139.	1.4	29
66	Large-scale fine mapping of the HNF1B locus and prostate cancer risk. Human Molecular Genetics, 2011, 20, 3322-3329.	2.9	28
67	Cytochrome P450 Allele CYP3A7*1C Associates with Adverse Outcomes in Chronic Lymphocytic Leukemia, Breast, and Lung Cancer. Cancer Research, 2016, 76, 1485-1493.	0.9	28
68	RAD51B in Familial Breast Cancer. PLoS ONE, 2016, 11, e0153788.	2.5	26
69	Fine-Scale Mapping of the 4q24 Locus Identifies Two Independent Loci Associated with Breast Cancer Risk. Cancer Epidemiology Biomarkers and Prevention, 2015, 24, 1680-1691.	2.5	24
70	ABCB1 (MDR1)rs1045642 is associated with increased overall survival in plasma cell myeloma. Leukemia and Lymphoma, 2009, 50, 566-570.	1.3	23
71	Epigenome-wide association study for lifetime estrogen exposure identifies an epigenetic signature associated with breast cancer risk. Clinical Epigenetics, 2019, 11, 66.	4.1	21
72	Large-scale Analysis Demonstrates Familial Testicular Cancer to have Polygenic Aetiology. European Urology, 2018, 74, 248-252.	1.9	20

#	Article	IF	Citations
73	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
74	Highâ€tthroughput automated scoring of Ki67 in breast cancer tissue microarrays from the Breast Cancer Association Consortium. Journal of Pathology: Clinical Research, 2016, 2, 138-153.	3.0	19
75	Reply to â€œAssociations of CFHR1â€“CFHR3 deletion and a CFH SNP to age-related macular degeneration are not independentâ€• Nature Genetics, 2010, 42, 555-556.	21.4	18
76	No clinical utility of KRAS variant rs61764370 for ovarian or breast cancer. Gynecologic Oncology, 2016, 141, 386-401.	1.4	18
77	Multidrug resistance gene expression and ABCB1 SNPs in plasma cell myeloma. Leukemia Research, 2011, 35, 1457-1463.	0.8	17
78	9q31.2-rs865686 as a Susceptibility Locus for Estrogen Receptor-Positive Breast Cancer: Evidence from the Breast Cancer Association Consortium. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 1783-1791.	2.5	17
79	Common variants in breast cancer risk loci predispose to distinct tumor subtypes. Breast Cancer Research, 2022, 24, 2.	5.0	15
80	Genetic variation at CYP3A is associated with age at menarche and breast cancer risk: a case-control study. Breast Cancer Research, 2014, 16, R51.	5.0	14
81	Genetic variation in mitotic regulatory pathway genes is associated with breast tumor grade. Human Molecular Genetics, 2014, 23, 6034-6046.	2.9	12
82	Fine-Mapping of the 1p11.2 Breast Cancer Susceptibility Locus. PLoS ONE, 2016, 11, e0160316.	2.5	12
83	Common Susceptibility Loci for Male Breast Cancer. Journal of the National Cancer Institute, 2021, 113, 453-461.	6.3	12
84	Validation of loci at 2q14.2 and 15q21.3 as risk factors for testicular cancer. Oncotarget, 2018, 9, 12630-12638.	1.8	8
85	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
86	Estimating Causal Effects of Genetic Risk Variants for Breast Cancer Using Marker Data from Bilateral and Familial Cases. Cancer Epidemiology Biomarkers and Prevention, 2012, 21, 262-272.	2.5	6
87	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
88	CYP3A7*1C allele: linking premenopausal oestrone and progesterone levels with risk of hormone receptor-positive breast cancers. British Journal of Cancer, 2021, 124, 842-854.	6.4	5
89	rs2735383, located at a microRNA binding site in the 3â€™UTR of NBS1, is not associated with breast cancer risk. Scientific Reports, 2016, 6, 36874.	3.3	2
90	Germline HOXB13 mutations p.G84E and p.R217C do not confer an increased breast cancer risk. Scientific Reports, 2020, 10, 9688.	3.3	2

#	Article	IF	Citations
91	Genome-wide interaction analysis of menopausal hormone therapy use and breast cancer risk among 62,370 women. Scientific Reports, 2022, 12, 6199.	3.3	2
92	Genetic Determinants of Breast Cancer Risk in Childhood Cancer Survivors. Journal of the National Cancer Institute, 2017, 109, .	6.3	0