

# Jacob Gratten

## List of Publications by Citations

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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	Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , <b>2014</b> , 511, 421-7	50.4	5249
66	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , <b>2016</b> , 533, 539-42	50.4	850
65	Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 576-92	11	649
64	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , <b>2016</b> , 48, 624-33	36.3	602
63	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> , <b>2019</b> , 18, 1091-1102	24.1	562
62	Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , <b>2017</b> , 49, 27-35	36.3	530
61	Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , <b>2018</b> , 173, 1705-1715.e16	56.2	360
60	Large-scale genomics unveils the genetic architecture of psychiatric disorders. <i>Nature Neuroscience</i> , <b>2014</b> , 17, 782-90	25.5	269
59	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> , <b>2019</b> , 51, 245-257	36.3	259
58	Life history trade-offs at a single locus maintain sexually selected genetic variation. <i>Nature</i> , <b>2013</b> , 502, 93-5	50.4	218
57	Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and Lysynuclein mechanisms. <i>Movement Disorders</i> , <b>2019</b> , 34, 866-875	7	136
56	Gene mapping in the wild with SNPs: guidelines and future directions. <i>Genetica</i> , <b>2009</b> , 136, 97-107	1.5	134
55	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> , <b>2007</b> , 274, 619-26	4.4	96
54	A localized negative genetic correlation constrains microevolution of coat color in wild sheep. <i>Science</i> , <b>2008</b> , 319, 318-20	33.3	91
53	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 13366-13371	11.5	90
52	Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , <b>2019</b> , 11, 54	14.4	81
51	Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. <i>Genome Medicine</i> , <b>2016</b> , 8, 78	14.4	77

50	Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. <i>Nature Genetics</i> , <b>2016</b> , 48, 718-24	36.3	74
49	Genome mapping in intensively studied wild vertebrate populations. <i>Trends in Genetics</i> , <b>2010</b> , 26, 275-848.5		72
48	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> , <b>2007</b> , 37, 121-9	4.3	72
47	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> , <b>2013</b> , 18, 38-52	15.1	66
46	Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. <i>Nature Genetics</i> , <b>2013</b> , 45, 234-8	36.3	64
45	Multiplex SNP-SCALE: a cost-effective medium-throughput single nucleotide polymorphism genotyping method. <i>Molecular Ecology Resources</i> , <b>2008</b> , 8, 1230-8	8.4	64
44	Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. <i>Genome Medicine</i> , <b>2016</b> , 8, 84	14.4	59
43	Characterisation of the transcriptome of a wild great tit <i>Parus major</i> population by next generation sequencing. <i>BMC Genomics</i> , <b>2011</b> , 12, 283	4.5	57
42	Heterogeneity of genetic architecture of body size traits in a free-living population. <i>Molecular Ecology</i> , <b>2015</b> , 24, 1810-30	5.7	55
41	Estimation of Genetic Correlation via Linkage Disequilibrium Score Regression and Genomic Restricted Maximum Likelihood. <i>American Journal of Human Genetics</i> , <b>2018</b> , 102, 1185-1194	11	55
40	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> , <b>2006</b> , 173, 1521-37	4	53
39	Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. <i>Nature Communications</i> , <b>2017</b> , 8, 611	17.4	45
38	Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , <b>2018</b> , 2, 948-954	12.8	45
37	Mapping quantitative trait Loci underlying fitness-related traits in a free-living sheep population. <i>Evolution; International Journal of Organic Evolution</i> , <b>2007</b> , 61, 1403-16	3.8	44
36	Identification of purebred <i>Crocodylus siamensis</i> for reintroduction in Vietnam. <i>The Journal of Experimental Zoology</i> , <b>2002</b> , 294, 373-81		44
35	Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. <i>JAMA Psychiatry</i> , <b>2016</b> , 73, 497-505	14.5	40
34	Introgression and the fate of domesticated genes in a wild mammal population. <i>Molecular Ecology</i> , <b>2013</b> , 22, 4210-4221	5.7	40
33	The genetic basis of recessive self-colour pattern in a wild sheep population. <i>Heredity</i> , <b>2010</b> , 104, 206-143.6		35

32	Autism-related dietary preferences mediate autism-gut microbiome associations. <i>Cell</i> , <b>2021</b> , 184, 5916-5931.e17	17.4	25
31	Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. <i>Nature Communications</i> , <b>2020</b> , 11, 1238	17.4	25
30	Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. <i>JAMA Psychiatry</i> , <b>2019</b> , 76, 1026-1034	14.5	24
29	Selection and microevolution of coat pattern are cryptic in a wild population of sheep. <i>Molecular Ecology</i> , <b>2012</b> , 21, 2977-90	5.7	22
28	Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. <i>Genome Medicine</i> , <b>2017</b> , 9, 97	14.4	17
27	Molecular assessment of the genetic integrity, distinctiveness and phylogeographic context of the Saltwater crocodile ( <i>Crocodylus porosus</i> ) on Palau. <i>Conservation Genetics</i> , <b>2007</b> , 8, 777-787	2.6	15
26	Small non-coding RNA expression from anterior cingulate cortex in schizophrenia shows sex specific regulation. <i>Schizophrenia Research</i> , <b>2017</b> , 183, 82-87	3.6	14
25	SNP-SCALE: SNP scoring by colour and length exclusion. <i>Molecular Ecology Notes</i> , <b>2007</b> , 7, 377-388		13
24	Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , <b>2020</b> , 5, 10	6.2	11
23	Gene networks associated with non-syndromic intellectual disability. <i>Journal of Neurogenetics</i> , <b>2018</b> , 32, 6-14	1.6	11
22	Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , <b>2018</b> , 8, 10168	4.9	11
21	Sizing up whole-genome sequencing studies of common diseases. <i>Nature Genetics</i> , <b>2018</b> , 50, 635-637	36.3	10
20	Study protocol for the Australian autism biobank: an international resource to advance autism discovery research. <i>BMC Pediatrics</i> , <b>2018</b> , 18, 284	2.6	9
19	Rare variants are common in schizophrenia. <i>Nature Neuroscience</i> , <b>2016</b> , 19, 1426-1428	25.5	8
18	Whole exome sequencing and DNA methylation analysis in a clinical amyotrophic lateral sclerosis cohort. <i>Molecular Genetics &amp; Genomic Medicine</i> , <b>2017</b> , 5, 418-428	2.3	8
17	Genetic Associations with Subjective Well-Being Also Implicate Depression and Neuroticism		7
16	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , <b>2022</b> ,	36.3	7
15	Improved prediction of chronological age from DNA methylation limits it as a biomarker of ageing		6

14	Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , <b>2021</b> , 22, 90	18.3	6
13	Mapping quantitative trait loci in a wild population using linkage and linkage disequilibrium analyses. <i>Genetical Research</i> , <b>2010</b> , 92, 273-81	1.1	5
12	The genetic relationship between female reproductive traits and six psychiatric disorders. <i>Scientific Reports</i> , <b>2019</b> , 9, 12041	4.9	4
11	No evidence for warming climate theory of coat colour change in Soay sheep: a comment on Maloney et al. <i>Biology Letters</i> , <b>2010</b> , 6, 678-9; discussion 680-1	3.6	4
10	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences <sup>1</sup>		4
9	Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. <i>Molecular Autism</i> , <b>2021</b> , 12, 12	6.5	4
8	Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. <i>Nature Communications</i> , <b>2021</b> , 12, 5641	17.4	2
7	Imprint of Assortative Mating on the Human Genome		2
6	Mapping and differential expression analysis from short-read RNA-Seq data in model organisms. <i>Quantitative Biology</i> , <b>2016</b> , 4, 22-35	3.9	2
5	Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <i>Genetics</i> , <b>2019</b> , 212, 577-586	4	1
4	Age at first birth in women is genetically associated with increased risk of schizophrenia		1
3	Trans-eQTLs identified in whole blood have limited influence on complex disease biology. <i>European Journal of Human Genetics</i> , <b>2018</b> , 26, 1361-1368	5.3	1
2	Comparing schizophrenia symptoms in the Iban of Sarawak with other populations to elucidate clinical heterogeneity. <i>Asia-Pacific Psychiatry</i> , <b>2015</b> , 7, 36-44	3.2	
1	Australian Parkinson's Genetics Study (APGS): pilot (n=1532).. <i>BMJ Open</i> , <b>2022</b> , 12, e052032	3	