

Full publication list based on archive at [google scholar](#).

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1. Lyon, M., Andrews, S., Elsworth, B., Gaunt, T., Hemani, G. & Marcora, E. The variant call format provides efficient and robust storage of gwas summary statistics. *Genome Biology* (2021).
2. Baird, D., Liu, J., Zheng, J., Sieberts, S., Perumal, T., Elsworth, B. & others. Identifying drug targets for neurological and psychiatric disease via genetics and the brain transcriptome. *PLoS genetics* (2021).
3. Hemani, G., Thomas, A., Walker, J., Trickey, A., Nixon, E., Ellis, D. & others. Modelling pooling strategies for sars-cov-2 testing in a university setting. *medRxiv* (2021).
4. Wootton, R., Richmond, R., Stuijzand, B., Lawn, R., Sallis, H. & others. Evidence for causal effects of lifetime smoking on risk for depression and schizophrenia: A mendelian randomisation study. *Psychological medicine* (2020).
5. Zhao, Q., Wang, J., Hemani, G., Bowden, J. & Small, D. Statistical inference in two-sample summary-data mendelian randomization using robust adjusted profile score. *Annals of Statistics* (2020).
6. Griffith, G., Morris, T., Tudball, M., Herbert, A., Mancano, G., Pike, L. & others. Collider bias undermines our understanding of covid-19 disease risk and severity. *Nature communications* (2020).
7. Brumpton, B., Sanderson, E., Heilbron, K., Hartwig, F., Harrison, S., Vie, G. & others. Avoiding dynastic, assortative mating, and population stratification biases in mendelian randomization through within-family analyses. *Nature communications* (2020).
8. Lawson, D., Davies, N., Haworth, S., Ashraf, B., Howe, L., Crawford, A. & others. Is population structure in the genetic biobank era irrelevant, a challenge, or an opportunity? *Human Genetics* (2020).
9. Zheng, J., Haberland, V., Baird, D., Walker, V., Haycock, P., Hurle, M. & others. Phenome-wide mendelian randomization mapping the influence of the plasma proteome on complex diseases. *Nature Genetics* (2020).
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13. Cho, Y., Haycock, P., Sanderson, E., Gaunt, T., Zheng, J., Morris, A. & others. Exploiting horizontal pleiotropy to search for causal pathways within a mendelian randomization framework. *Nature communications* (2020).
14. Zheng, J., Brion, M., Kemp, J., Warrington, N., Borges, M., Hemani, G. & others. The effect of plasma lipids and lipid-lowering interventions on bone mineral density: A mendelian randomization study. *Journal of Bone and Mineral Research* (2020).

15. Neumeyer, S., Hemani, G. & Zeggini, E. Strengthening causal inference for complex disease using molecular quantitative trait loci. *Trends in molecular medicine* (2020).
16. Banos, D., McCartney, D., Patxot, M., Anchieri, L., Battram, T., Christiansen, C. & others. Bayesian reassessment of the epigenetic architecture of complex traits. *Nature communications* (2020).
17. Elsworth, B., Lyon, M., Alexander, T., Liu, Y. & Matthews, P. *et al.* The mrc ieu opengwas data infrastructure. *bioRxiv* (2020).
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33. Howe, L., Battram, T., Morris, T., Hartwig, F., Hemani, G., Davies, N. & others. Assortative mating and within-spouse pair comparisons. *BioRxiv* (2020).
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46. Moen, G., Hemani, G., Warrington, N. & Evans, D. Calculating power to detect maternal and offspring genetic effects in genetic association studies. *Behavior genetics* (2019).
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