

Paul F. O'Reilly

List of Publications by Year in descending order

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Version: 2024-02-01

87
papers

20,189
citations

36203

51
h-index

48187

88
g-index

109
all docs

109
docs citations

109
times ranked

29685
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018, 50, 668-681.	9.4	2,224
2	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
3	Common genetic determinants of vitamin D insufficiency: a genome-wide association study. <i>Lancet</i> , The, 2010, 376, 180-188.	6.3	1,385
4	PRSice: Polygenic Risk Score software. <i>Bioinformatics</i> , 2015, 31, 1466-1468.	1.8	1,109
5	Genome-wide association study identifies eight loci associated with blood pressure. <i>Nature Genetics</i> , 2009, 41, 666-676.	9.4	1,104
6	PRSice-2: Polygenic Risk Score software for biobank-scale data. <i>GigaScience</i> , 2019, 8, .	3.3	940
7	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
8	Tutorial: a guide to performing polygenic risk score analyses. <i>Nature Protocols</i> , 2020, 15, 2759-2772.	5.5	918
9	Identification of seven loci affecting mean telomere length and their association with disease. <i>Nature Genetics</i> , 2013, 45, 422-427.	9.4	808
10	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
11	Genome-wide association analysis identifies novel blood pressure loci and offers biological insights into cardiovascular risk. <i>Nature Genetics</i> , 2017, 49, 403-415.	9.4	492
12	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
13	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	13.7	401
14	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
15	MultiPhen: Joint Model of Multiple Phenotypes Can Increase Discovery in GWAS. <i>PLoS ONE</i> , 2012, 7, e34861.	1.1	339
16	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
17	Using genetic data to strengthen causal inference in observational research. <i>Nature Reviews Genetics</i> , 2018, 19, 566-580.	7.7	298
18	Genome-wide association study in 79,366 European-ancestry individuals informs the genetic architecture of 25-hydroxyvitamin D levels. <i>Nature Communications</i> , 2018, 9, 260.	5.8	295

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19	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
20	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 7119-7124.	3.3	258
21	A Bivariate Genome-Wide Approach to Metabolic Syndrome. <i>Diabetes</i> , 2011, 60, 1329-1339.	0.3	226
22	Variants in ADCY5 and near CCNL1 are associated with fetal growth and birth weight. <i>Nature Genetics</i> , 2010, 42, 430-435.	9.4	223
23	KLB is associated with alcohol drinking, and its gene product Klotho is necessary for FGF21 regulation of alcohol preference. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 14372-14377.	3.3	208
24	Long-term Leisure-time Physical Activity and Serum Metabolome. <i>Circulation</i> , 2013, 127, 340-348.	1.6	193
25	Comparing Within- and Between-Family Polygenic Score Prediction. <i>American Journal of Human Genetics</i> , 2019, 105, 351-363.	2.6	190
26	An Examination of Polygenic Score Risk Prediction in Individuals With First-Episode Psychosis. <i>Biological Psychiatry</i> , 2017, 81, 470-477.	0.7	176
27	Machine Learning to Predict Mortality and Critical Events in a Cohort of Patients With COVID-19 in New York City: Model Development and Validation. <i>Journal of Medical Internet Research</i> , 2020, 22, e24018.	2.1	174
28	Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource study. <i>Human Molecular Genetics</i> , 2011, 20, 2273-2284.	1.4	168
29	Phenome-wide analysis of genome-wide polygenic scores. <i>Molecular Psychiatry</i> , 2016, 21, 1188-1193.	4.1	154
30	Predicting educational achievement from DNA. <i>Molecular Psychiatry</i> , 2017, 22, 267-272.	4.1	137
31	The Genetics of the Mood Disorder Spectrum: Genome-wide Association Analyses of More Than 185,000 Cases and 439,000 Controls. <i>Biological Psychiatry</i> , 2020, 88, 169-184.	0.7	137
32	Portability of 245 polygenic scores when derived from the UK Biobank and applied to 9 ancestry groups from the same cohort. <i>American Journal of Human Genetics</i> , 2022, 109, 12-23.	2.6	136
33	Genetic Determinants of Height Growth Assessed Longitudinally from Infancy to Adulthood in the Northern Finland Birth Cohort 1966. <i>PLoS Genetics</i> , 2009, 5, e1000409.	1.5	131
34	Common variants at 12q15 and 12q24 are associated with infant head circumference. <i>Nature Genetics</i> , 2012, 44, 532-538.	9.4	130
35	Lumbar disc degeneration is linked to a carbohydrate sulfotransferase 3 variant. <i>Journal of Clinical Investigation</i> , 2013, 123, 4909-4917.	3.9	126
36	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123

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37	Genome-wide gene-environment analyses of major depressive disorder and reported lifetime traumatic experiences in UK Biobank. <i>Molecular Psychiatry</i> , 2020, 25, 1430-1446.	4.1	116
38	Translating genome-wide association findings into new therapeutics for psychiatry. <i>Nature Neuroscience</i> , 2016, 19, 1392-1396.	7.1	115
39	Multivariate simulation framework reveals performance of multi-trait GWAS methods. <i>Scientific Reports</i> , 2017, 7, 38837.	1.6	100
40	Detailed metabolic and genetic characterization reveals new associations for 30 known lipid loci. <i>Human Molecular Genetics</i> , 2012, 21, 1444-1455.	1.4	89
41	Causal Effect of Plasminogen Activator Inhibitor Type 1 on Coronary Heart Disease. <i>Journal of the American Heart Association</i> , 2017, 6, .	1.6	89
42	The Genetic Architecture of Depression in Individuals of East Asian Ancestry. <i>JAMA Psychiatry</i> , 2021, 78, 1258.	6.0	88
43	Does Childhood Trauma Moderate Polygenic Risk for Depression? A Meta-analysis of 5765 Subjects From the Psychiatric Genomics Consortium. <i>Biological Psychiatry</i> , 2018, 84, 138-147.	0.7	87
44	Genomics of body fat percentage may contribute to sex bias in anorexia nervosa. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 428-438.	1.1	87
45	Common genetic variants regulating ADD3 gene expression alter biliary atresia risk. <i>Journal of Hepatology</i> , 2013, 59, 1285-1291.	1.8	84
46	Common variation near ROBO2 is associated with expressive vocabulary in infancy. <i>Nature Communications</i> , 2014, 5, 4831.	5.8	82
47	Causal Associations Between Modifiable Risk Factors and the Alzheimer's Phenome. <i>Annals of Neurology</i> , 2021, 89, 54-65.	2.8	82
48	Confounding between recombination and selection, and the Ped/Pop method for detecting selection. <i>Genome Research</i> , 2008, 18, 1304-1313.	2.4	81
49	Evidence for gene-environment correlation in child feeding: Links between common genetic variation for BMI in children and parental feeding practices. <i>PLoS Genetics</i> , 2018, 14, e1007757.	1.5	67
50	Genome-Wide Association Study Reveals Multiple Loci Associated with Primary Tooth Development during Infancy. <i>PLoS Genetics</i> , 2010, 6, e1000856.	1.5	64
51	Genetic correlations of psychiatric traits with body composition and glycemic traits are sex- and age-dependent. <i>Nature Communications</i> , 2019, 10, 5765.	5.8	59
52	Fregene: Simulation of realistic sequence-level data in populations and ascertained samples. <i>BMC Bioinformatics</i> , 2008, 9, 364.	1.2	57
53	Rsu1 regulates ethanol consumption in <i>Drosophila</i> and humans. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E4085-93.	3.3	57
54	Association of Polygenic Risk for Attention-Deficit/Hyperactivity Disorder With Co-occurring Traits and Disorders. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2018, 3, 635-643.	1.1	57

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55	Retrospective cohort study of clinical characteristics of 2199 hospitalised patients with COVID-19 in New York City. <i>BMJ Open</i> , 2020, 10, e040736.	0.8	50
56	Hospitalised COVID-19 patients of the Mount Sinai Health System: a retrospective observational study using the electronic medical records. <i>BMJ Open</i> , 2020, 10, e040441.	0.8	48
57	Association of polygenic score for major depression with response to lithium in patients with bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 2457-2470.	4.1	44
58	The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645.	1.1	43
59	Body composition in anorexia nervosa: Meta-analysis and meta-regression of cross-sectional and longitudinal studies. <i>International Journal of Eating Disorders</i> , 2019, 52, 1205-1223.	2.1	37
60	Evolutionary and functional impact of common polymorphic inversions in the human genome. <i>Nature Communications</i> , 2019, 10, 4222.	5.8	34
61	Genome-Wide Polygenic Scores Predict Reading Performance Throughout the School Years. <i>Scientific Studies of Reading</i> , 2017, 21, 334-349.	1.3	32
62	Identifying the Common Genetic Basis of Antidepressant Response. <i>Biological Psychiatry Global Open Science</i> , 2022, 2, 115-126.	1.0	31
63	Prognostic value of polygenic risk scores for adults with psychosis. <i>Nature Medicine</i> , 2021, 27, 1576-1581.	15.2	31
64	Genetic sensitivity analysis: Adjusting for genetic confounding in epidemiological associations. <i>PLoS Genetics</i> , 2021, 17, e1009590.	1.5	30
65	Investigating Pleiotropy Between Depression and Autoimmune Diseases Using the UK Biobank. <i>Biological Psychiatry Global Open Science</i> , 2021, 1, 48-58.	1.0	29
66	Assessing multivariate gene-metabolome associations with rare variants using Bayesian reduced rank regression. <i>Bioinformatics</i> , 2014, 30, 2026-2034.	1.8	28
67	Classical Human Leukocyte Antigen Alleles and C4 Haplotypes Are Not Significantly Associated With Depression. <i>Biological Psychiatry</i> , 2020, 87, 419-430.	0.7	27
68	Multiple measures of depression to enhance validity of major depressive disorder in the UK Biobank. <i>BJPsych Open</i> , 2021, 7, e44.	0.3	27
69	Assortative Mating—A Missing Piece in the Jigsaw of Psychiatric Genetics. <i>JAMA Psychiatry</i> , 2016, 73, 323.	6.0	24
70	Multiple Measures of Adiposity Are Associated with Mean Leukocyte Telomere Length in the Northern Finland Birth Cohort 1966. <i>PLoS ONE</i> , 2014, 9, e99133.	1.1	22
71	Exploring the role of genetic confounding in the association between maternal and offspring body mass index: evidence from three birth cohorts. <i>International Journal of Epidemiology</i> , 2020, 49, 233-243.	0.9	18
72	A new method for identifying causal genes of schizophrenia and anti-tuberculosis drug-induced hepatotoxicity. <i>Scientific Reports</i> , 2016, 6, 32571.	1.6	16

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73	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€™Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019, 4, 91-100.	1.1	16
74	Exploring the causal effect of maternal pregnancy adiposity on offspring adiposity: Mendelian randomisation using polygenic risk scores. <i>BMC Medicine</i> , 2022, 20, 34.	2.3	14
75	invertFREGENE: software for simulating inversions in population genetic data. <i>Bioinformatics</i> , 2010, 26, 838-840.	1.8	12
76	The Effect of Genomic Inversions on Estimation of Population Genetic Parameters from SNP Data. <i>Genetics</i> , 2013, 193, 243-253.	1.2	12
77	Differential predictors for alcohol use in adolescents as a function of familial risk. <i>Translational Psychiatry</i> , 2021, 11, 157.	2.4	11
78	Investigating the effects of genetic risk of schizophrenia on behavioural traits. <i>NPJ Schizophrenia</i> , 2021, 7, 2.	2.0	10
79	Maternal health around pregnancy and autism risk: a diagnosis-wide, population-based study. <i>Psychological Medicine</i> , 2022, 52, 4076-4084.	2.7	10
80	Fine-Scale Estimation of Location of Birth from Genome-Wide Single-Nucleotide Polymorphism Data. <i>Genetics</i> , 2012, 190, 669-677.	1.2	8
81	Multifactorial disorders and polygenic risk scores: predicting common diseases and the possibility of adverse selection in life and protection insurance. <i>Annals of Actuarial Science</i> , 2020, , 1-16.	1.0	8
82	An Emerging Syndemic of Smoking and Cardiopulmonary Diseases in People Living with HIV in Africa. <i>International Journal of Environmental Research and Public Health</i> , 2021, 18, 3111.	1.2	7
83	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. <i>Frontiers in Endocrinology</i> , 2022, 13, 863893.	1.5	7
84	Heterogeneous effects of genetic risk for Alzheimerâ€™s disease on the phenome. <i>Translational Psychiatry</i> , 2021, 11, 406.	2.4	4
85	Admixture provides new insights into recombination. <i>Nature Genetics</i> , 2011, 43, 819-820.	9.4	3
86	Common Genetic Determinants of Vitamin D Insufficiency: A Genome-Wide Association Study. <i>Obstetrical and Gynecological Survey</i> , 2011, 66, 91-93.	0.2	0
87	Genetic Effects, Categorical Disorders, and Quantitative Traits. <i>Journal of the American Academy of Child and Adolescent Psychiatry</i> , 2015, 54, 702-703.	0.3	0