

# Matthew R Robinson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1908278/publications.pdf>

Version: 2024-02-01

31  
papers

5,642  
citations

304743

22  
h-index

414414

32  
g-index

43  
all docs

43  
docs citations

43  
times ranked

12146  
citing authors

| #  | ARTICLE  | IF   | CITATIONS |
|----|--|------|-----------|
| 1  | Integration of summary data from GWAS and eQTL studies predicts complex trait gene targets. <i>Nature Genetics</i> , 2016, 48, 481-487.  | 21.4 | 1,757     |
| 2  | Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. <i>Nature Genetics</i> , 2015, 47, 1114-1120.                                    | 21.4 | 709       |
| 3  | Causal associations between risk factors and common diseases inferred from GWAS summary data. <i>Nature Communications</i> , 2018, 9, 224.   | 12.8 | 629       |
| 4  | Accurate, scalable and integrative haplotype estimation. <i>Nature Communications</i> , 2019, 10, 5436.  | 12.8 | 336       |
| 5  | Signatures of negative selection in the genetic architecture of human complex traits. <i>Nature Genetics</i> , 2018, 50, 746-753.  | 21.4 | 304       |
| 6  | Genetic evidence of assortative mating in humans. <i>Nature Human Behaviour</i> , 2017, 1, .   | 12.0 | 242       |
| 7  | Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.  | 21.4 | 227       |
| 8  | Hidden heritability due to heterogeneity across seven populations. <i>Nature Human Behaviour</i> , 2017, 1, 757-765.   | 12.0 | 137       |
| 9  | Improving genetic prediction by leveraging genetic correlations among human diseases and traits. <i>Nature Communications</i> , 2018, 9, 989.  | 12.8 | 136       |
| 10 | Explaining additional genetic variation in complex traits. <i>Trends in Genetics</i> , 2014, 30, 124-132.  | 6.7  | 128       |
| 11 | Genotype-covariate interaction effects and the heritability of adult body mass index. <i>Nature Genetics</i> , 2017, 49, 1174-1181.  | 21.4 | 119       |
| 12 | LIVE FAST, DIE YOUNG: TRADE-OFFS BETWEEN FITNESS COMPONENTS AND SEXUALLY ANTAGONISTIC SELECTION ON WEAPONRY IN SOAY SHEEP. <i>Evolution; International Journal of Organic Evolution</i> , 2006, 60, 2168-2181. | 2.3  | 114       |
| 13 | Environmental Heterogeneity Generates Fluctuating Selection on a Secondary Sexual Trait. <i>Current Biology</i> , 2008, 18, 751-757.   | 3.9  | 99        |
| 14 | Imprint of assortative mating on the human genome. <i>Nature Human Behaviour</i> , 2018, 2, 948-954.   | 12.0 | 97        |
| 15 | Global genetic differentiation of complex traits shaped by natural selection in humans. <i>Nature Communications</i> , 2018, 9, 1865.  | 12.8 | 70        |
| 16 | The Impact of Environmental Heterogeneity on Genetic Architecture in a Wild Population of Soay Sheep. <i>Genetics</i> , 2009, 181, 1639-1648.  | 2.9  | 58        |
| 17 | Evolutionary history and adaptation of a human pygmy population of Flores Island, Indonesia. <i>Science</i> , 2018, 361, 511-516.  | 12.6 | 56        |
| 18 | Function of weaponry in females: the use of horns in intrasexual competition for resources in female Soay sheep. <i>Biology Letters</i> , 2007, 3, 651-654.  | 2.3  | 49        |

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|----|---|------|-----------|
| 19 | Detection and quantification of inbreeding depression for complex traits from SNP data. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 8602-8607.                              | 7.1  | 48        |
| 20 | Bayesian reassessment of the epigenetic architecture of complex traits. Nature Communications, 2020, 11, 2865.  | 12.8 | 43        |
| 21 | Live fast, die young: trade-offs between fitness components and sexually antagonistic selection on weaponry in Soay sheep. Evolution; International Journal of Organic Evolution, 2006, 60, 2168-81.                        | 2.3  | 42        |
| 22 | Predation drives local adaptation of phenotypic plasticity. Nature Ecology and Evolution, 2018, 2, 100-107.   | 7.8  | 40        |
| 23 | Quantification of the overall contribution of gene-environment interaction for obesity-related traits. Nature Communications, 2020, 11, 1385.   | 12.8 | 31        |
| 24 | Inference on the Genetic Basis of Eye and Skin Color in an Admixed Population via Bayesian Linear Mixed Models. Genetics, 2017, 206, 1113-1126.   | 2.9  | 30        |
| 25 | Multi-method genome- and epigenome-wide studies of inflammatory protein levels in healthy older adults. Genome Medicine, 2020, 12, 60.  | 8.2  | 30        |
| 26 | Blood-based epigenome-wide analyses of cognitive abilities. Genome Biology, 2022, 23, 26.   | 8.8  | 20        |
| 27 | Major histocompatibility complex-linked social signalling affects female fertility. Proceedings of the Royal Society B: Biological Sciences, 2017, 284, 20171824.   | 2.6  | 17        |
| 28 | Probabilistic inference of the genetic architecture underlying functional enrichment of complex traits. Nature Communications, 2021, 12, 6972.  | 12.8 | 14        |
| 29 | Genomic architecture and prediction of censored time-to-event phenotypes with a Bayesian genome-wide analysis. Nature Communications, 2021, 12, 2337.   | 12.8 | 11        |
| 30 | Genome- and epigenome-wide studies of plasma protein biomarkers for Alzheimer's disease implicate TBCA and TREM2 in disease risk. Alzheimer's and Dementia: Diagnosis, Assessment and Disease Monitoring, 2022, 14, e12280. | 2.4  | 4         |
| 31 | Postpartum hemorrhage risk is driven by changes in blood composition through pregnancy. Scientific Reports, 2021, 11, 19238.  | 3.3  | 3         |