

Jonathan P Tyrer

List of Publications by Year in descending order

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Version: 2024-02-01

93
papers

17,023
citations

61687

45
h-index

38517

99
g-index

104
all docs

104
docs citations

104
times ranked

28718
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
2	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
3	Association analysis identifies 65 new breast cancer risk loci. <i>Nature</i> , 2017, 551, 92-94.	13.7	1,099
4	Polygenic Risk Scores for Prediction of Breast Cancer and Breast Cancer Subtypes. <i>American Journal of Human Genetics</i> , 2019, 104, 21-34.	2.6	711
5	Association analyses of more than 140,000 men identify 63 new prostate cancer susceptibility loci. <i>Nature Genetics</i> , 2018, 50, 928-936.	9.4	652
6	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
7	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
8	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.	9.4	493
9	Prediction of Breast Cancer Risk Based on Profiling With Common Genetic Variants. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	428
10	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	9.4	426
11	A meta-analysis of 87,040 individuals identifies 23 new susceptibility loci for prostate cancer. <i>Nature Genetics</i> , 2014, 46, 1103-1109.	9.4	408
12	Identification of 12 new susceptibility loci for different histotypes of epithelial ovarian cancer. <i>Nature Genetics</i> , 2017, 49, 680-691.	9.4	356
13	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
14	GWAS meta-analysis and replication identifies three new susceptibility loci for ovarian cancer. <i>Nature Genetics</i> , 2013, 45, 362-370.	9.4	326
15	Heterogeneity of Breast Cancer Associations with Five Susceptibility Loci by Clinical and Pathological Characteristics. <i>PLoS Genetics</i> , 2008, 4, e1000054.	1.5	315
16	Germline Mutations in the BRIP1, BARD1, PALB2, and NBN Genes in Women With Ovarian Cancer. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	311
17	Identification of ten variants associated with risk of estrogen-receptor-negative breast cancer. <i>Nature Genetics</i> , 2017, 49, 1767-1778.	9.4	289
18	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	9.4	286

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19	Contribution of Germline Mutations in the <i>RAD51B</i> , <i>RAD51C</i> , and <i>RAD51D</i> Genes to Ovarian Cancer in the Population. <i>Journal of Clinical Oncology</i> , 2015, 33, 2901-2907.	0.8	266
20	Identification of six new susceptibility loci for invasive epithelial ovarian cancer. <i>Nature Genetics</i> , 2015, 47, 164-171.	9.4	221
21	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.	2.6	201
22	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018, 9, 3166.	5.8	178
23	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.	7.7	157
24	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.	0.8	152
25	A genome wide association study (GWAS) providing evidence of an association between common genetic variants and late radiotherapy toxicity. <i>Radiotherapy and Oncology</i> , 2014, 111, 178-185.	0.3	128
26	Fine-mapping of 150 breast cancer risk regions identifies 191 likely target genes. <i>Nature Genetics</i> , 2020, 52, 56-73.	9.4	120
27	The contribution of deleterious germline mutations in <i>BRCA1</i> , <i>BRCA2</i> and the mismatch repair genes to ovarian cancer in the population. <i>Human Molecular Genetics</i> , 2014, 23, 4703-4709.	1.4	112
28	Association of vitamin D levels and risk of ovarian cancer: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 1619-1630.	0.9	111
29	Fine-Scale Mapping of the <i>FGFR2</i> Breast Cancer Risk Locus: Putative Functional Variants Differentially Bind <i>FOXA1</i> and <i>E2F1</i> . <i>American Journal of Human Genetics</i> , 2013, 93, 1046-1060.	2.6	98
30	Replication of Genetic Polymorphisms Reported to Be Associated with Taxane-Related Sensory Neuropathy in Patients with Early Breast Cancer Treated with Paclitaxel. <i>Clinical Cancer Research</i> , 2014, 20, 2466-2475.	3.2	91
31	Shared heritability and functional enrichment across six solid cancers. <i>Nature Communications</i> , 2019, 10, 431.	5.8	88
32	European polygenic risk score for prediction of breast cancer shows similar performance in Asian women. <i>Nature Communications</i> , 2020, 11, 3833.	5.8	88
33	Genome-wide significant risk associations for mucinous ovarian carcinoma. <i>Nature Genetics</i> , 2015, 47, 888-897.	9.4	78
34	Functional mechanisms underlying pleiotropic risk alleles at the 19p13.1 breast-ovarian cancer susceptibility locus. <i>Nature Communications</i> , 2016, 7, 12675.	5.8	78
35	Five endometrial cancer risk loci identified through genome-wide association analysis. <i>Nature Genetics</i> , 2016, 48, 667-674.	9.4	77
36	Adult body mass index and risk of ovarian cancer by subtype: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2016, 45, 884-895.	0.9	71

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37	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.	2.7	69
38	Fine scale mapping of the breast cancer 16q12 locus. <i>Human Molecular Genetics</i> , 2010, 19, 2507-2515.	1.4	68
39	Genetic Risk Score Mendelian Randomization Shows that Obesity Measured as Body Mass Index, but not Waist:Hip Ratio, Is Causal for Endometrial Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 1503-1510.	1.1	64
40	Cis-eQTL analysis and functional validation of candidate susceptibility genes for high-grade serous ovarian cancer. <i>Nature Communications</i> , 2015, 6, 8234.	5.8	63
41	CYP19A1 fine-mapping and Mendelian randomization: estradiol is causal for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2016, 23, 77-91.	1.6	62
42	Genetic overlap between endometriosis and endometrial cancer: evidence from cross-disease genetic correlation and GWAS meta-analyses. <i>Cancer Medicine</i> , 2018, 7, 1978-1987.	1.3	62
43	Identification of Novel Genetic Markers of Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2015, 107, .	3.0	56
44	Fine-mapping of the HNF1B multicancer locus identifies candidate variants that mediate endometrial cancer risk. <i>Human Molecular Genetics</i> , 2015, 24, 1478-1492.	1.4	50
45	Genetic Data from Nearly 63,000 Women of European Descent Predicts DNA Methylation Biomarkers and Epithelial Ovarian Cancer Risk. <i>Cancer Research</i> , 2019, 79, 505-517.	0.4	49
46	Association Between a Germline OCA2 Polymorphism at Chromosome 15q13.1 and Estrogen Receptor-Negative Breast Cancer Survival. <i>Journal of the National Cancer Institute</i> , 2010, 102, 650-662.	3.0	48
47	Common Genetic Variation In Cellular Transport Genes and Epithelial Ovarian Cancer (EOC) Risk. <i>PLoS ONE</i> , 2015, 10, e0128106.	1.1	44
48	Germline whole exome sequencing and large-scale replication identifies FANCM as a likely high grade serous ovarian cancer susceptibility gene. <i>Oncotarget</i> , 2017, 8, 50930-50940.	0.8	43
49	Cell-type-specific enrichment of risk-associated regulatory elements at ovarian cancer susceptibility loci. <i>Human Molecular Genetics</i> , 2015, 24, 3595-3607.	1.4	40
50	Evaluation of polygenic risk scores for ovarian cancer risk prediction in a prospective cohort study. <i>Journal of Medical Genetics</i> , 2018, 55, 546-554.	1.5	38
51	Evidence of a genetic link between endometriosis and ovarian cancer. <i>Fertility and Sterility</i> , 2016, 105, 35-43.e10.	0.5	37
52	Meta-analysis of genome-wide association studies identifies common susceptibility polymorphisms for colorectal and endometrial cancer near SH2B3 and TSHZ1. <i>Scientific Reports</i> , 2015, 5, 17369.	1.6	35
53	Mendelian randomization analyses suggest a role for cholesterol in the development of endometrial cancer. <i>International Journal of Cancer</i> , 2021, 148, 307-319.	2.3	35
54	Genome-wide Analysis Identifies Novel Loci Associated with Ovarian Cancer Outcomes: Findings from the Ovarian Cancer Association Consortium. <i>Clinical Cancer Research</i> , 2015, 21, 5264-5276.	3.2	33

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55	Comprehensive epithelial tubo-ovarian cancer risk prediction model incorporating genetic and epidemiological risk factors. <i>Journal of Medical Genetics</i> , 2022, 59, 632-643.	1.5	33
56	Reducing overdiagnosis by polygenic risk-stratified screening: findings from the Finnish section of the ERSPC. <i>British Journal of Cancer</i> , 2015, 113, 1086-1093.	2.9	32
57	The admixture maximum likelihood test: a novel experiment-wise test of association between disease and multiple SNPs. <i>Genetic Epidemiology</i> , 2006, 30, 636-643.	0.6	31
58	Network-Based Integration of GWAS and Gene Expression Identifies a <i>HOX</i> -Centric Network Associated with Serous Ovarian Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1574-1584.	1.1	28
59	Genome-wide association studies identify susceptibility loci for epithelial ovarian cancer in east Asian women. <i>Gynecologic Oncology</i> , 2019, 153, 343-355.	0.6	28
60	Common germline polymorphisms associated with breast cancer-specific survival. <i>Breast Cancer Research</i> , 2015, 17, 58.	2.2	26
61	Population-based targeted sequencing of 54 candidate genes identifies <i>PALB2</i> as a susceptibility gene for high-grade serous ovarian cancer. <i>Journal of Medical Genetics</i> , 2021, 58, 305-313.	1.5	26
62	Comprehensive genetic assessment of the <i>ESR1</i> locus identifies a risk region for endometrial cancer. <i>Endocrine-Related Cancer</i> , 2015, 22, 851-861.	1.6	25
63	Common Genetic Variation in Circadian Rhythm Genes and Risk of Epithelial Ovarian Cancer (EOC). <i>Journal of Genetics and Genome Research</i> , 2015, 2, .	0.3	25
64	Common variants at the <i>CHEK2</i> gene locus and risk of epithelial ovarian cancer. <i>Carcinogenesis</i> , 2015, 36, 1341-1353.	1.3	24
65	Enrichment of putative PAX8 target genes at serous epithelial ovarian cancer susceptibility loci. <i>British Journal of Cancer</i> , 2017, 116, 524-535.	2.9	23
66	Polygenic risk modeling for prediction of epithelial ovarian cancer risk. <i>European Journal of Human Genetics</i> , 2022, 30, 349-362.	1.4	23
67	Epithelial-Mesenchymal Transition (EMT) Gene Variants and Epithelial Ovarian Cancer (EOC) Risk. <i>Genetic Epidemiology</i> , 2015, 39, 689-697.	0.6	22
68	Functional Analysis and Fine Mapping of the 9p22.2 Ovarian Cancer Susceptibility Locus. <i>Cancer Research</i> , 2019, 79, 467-481.	0.4	22
69	Assessing the genetic architecture of epithelial ovarian cancer histological subtypes. <i>Human Genetics</i> , 2016, 135, 741-756.	1.8	19
70	A case-only study to identify genetic modifiers of breast cancer risk for BRCA1/BRCA2 mutation carriers. <i>Nature Communications</i> , 2021, 12, 1078.	5.8	19
71	Identification of novel epithelial ovarian cancer loci in women of African ancestry. <i>International Journal of Cancer</i> , 2020, 146, 2987-2998.	2.3	18
72	Evaluating the ovarian cancer gonadotropin hypothesis: A candidate gene study. <i>Gynecologic Oncology</i> , 2015, 136, 542-548.	0.6	15

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73	Adult height is associated with increased risk of ovarian cancer: a Mendelian randomisation study. <i>British Journal of Cancer</i> , 2018, 118, 1123-1129.	2.9	15
74	The admixture maximum likelihood test to test for association between rare variants and disease phenotypes. <i>BMC Bioinformatics</i> , 2013, 14, 177.	1.2	14
75	Ovarian Cancer Risk Variants Are Enriched in Histotype-Specific Enhancers and Disrupt Transcription Factor Binding Sites. <i>American Journal of Human Genetics</i> , 2020, 107, 622-635.	2.6	14
76	A comprehensive gene-environment interaction analysis in Ovarian Cancer using genome-wide significant common variants. <i>International Journal of Cancer</i> , 2019, 144, 2192-2205.	2.3	12
77	Assessment of Multifactor Gene-Environment Interactions and Ovarian Cancer Risk: Candidate Genes, Obesity, and Hormone-Related Risk Factors. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 780-790.	1.1	10
78	Detecting rare copy number variants from Illumina genotyping arrays with the CamCNV pipeline: Segmentation of Δ scores improves detection and reliability. <i>Genetic Epidemiology</i> , 2021, 45, 237-248.	0.6	10
79	Investigation of Exomic Variants Associated with Overall Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2016, 25, 446-454.	1.1	9
80	Variants in genes encoding small GTPases and association with epithelial ovarian cancer susceptibility. <i>PLoS ONE</i> , 2018, 13, e0197561.	1.1	9
81	Genome-Wide Association Study for Ovarian Cancer Susceptibility Using Pooled DNA. <i>Twin Research and Human Genetics</i> , 2012, 15, 615-623.	0.3	8
82	Robust Tests for Additive Gene-Environment Interaction in Case-Control Studies Using Gene-Environment Independence. <i>American Journal of Epidemiology</i> , 2018, 187, 366-377.	1.6	8
83	The effect of rare variants on inflation of the test statistics in case-control analyses. <i>BMC Bioinformatics</i> , 2015, 16, 53.	1.2	7
84	Analyses of germline variants associated with ovarian cancer survival identify functional candidates at the 1q22 and 19p12 outcome loci. <i>Oncotarget</i> , 2017, 8, 64670-64684.	0.8	7
85	Pleiotropy-guided transcriptome imputation from normal and tumor tissues identifies candidate susceptibility genes for breast and ovarian cancer. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100042.	1.0	6
86	Large-scale cross-cancer fine-mapping of the 5p15.33 region reveals multiple independent signals. <i>Human Genetics and Genomics Advances</i> , 2021, 2, 100041.	1.0	6
87	Rare germline copy number variants (CNVs) and breast cancer risk. <i>Communications Biology</i> , 2022, 5, 65.	2.0	6
88	Identification of a Locus Near <i>ULK1</i> Associated With Progression-Free Survival in Ovarian Cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2021, 30, 1669-1680.	1.1	5
89	Assessment of variation in immunosuppressive pathway genes reveals <i>TGFB2</i> to be associated with risk of clear cell ovarian cancer. <i>Oncotarget</i> , 2016, 7, 69097-69110.	0.8	5
90	Genomic risk prediction of coronary artery disease in women with breast cancer: a prospective cohort study. <i>Breast Cancer Research</i> , 2021, 23, 94.	2.2	4

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91	rs495139 in the TYMS-ENOSF1 Region and Risk of Ovarian Carcinoma of Mucinous Histology. International Journal of Molecular Sciences, 2018, 19, 2473.	1.8	3
92	Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. American Journal of Human Genetics, 2022, 109, 116-135.	2.6	3
93	chromMAGMA: regulatory element-centric interrogation of risk variants. Life Science Alliance, 2022, 5, e202201446.	1.3	1