

Jacob Gratten

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.

67
papers

11,554
citations

35
h-index

71
g-index

71
ext. papers

15,312
ext. citations

15.6
avg, IF

7.56
L-index

#	Paper	IF	Citations
67	Australian Parkinson's Genetics Study (APGS): pilot (n=1532).. <i>BMJ Open</i> , 2022 , 12, e052032	3	
66	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , 2022 ,	36.3	7
65	Autism-related dietary preferences mediate autism-gut microbiome associations. <i>Cell</i> , 2021 , 184, 5916-5931.e17	39.1	17
64	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. <i>Nature Communications</i> , 2021 , 12, 5641	17.4	2
63	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021 , 22, 90	18.3	6
62	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. <i>Molecular Autism</i> , 2021 , 12, 12	6.5	4
61	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , 2020 , 11, 1238	17.4	25
60	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020 , 5, 10	6.2	11
59	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019 , 11, 54	14.4	81
58	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <i>Genetics</i> , 2019 , 212, 577-586	4	1
57	Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and Lysynuclein mechanisms. <i>Movement Disorders</i> , 2019 , 34, 866-875	7	136
56	The genetic relationship between female reproductive traits and six psychiatric disorders. <i>Scientific Reports</i> , 2019 , 9, 12041	4.9	4
55	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. <i>JAMA Psychiatry</i> , 2019 , 76, 1026-1034	14.5	24
54	Identification of novel risk loci, causal insights, and heritable risk for Parkinson's disease: a meta-analysis of genome-wide association studies. <i>Lancet Neurology</i> , 2019 , 18, 1091-1102	24.1	562
53	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019 , 51, 245-257	36.3	259
52	Sizing up whole-genome sequencing studies of common diseases. <i>Nature Genetics</i> , 2018 , 50, 635-637	36.3	10
51	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018 , 173, 1705-1715.e16	56.2	360

50	Gene networks associated with non-syndromic intellectual disability. <i>Journal of Neurogenetics</i> , 2018 , 32, 6-14	1.6	11
49	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018 , 2, 948-954	12.8	45
48	Study protocol for the Australian autism biobank: an international resource to advance autism discovery research. <i>BMC Pediatrics</i> , 2018 , 18, 284	2.6	9
47	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , 2018 , 102, 1185-1194	11	55
46	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , 2018 , 8, 10168	4.9	11
45	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. <i>European Journal of Human Genetics</i> , 2018 , 26, 1361-1368	5.3	1
44	Small non-coding RNA expression from anterior cingulate cortex in schizophrenia shows sex specific regulation. <i>Schizophrenia Research</i> , 2017 , 183, 82-87	3.6	14
43	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. <i>Genome Medicine</i> , 2017 , 9, 97	14.4	17
42	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , 2017 , 8, 611	17.4	45
41	Whole exome sequencing and DNA methylation analysis in a clinical amyotrophic lateral sclerosis cohort. <i>Molecular Genetics & Genomic Medicine</i> , 2017 , 5, 418-428	2.3	8
40	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017 , 49, 27-35	36.3	530
39	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. <i>Genome Medicine</i> , 2016 , 8, 78	14.4	77
38	Rare variants are common in schizophrenia. <i>Nature Neuroscience</i> , 2016 , 19, 1426-1428	25.5	8
37	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 13366-13371	11.5	90
36	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , 2016 , 73, 497-505	14.5	40
35	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , 2016 , 8, 84	14.4	59
34	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. <i>Nature Genetics</i> , 2016 , 48, 718-24	36.3	74
33	Mapping and differential expression analysis from short-read RNA-Seq data in model organisms. <i>Quantitative Biology</i> , 2016 , 4, 22-35	3.9	2

32	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
31	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
30	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015 , 97, 576-92	11	649
29	Comparing schizophrenia symptoms in the Iban of Sarawak with other populations to elucidate clinical heterogeneity. <i>Asia-Pacific Psychiatry</i> , 2015 , 7, 36-44	3.2	
28	Heterogeneity of genetic architecture of body size traits in a free-living population. <i>Molecular Ecology</i> , 2015 , 24, 1810-30	5.7	55
27	Large-scale genomics unveils the genetic architecture of psychiatric disorders. <i>Nature Neuroscience</i> , 2014 , 17, 782-90	25.5	269
26	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , 2014 , 511, 421-7	50.4	5249
25	The emerging spectrum of allelic variation in schizophrenia: current evidence and strategies for the identification and functional characterization of common and rare variants. <i>Molecular Psychiatry</i> , 2013 , 18, 38-52	15.1	66
24	Life history trade-offs at a single locus maintain sexually selected genetic variation. <i>Nature</i> , 2013 , 502, 93-5	50.4	218
23	Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. <i>Nature Genetics</i> , 2013 , 45, 234-8	36.3	64
22	Introgression and the fate of domesticated genes in a wild mammal population. <i>Molecular Ecology</i> , 2013 , 22, 4210-4221	5.7	40
21	Selection and microevolution of coat pattern are cryptic in a wild population of sheep. <i>Molecular Ecology</i> , 2012 , 21, 2977-90	5.7	22
20	Characterisation of the transcriptome of a wild great tit <i>Parus major</i> population by next generation sequencing. <i>BMC Genomics</i> , 2011 , 12, 283	4.5	57
19	The genetic basis of recessive self-colour pattern in a wild sheep population. <i>Heredity</i> , 2010 , 104, 206-14	3.6	35
18	No evidence for warming climate theory of coat colour change in Soay sheep: a comment on Maloney et al. <i>Biology Letters</i> , 2010 , 6, 678-9; discussion 680-1	3.6	4
17	Mapping quantitative trait loci in a wild population using linkage and linkage disequilibrium analyses. <i>Genetical Research</i> , 2010 , 92, 273-81	1.1	5
16	Genome mapping in intensively studied wild vertebrate populations. <i>Trends in Genetics</i> , 2010 , 26, 275-84	8.5	72
15	Gene mapping in the wild with SNPs: guidelines and future directions. <i>Genetica</i> , 2009 , 136, 97-107	1.5	134

14	Multiplex SNP-SCALE: a cost-effective medium-throughput single nucleotide polymorphism genotyping method. <i>Molecular Ecology Resources</i> , 2008 , 8, 1230-8	8.4	64
13	A localized negative genetic correlation constrains microevolution of coat color in wild sheep. <i>Science</i> , 2008 , 319, 318-20	33.3	91
12	SNP-SCALE: SNP scoring by colour and length exclusion. <i>Molecular Ecology Notes</i> , 2007 , 7, 377-388		13
11	Mapping quantitative trait Loci underlying fitness-related traits in a free-living sheep population. <i>Evolution; International Journal of Organic Evolution</i> , 2007 , 61, 1403-16	3.8	44
10	Quantitative trait loci (QTL) mapping of resistance to strongyles and coccidia in the free-living Soay sheep (<i>Ovis aries</i>). <i>International Journal for Parasitology</i> , 2007 , 37, 121-9	4.3	72
9	Molecular assessment of the genetic integrity, distinctiveness and phylogeographic context of the Saltwater crocodile (<i>Crocodylus porosus</i>) on Palau. <i>Conservation Genetics</i> , 2007 , 8, 777-787	2.6	15
8	Compelling evidence that a single nucleotide substitution in TYRP1 is responsible for coat-colour polymorphism in a free-living population of Soay sheep. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2007 , 274, 619-26	4.4	96
7	Development of a linkage map and mapping of phenotypic polymorphisms in a free-living population of Soay sheep (<i>Ovis aries</i>). <i>Genetics</i> , 2006 , 173, 1521-37	4	53
6	Identification of purebred <i>Crocodylus siamensis</i> for reintroduction in Vietnam. <i>The Journal of Experimental Zoology</i> , 2002 , 294, 373-81		44
5	Genetic Associations with Subjective Well-Being Also Implicate Depression and Neuroticism		7
4	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences ¹		4
3	Imprint of Assortative Mating on the Human Genome		2
2	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing		6
1	Age at first birth in women is genetically associated with increased risk of schizophrenia		1