Doug Speed

List of Publications by Year
in descending order

37 papers	8,458 citations	361413 20 h-index	345221 36 g-index
53 all docs	53 docs citations	53 times ranked	18279 citing authors

#	Article	IF	Citations
1	The genomic and transcriptomic architecture of 2,000 breast tumours reveals novel subgroups. Nature, 2012, 486, 346-352.	27.8	4,708
2	Improved Heritability Estimation from Genome-wide SNPs. American Journal of Human Genetics, 2012, 91, 1011-1021.	6.2	656
3	Transient structural variations have strong effects on quantitative traits and reproductive isolation in fission yeast. Nature Communications, 2017, 8, 14061.	12.8	472
4	Reevaluation of SNP heritability in complex human traits. Nature Genetics, 2017, 49, 986-992.	21.4	427
5	MultiBLUP: improved SNP-based prediction for complex traits. Genome Research, 2014, 24, 1550-1557.	5.5	258
6	Relatedness in the post-genomic era: is it still useful?. Nature Reviews Genetics, 2015, 16, 33-44.	16.3	228
7	SumHer better estimates the SNP heritability of complex traits from summary statistics. Nature Genetics, 2019, 51, 277-284.	21.4	181
8	The genomic and phenotypic diversity of Schizosaccharomyces pombe. Nature Genetics, 2015, 47, 235-241.	21.4	174
9	Systems genetics identifies Sestrin 3 as a regulator of a proconvulsant gene network in human epileptic hippocampus. Nature Communications, 2015, 6, 6031.	12.8	158
10	Genetic correlations among psychiatric and immuneâ€related phenotypes based on genomeâ€wide association data. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2018, 177, 641-657.	1.7	158
11	Systems genetics identifies a convergent gene network for cognition and neurodevelopmental disease. Nature Neuroscience, 2016, 19, 223-232.	14.8	131
12	Graph pangenome captures missing heritability and empowers tomato breeding. Nature, 2022, 606, 527-534.	27.8	131
13	Evaluating and improving heritability models using summary statistics. Nature Genetics, 2020, 52, 458-462.	21.4	128
14	Investigating the association between body fat and depression via Mendelian randomization. Translational Psychiatry, 2019, 9, 184.	4.8	90
15	Describing the genetic architecture of epilepsy through heritability analysis. Brain, 2014, 137, 2680-2689.	7.6	87
16	GWAS on longitudinal growth traits reveals different genetic factors influencing infant, child, and adult BMI. Science Advances, 2019, 5, eaaw3095.	10.3	86
17	Improved genetic prediction of complex traits from individual-level data or summary statistics. Nature Communications, 2021, 12, 4192.	12.8	76
18	Genetic Complexity of Crohnâ€™s Disease in Two Large Ashkenazi Jewish Families. Gastroenterology, 2016, 151, 698-709.	1.3	54

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19	Mendelian randomization study shows no causal relationship between circulating urate levels and Parkinson's disease. Annals of Neurology, 2018, 84, 191-199.	5.3	43
20	A genome-wide association study and biological pathway analysis of epilepsy prognosis in a prospective cohort of newly treated epilepsy. Human Molecular Genetics, 2014, 23, 247-258.	2.9	33
21	Investigating the causal relationship between neuroticism and depression via Mendelian randomization. Acta Psychiatrica Scandinavica, 2019, 139, 395-397.	4.5	20
22	Response to Lee etÂal.: SNP-Based Heritability Analysis with Dense Data. American Journal of Human Genetics, 2013, 93, 1155-1157.	6.2	17
23	Genomeâ€wide association study of the sensitivity to environmental stress and adversity neuroticism cluster. Acta Psychiatrica Scandinavica, 2020, 141, 476-478.	4.5	16
24	SNPâ€based heritability and selection analyses: Improved models and new results. BioEssays, 2022, 44, e2100170.	2.5	14
25	Genetic Interactions with Sex Make a Relatively Small Contribution to the Heritability of Complex Traits in Mice. PLoS ONE, 2014, 9, e96450.	2.5	9
26	Bipolar disorder and cannabis use: A bidirectional twoâ€sample Mendelian randomization study. Addiction Biology, 2021, 26, e13030.	2.6	9
27	Using common genetic variants to find drugs for common epilepsies. Brain Communications, 2021, 3, fcab287.	3.3	9
28	Summary statistic analyses can mistake confounding bias for heritability. Genetic Epidemiology, 2019, 43, 930-940.	1.3	8
29	Estimating narrow-sense heritability using family data from admixed populations. Heredity, 2020, 124, 751-762.	2.6	6
30	The Effects of Common Genetic Variation in 96 Genes Involved in Thyroid Hormone Regulation on TSH and FT4 Concentrations. Journal of Clinical Endocrinology and Metabolism, 2022, 107, e2276-e2283.	3.6	6
31	Shared genetic basis between genetic generalized epilepsy and background electroencephalographic oscillations. Epilepsia, 2021, 62, 1518-1527.	5.1	5
32	Signatures of TSPAN8 variants associated with human metabolic regulation and diseases. IScience, 2021, 24, 102893.	4.1	5
33	Genome-wide association, prediction and heritability in bacteria with application to Streptococcus pneumoniae. NAR Genomics and Bioinformatics, 2022, 4, lqac011.	3.2	5
34	Sparse Partitioning: Nonlinear regression with binary or tertiary predictors, with application to association studies. Annals of Applied Statistics, 2011, 5, .	1.1	3
35	Long-stay patients with cancer on the intensive care unit: characteristics, risk factors, and clinical outcomes. British Journal of Anaesthesia, 2013, 111, 1026-1027.	3.4	3
36	Understanding complex traits: from farmers to pharmas. Genome Medicine, 2012, 4, 59.	8.2	1

#	Article	IF	Citations
37	P117. Predicting Genetic Risk for Depression and Anxiety Disorders. Biological Psychiatry, 2022, 91, S134-S135.	1.3	0