

# Jacob Gratten

## List of Publications by Year in descending order

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Version: 2024-02-01

62  
papers

17,511  
citations

81839

39  
h-index

110317

64  
g-index

71  
all docs

71  
docs citations

71  
times ranked

24669  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Biological insights from 108 schizophrenia-associated genetic loci. <i>Nature</i> , 2014, 511, 421-427.  | 13.7 | 6,934     |
| 2  | 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> , The, 2019, 18, 1091-1102.  | 4.9  | 1,414     |
| 3  | Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.   | 13.7 | 1,204     |
| 4  | Modeling Linkage Disequilibrium Increases Accuracy of Polygenic Risk Scores. <i>American Journal of Human Genetics</i> , 2015, 97, 576-592.  | 2.6  | 1,098     |
| 5  | Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016, 48, 624-633.  | 9.4  | 870       |
| 6  | Contribution of copy number variants to schizophrenia from a genome-wide study of 41,321 subjects. <i>Nature Genetics</i> , 2017, 49, 27-35.   | 9.4  | 838       |
| 7  | Genomic Dissection of Bipolar Disorder and Schizophrenia, Including 28 Subphenotypes. <i>Cell</i> , 2018, 173, 1705-1715.e16.  | 13.5 | 623       |
| 8  | 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.                                      | 9.4  | 536       |
| 9  | Large-scale genomics unveils the genetic architecture of psychiatric disorders. <i>Nature Neuroscience</i> , 2014, 17, 782-790.  | 7.1  | 321       |
| 10 | Life history trade-offs at a single locus maintain sexually selected genetic variation. <i>Nature</i> , 2013, 502, 93-95.  | 13.7 | 296       |
| 11 | Parkinson's disease age at onset genome-wide association study: Defining heritability, genetic loci, and $\alpha$ -synuclein mechanisms. <i>Movement Disorders</i> , 2019, 34, 866-875.  | 2.2  | 258       |
| 12 | Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.   | 9.4  | 215       |
| 13 | Improved precision of epigenetic clock estimates across tissues and its implication for biological ageing. <i>Genome Medicine</i> , 2019, 11, 54.  | 3.6  | 191       |
| 14 | Gene mapping in the wild with SNPs: guidelines and future directions. <i>Genetica</i> , 2009, 136, 97-107.   | 0.5  | 181       |
| 15 | Autism-related dietary preferences mediate autism-gut microbiome associations. <i>Cell</i> , 2021, 184, 5916-5931.e17.   | 13.5 | 172       |
| 16 | Genetic pleiotropy in complex traits and diseases: implications for genomic medicine. <i>Genome Medicine</i> , 2016, 8, 78.  | 3.6  | 135       |
| 17 | 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.   | 2.6  | 119       |
| 18 | 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, 619-626. | 1.2  | 116       |

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|----|---|-----|-----------|
| 19 | Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.  | 3.3 | 110       |
| 20 | Risk of psychiatric illness from advanced paternal age is not predominantly from de novo mutations. Nature Genetics, 2016, 48, 718-724.   | 9.4 | 98        |
| 21 | A Localized Negative Genetic Correlation Constrains Microevolution of Coat Color in Wild Sheep. Science, 2008, 319, 318-320.  | 6.0 | 97        |
| 22 | Imprint of assortative mating on the human genome. Nature Human Behaviour, 2018, 2, 948-954.  | 6.2 | 97        |
| 23 | Cross-ethnic meta-analysis identifies association of the GPX3-TNIP1 locus with amyotrophic lateral sclerosis. Nature Communications, 2017, 8, 611.  | 5.8 | 93        |
| 24 | Predicting gene targets from integrative analyses of summary data from GWAS and eQTL studies for 28 human complex traits. Genome Medicine, 2016, 8, 84.   | 3.6 | 91        |
| 25 | Quantitative trait loci (QTL) mapping of resistance to strongyles and coccidia in the free-living Soay sheep ( <i>Ovis aries</i> ). International Journal for Parasitology, 2007, 37, 121-129.                          | 1.3 | 87        |
| 26 | Genome mapping in intensively studied wild vertebrate populations. Trends in Genetics, 2010, 26, 275-284.   | 2.9 | 85        |
| 27 | Analysis of DNA methylation associates the cystine-glutamate antiporter SLC7A11 with risk of Parkinson's disease. Nature Communications, 2020, 11, 1238.  | 5.8 | 85        |
| 28 | Interpreting the role of de novo protein-coding mutations in neuropsychiatric disease. Nature Genetics, 2013, 45, 234-238.  | 9.4 | 76        |
| 29 | The emerging spectrum of allelic variation in schizophrenia: current evidence and strategies for the identification and functional characterization of common and rare variants. Molecular Psychiatry, 2013, 18, 38-52. | 4.1 | 75        |
| 30 | Heterogeneity of genetic architecture of body size traits in a free-living population. Molecular Ecology, 2015, 24, 1810-1830.  | 2.0 | 72        |
| 31 | Characterisation of the transcriptome of a wild great tit <i>Parus major</i> population by next generation sequencing. BMC Genomics, 2011, 12, 283.   | 1.2 | 67        |
| 32 | Multiplex SNP-SCALE: a cost-effective medium-throughput single nucleotide polymorphism genotyping method. Molecular Ecology Resources, 2008, 8, 1230-1238.  | 2.2 | 65        |
| 33 | Development of a Linkage Map and Mapping of Phenotypic Polymorphisms in a Free-Living Population of Soay Sheep ( <i>Ovis aries</i> ). Genetics, 2006, 173, 1521-1537.   | 1.2 | 57        |
| 34 | Identification of purebred <i>Crocodylus siamensis</i> for reintroduction in Vietnam. The Journal of Experimental Zoology, 2002, 294, 373-381.  | 1.4 | 54        |
| 35 | Introgression and the fate of domesticated genes in a wild mammal population. Molecular Ecology, 2013, 22, 4210-4221.   | 2.0 | 53        |
| 36 | Evidence for Genetic Overlap Between Schizophrenia and Age at First Birth in Women. JAMA Psychiatry, 2016, 73, 497.   | 6.0 | 51        |

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|----|--|-----|-----------|
| 37 | Association of Schizophrenia Risk With Disordered Niacin Metabolism in an Indian Genome-wide Association Study. <i>JAMA Psychiatry</i> , 2019, 76, 1026.   | 6.0 | 51        |
| 38 | Meta-analysis of genome-wide DNA methylation identifies shared associations across neurodegenerative disorders. <i>Genome Biology</i> , 2021, 22, 90.  | 3.8 | 49        |
| 39 | MAPPING QUANTITATIVE TRAIT LOCI UNDERLYING FITNESS-RELATED TRAITS IN A FREE-LIVING SHEEP POPULATION. <i>Evolution; International Journal of Organic Evolution</i> , 2007, 61, 1403-1416.                       | 1.1 | 48        |
| 40 | Investigating the shared genetic architecture between multiple sclerosis and inflammatory bowel diseases. <i>Nature Communications</i> , 2021, 12, 5641.   | 5.8 | 46        |
| 41 | The genetic basis of recessive self-colour pattern in a wild sheep population. <i>Heredity</i> , 2010, 104, 206-214.   | 1.2 | 43        |
| 42 | Selection and microevolution of coat pattern are cryptic in a wild population of sheep. <i>Molecular Ecology</i> , 2012, 21, 2977-2990.  | 2.0 | 31        |
| 43 | Significant out-of-sample classification from methylation profile scoring for amyotrophic lateral sclerosis. <i>Npj Genomic Medicine</i> , 2020, 5, 10.  | 1.7 | 25        |
| 44 | Whole-exome sequencing in amyotrophic lateral sclerosis suggests NEK1 is a risk gene in Chinese. <i>Genome Medicine</i> , 2017, 9, 97.   | 3.6 | 23        |
| 45 | Study protocol for the Australian autism biobank: an international resource to advance autism discovery research. <i>BMC Pediatrics</i> , 2018, 18, 284.   | 0.7 | 20        |
| 46 | The genetic relationship between female reproductive traits and six psychiatric disorders. <i>Scientific Reports</i> , 2019, 9, 12041.   | 1.6 | 18        |
| 47 | 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. | 0.8 | 17        |
| 48 | Small non-coding RNA expression from anterior cingulate cortex in schizophrenia shows sex specific regulation. <i>Schizophrenia Research</i> , 2017, 183, 82-87.   | 1.1 | 17        |
| 49 | Age at first birth in women is genetically associated with increased risk of schizophrenia. <i>Scientific Reports</i> , 2018, 8, 10168.  | 1.6 | 17        |
| 50 | TECHNICAL ARTICLE: SNP-SCALE: SNP scoring by colour and length exclusion. <i>Molecular Ecology Notes</i> , 2007, 7, 377-388.   | 1.7 | 15        |
| 51 | Whole exome sequencing and <sc>DNA</sc> methylation analysis in a clinical amyotrophic lateral sclerosis cohort. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2017, 5, 418-428.                          | 0.6 | 14        |
| 52 | Sizing up whole-genome sequencing studies of common diseases. <i>Nature Genetics</i> , 2018, 50, 635-637.  | 9.4 | 13        |
| 53 | Gene networks associated with non-syndromic intellectual disability. <i>Journal of Neurogenetics</i> , 2018, 32, 6-14.   | 0.6 | 13        |
| 54 | Rare variants are common in schizophrenia. <i>Nature Neuroscience</i> , 2016, 19, 1426-1428.   | 7.1 | 11        |

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|----|--|-----|-----------|
| 55 | Analysis of common genetic variation and rare CNVs in the Australian Autism Biobank. <i>Molecular Autism</i> , 2021, 12, 12.   | 2.6 | 11        |
| 56 | Mapping quantitative trait loci in a wild population using linkage and linkage disequilibrium analyses. <i>Genetical Research</i> , 2010, 92, 273-281.               | 0.3 | 6         |
| 57 | 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, 678-679.                 | 1.0 | 6         |
| 58 | Mapping and differential expression analysis from short-read RNA-seq data in model organisms. <i>Quantitative Biology</i> , 2016, 4, 22-35.                          | 0.3 | 3         |
| 59 | Trans-eQTLs identified in whole blood have limited influence on complex disease biology. <i>European Journal of Human Genetics</i> , 2018, 26, 1361-1368.            | 1.4 | 3         |
| 60 | Comparing schizophrenia symptoms in the Iban of Sarawak with other populations to elucidate clinical heterogeneity. <i>Asia-Pacific Psychiatry</i> , 2015, 7, 36-44. | 1.2 | 2         |
| 61 | Examining the Impact of Imputation Errors on Fine-Mapping Using DNA Methylation QTL as a Model Trait. <i>Genetics</i> , 2019, 212, 577-586.                          | 1.2 | 2         |
| 62 | Australian Parkinson's Genetics Study (APGS): pilot (n=1532). <i>BMJ Open</i> , 2022, 12, e052032.   | 0.8 | 1         |