

John R B Perry

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

108
papers

18,089
citations

57
h-index

117
g-index

117
ext. papers

24,579
ext. citations

19.1
avg, IF

5.61
L-index

#	Paper	IF	Citations
108	Using genetic variation to disentangle the complex relationship between food intake and health outcomes. <i>PLoS Genetics</i> , 2022 , 18, e1010162	6	0
107	MC3R links nutritional state to childhood growth and the timing of puberty. <i>Nature</i> , 2021 , 599, 436-441	50.4	9
106	Serum Estradiol and 20 Site-Specific Cancers in Women: Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	2
105	A Polygenic Risk Score to Predict Future Adult Short Stature Among Children. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 , 106, 1918-1928	5.6	5
104	Response to Comment on "Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior". <i>Science</i> , 2021 , 371,	33.3	2
103	Immune cells lacking Y chromosome show dysregulation of autosomal gene expression. <i>Cellular and Molecular Life Sciences</i> , 2021 , 78, 4019-4033	10.3	13
102	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021 , 53, 663-674	31.3	20
101	Prepubertal Dietary and Plasma Phospholipid Fatty Acids Related to Puberty Timing: Longitudinal Cohort and Mendelian Randomization Analyses. <i>Nutrients</i> , 2021 , 13,	6.7	2
100	The CD94/NKG2A inhibitory receptor educates uterine NK cells to optimize pregnancy outcomes in humans and mice. <i>Immunity</i> , 2021 , 54, 1231-1244.e4	32.3	13
99	GIGYF1 loss of function is associated with clonal mosaicism and adverse metabolic health. <i>Nature Communications</i> , 2021 , 12, 4178	17.4	3
98	Genetic association study of childhood aggression across raters, instruments, and age. <i>Translational Psychiatry</i> , 2021 , 11, 413	8.6	7
97	Identification of a unique epigenetic profile in women with diminished ovarian reserve. <i>Fertility and Sterility</i> , 2021 , 115, 732-741	4.8	3
96	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
95	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021 , 596, 393-397	50.4	28
94	Continuity of Genetic Risk for Aggressive Behavior Across the Life-Course. <i>Behavior Genetics</i> , 2021 , 51, 592-606	3.2	2
93	Genomic and phenotypic insights from an atlas of genetic effects on DNA methylation. <i>Nature Genetics</i> , 2021 , 53, 1311-1321	36.3	27
92	Identification of rare loss of function genetic variation regulating body fat distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021 ,	5.6	1

91	A distinctive epigenetic ageing profile in human granulosa cells. <i>Human Reproduction</i> , 2020 , 35, 1332-1345	5.7	9
90	Genomic analysis of male puberty timing highlights shared genetic basis with hair colour and lifespan. <i>Nature Communications</i> , 2020 , 11, 1536	17.4	12
89	Using human genetics to understand the disease impacts of testosterone in men and women. <i>Nature Medicine</i> , 2020 , 26, 252-258	50.5	121
88	The NEMP family supports metazoan fertility and nuclear envelope stiffness. <i>Science Advances</i> , 2020 , 6, eabb4591	14.3	3
87	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. <i>Science</i> , 2019 , 365,	33.3	139
86	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. <i>Science Advances</i> , 2019 , 5, eaaw3095	14.3	39
85	Voice break in boys-temporal relations with other pubertal milestones and likely causal effects of BMI. <i>Human Reproduction</i> , 2019 , 34, 1514-1522	5.7	14
84	Human Gain-of-Function MC4R Variants Show Signaling Bias and Protect against Obesity. <i>Cell</i> , 2019 , 177, 597-607.e9	56.2	113
83	GWAS of mosaic loss of chromosome Y highlights genetic effects on blood cell differentiation. <i>Nature Communications</i> , 2019 , 10, 4719	17.4	18
82	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. <i>Nature Communications</i> , 2019 , 10, 4857	17.4	34
81	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019 , 51, 452-469	36.3	44
80	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019 , 575, 652-657	50.4	83
79	Genome studies must account for history-Response. <i>Science</i> , 2019 , 366, 1461-1462	33.3	4
78	Epigenome-Wide Association Study of Incident Type 2 Diabetes in a British Population: EPIC-Norfolk Study. <i>Diabetes</i> , 2019 , 68, 2315-2326	0.9	40
77	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018 , 27, 1664-1674	5.6	20
76	Heritability enrichment of specifically expressed genes identifies disease-relevant tissues and cell types. <i>Nature Genetics</i> , 2018 , 50, 621-629	36.3	400
75	GWAS of epigenetic aging rates in blood reveals a critical role for TERT. <i>Nature Communications</i> , 2018 , 9, 387	17.4	106
74	Genome-wide association study for risk taking propensity indicates shared pathways with body mass index. <i>Communications Biology</i> , 2018 , 1, 36	6.7	30

73	Genetic Determinants of Circulating Estrogen Levels and Evidence of a Causal Effect of Estradiol on Bone Density in Men. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018 , 103, 991-1004	5.6	37
72	Gene discovery and polygenic prediction from a genome-wide association study of educational attainment in 1.1 million individuals. <i>Nature Genetics</i> , 2018 , 50, 1112-1121	36.3	950
71	Identification of nine new susceptibility loci for endometrial cancer. <i>Nature Communications</i> , 2018 , 9, 3166	17.4	70
70	GWAS of lifetime cannabis use reveals new risk loci, genetic overlap with psychiatric traits, and a causal influence of schizophrenia. <i>Nature Neuroscience</i> , 2018 , 21, 1161-1170	25.5	270
69	Associations of vomiting and antiemetic use in pregnancy with levels of circulating GDF15 early in the second trimester: A nested case-control study. <i>Wellcome Open Research</i> , 2018 , 3, 123	4.8	21
68	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	36.3	186
67	Exploring the genetic correlations of antisocial behaviour and life history traits. <i>BJPsych Open</i> , 2018 , 4, 467-470	5	8
66	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. <i>PLoS Genetics</i> , 2018 , 14, e1007813	6	166
65	Association of Genetic Variants Related to Gluteofemoral vs Abdominal Fat Distribution With Type 2 Diabetes, Coronary Disease, and Cardiovascular Risk Factors. <i>JAMA - Journal of the American Medical Association</i> , 2018 , 320, 2553-2563	27.4	78
64	Association of Genetically Enhanced Lipoprotein Lipase-Mediated Lipolysis and Low-Density Lipoprotein Cholesterol-Lowering Alleles With Risk of Coronary Disease and Type 2 Diabetes. <i>JAMA Cardiology</i> , 2018 , 3, 957-966	16.2	30
63	Elucidating the genetic architecture of reproductive ageing in the Japanese population. <i>Nature Communications</i> , 2018 , 9, 1977	17.4	28
62	Elucidating the genetic basis of social interaction and isolation. <i>Nature Communications</i> , 2018 , 9, 2457	17.4	81
61	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017 , 542, 186-190	50.4	412
60	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	36.3	257
59	Genome-wide association study meta-analysis for quantitative ultrasound parameters of bone identifies five novel loci for broadband ultrasound attenuation. <i>Human Molecular Genetics</i> , 2017 , 26, 2791-2802	5.6	20
58	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017 , 100, 865-884	11	74
57	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017 , 66, 2888-2902	29.0	414
56	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. <i>Nature Genetics</i> , 2017 , 49, 674-679	36.3	70

55	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017 , 66, 2019-2032	0.9	29
54	Genome-Wide Association Studies of a Broad Spectrum of Antisocial Behavior. <i>JAMA Psychiatry</i> , 2017 , 74, 1242-1250	14.5	124
53	Identifying genetic variants that affect viability in large cohorts. <i>PLoS Biology</i> , 2017 , 15, e2002458	9.7	49
52	Dissecting Causal Pathways Using Mendelian Randomization with Summarized Genetic Data: Application to Age at Menarche and Risk of Breast Cancer. <i>Genetics</i> , 2017 , 207, 481-487	4	91
51	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. <i>Scientific Reports</i> , 2017 , 7, 11008	4.9	49
50	Replication and characterization of and genes on human behavior. <i>Heliyon</i> , 2017 , 3, e00349	3.6	61
49	Integrative genomic analysis implicates limited peripheral adipose storage capacity in the pathogenesis of human insulin resistance. <i>Nature Genetics</i> , 2017 , 49, 17-26	36.3	312
48	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017 , 4, 170179	8.2	22
47	Genome-wide association study with 1000 genomes imputation identifies signals for nine sex hormone-related phenotypes. <i>European Journal of Human Genetics</i> , 2016 , 24, 284-90	5.3	61
46	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016 , 48, 1462-1472	36.3	198
45	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016 , 7, 10495	17.4	180
44	A Robust Example of Collider Bias in a Genetic Association Study. <i>American Journal of Human Genetics</i> , 2016 , 98, 392-3	11	60
43	Investigating the Causal Relationship of C-Reactive Protein with 32 Complex Somatic and Psychiatric Outcomes: A Large-Scale Cross-Consortium Mendelian Randomization Study. <i>PLoS Medicine</i> , 2016 , 13, e1001976	11.6	100
42	Genetic Predisposition to an Impaired Metabolism of the Branched-Chain Amino Acids and Risk of Type 2 Diabetes: A Mendelian Randomisation Analysis. <i>PLoS Medicine</i> , 2016 , 13, e1002179	11.6	214
41	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016 , 536, 41-47	50.4	704
40	Events in Early Life are Associated with Female Reproductive Ageing: A UK Biobank Study. <i>Scientific Reports</i> , 2016 , 6, 24710	4.9	31
39	Physical and neurobehavioral determinants of reproductive onset and success. <i>Nature Genetics</i> , 2016 , 48, 617-623	36.3	118
38	Identification of Common Genetic Variants Influencing Spontaneous Dizygotic Twinning and Female Fertility. <i>American Journal of Human Genetics</i> , 2016 , 98, 898-908	11	66

37	Genome-wide association study identifies common and low-frequency variants at the AMH gene locus that strongly predict serum AMH levels in males. <i>Human Molecular Genetics</i> , 2016 , 25, 382-8	5.6	12
36	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. <i>Nature Genetics</i> , 2016 , 48, 1303-1312	36.3	51
35	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016 , 538, 248-252	52.4	266
34	Association Between Low-Density Lipoprotein Cholesterol-Lowering Genetic Variants and Risk of Type 2 Diabetes: A Meta-analysis. <i>JAMA - Journal of the American Medical Association</i> , 2016 , 316, 1383-1391	37.4	225
33	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015 , 523, 459-462	50.4	119
32	Puberty timing associated with diabetes, cardiovascular disease and also diverse health outcomes in men and women: the UK Biobank study. <i>Scientific Reports</i> , 2015 , 5, 11208	4.9	254
31	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. <i>Human Molecular Genetics</i> , 2015 , 24, 1504-12	5.6	7
30	Partitioning heritability by functional annotation using genome-wide association summary statistics. <i>Nature Genetics</i> , 2015 , 47, 1228-35	36.3	1143
29	An atlas of genetic correlations across human diseases and traits. <i>Nature Genetics</i> , 2015 , 47, 1236-41	36.3	1841
28	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015 , 47, 1294-1303	36.3	226
27	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015 , 6, 8464	17.4	203
26	Season of birth is associated with birth weight, pubertal timing, adult body size and educational attainment: a UK Biobank study. <i>Heliyon</i> , 2015 , 1, e00031	3.6	31
25	Molecular insights into the aetiology of female reproductive ageing. <i>Nature Reviews Endocrinology</i> , 2015 , 11, 725-34	15.2	47
24	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015 , 47, 1114-20	36.3	522
23	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015 , 47, 1415-25	36.3	292
22	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. <i>Nature Communications</i> , 2015 , 6, 8842	17.4	75
21	Evidence of a Causal Association Between Insulinemia and Endometrial Cancer: A Mendelian Randomization Analysis. <i>Journal of the National Cancer Institute</i> , 2015 , 107,	9.7	96
20	Associations between Potentially Modifiable Risk Factors and Alzheimer Disease: A Mendelian Randomization Study. <i>PLoS Medicine</i> , 2015 , 12, e1001841; discussion e1001841	11.6	115

19	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015 , 6, 5681	17.4	56
18	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015 , 6, 7756	17.4	23
17	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015 , 518, 187-196	50.4	920
16	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015 , 518, 197-206	50.4	2687
15	Genome-wide association study of sexual maturation in males and females highlights a role for body mass and menarche loci in male puberty. <i>Human Molecular Genetics</i> , 2014 , 23, 4452-64	5.6	66
14	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. <i>Nature Communications</i> , 2014 , 5, 4871	17.4	46
13	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
12	Genetic evidence for a normal-weight "metabolically obese" phenotype linking insulin resistance, hypertension, coronary artery disease, and type 2 diabetes. <i>Diabetes</i> , 2014 , 63, 4369-77	0.9	131
11	A genome-wide association study of early menopause and the combined impact of identified variants. <i>Human Molecular Genetics</i> , 2013 , 22, 1465-72	5.6	82
10	Genome-wide meta-analysis of common variant differences between men and women. <i>Human Molecular Genetics</i> , 2012 , 21, 4805-15	5.6	24
9	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012 , 44, 260-8	36.3	243
8	A genome-wide association meta-analysis of circulating sex hormone-binding globulin reveals multiple Loci implicated in sex steroid hormone regulation. <i>PLoS Genetics</i> , 2012 , 8, e1002805	6	116
7	Stratifying type 2 diabetes cases by BMI identifies genetic risk variants in LAMA1 and enrichment for risk variants in lean compared to obese cases. <i>PLoS Genetics</i> , 2012 , 8, e1002741	6	162
6	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. <i>Human Molecular Genetics</i> , 2010 , 19, 535-44	5.6	150
5	Interrogating type 2 diabetes genome-wide association data using a biological pathway-based approach. <i>Diabetes</i> , 2009 , 58, 1463-7	0.9	87
4	Circulating beta-carotene levels and type 2 diabetes-cause or effect?. <i>Diabetologia</i> , 2009 , 52, 2117-21	10.3	21
3	Meta-analysis of genome-wide association data identifies two loci influencing age at menarche. <i>Nature Genetics</i> , 2009 , 41, 648-50	36.3	223
2	New gene variants alter type 2 diabetes risk predominantly through reduced beta-cell function. <i>Current Opinion in Clinical Nutrition and Metabolic Care</i> , 2008 , 11, 371-7	3.8	86

1 Elucidating the genetic architecture underlying IGF1 levels and its impact on genomic instability and cancer risk. *Wellcome Open Research*, 6, 20

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