

Andrew R Wood

List of Publications by Year in descending order

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Version: 2024-02-01

114
papers

30,195
citations

25034

57
h-index

21540

114
g-index

132
all docs

132
docs citations

132
times ranked

36633
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
2	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	21.4	2,634
3	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , 2016, 48, 1279-1283.	21.4	2,421
4	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
5	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	21.4	1,748
6	Meta-analysis of genome-wide association studies for height and body mass index in $\sim 700,000$ individuals of European ancestry. <i>Human Molecular Genetics</i> , 2018, 27, 3641-3649.	2.9	1,541
7	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
8	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
9	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	27.8	952
10	Meta-analysis of genome-wide association studies for body fat distribution in 694,649 individuals of European ancestry. <i>Human Molecular Genetics</i> , 2019, 28, 166-174.	2.9	752
11	Biological interpretation of genome-wide association studies using predicted gene functions. <i>Nature Communications</i> , 2015, 6, 5890.	12.8	706
12	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
13	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
14	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. <i>Nature Communications</i> , 2019, 10, 343.	12.8	417
15	Genome-wide associations for birth weight and correlations with adult disease. <i>Nature</i> , 2016, 538, 248-252.	27.8	406
16	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. <i>Nature Genetics</i> , 2019, 51, 804-814.	21.4	402
17	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014, 9, 1192-1212.	12.0	398
18	Using human genetics to understand the disease impacts of testosterone in men and women. <i>Nature Medicine</i> , 2020, 26, 252-258.	30.7	384

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19	Genome-wide association study identifies genetic loci for self-reported habitual sleep duration supported by accelerometer-derived estimates. <i>Nature Communications</i> , 2019, 10, 1100.	12.8	369
20	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	21.4	365
21	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <i>Nature Genetics</i> , 2018, 50, 559-571.	21.4	356
22	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	27.8	353
23	The trans-ancestral genomic architecture of glycemic traits. <i>Nature Genetics</i> , 2021, 53, 840-860.	21.4	341
24	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016, 12, e1006125.	3.5	308
25	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
26	Biological and clinical insights from genetics of insomnia symptoms. <i>Nature Genetics</i> , 2019, 51, 387-393.	21.4	250
27	Height, body mass index, and socioeconomic status: mendelian randomisation study in UK Biobank. <i>BMJ</i> , 2016, 352, i582.	6.0	247
28	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	21.4	227
29	Genetic Evidence for Causal Relationships Between Maternal Obesity-Related Traits and Birth Weight. <i>JAMA - Journal of the American Medical Association</i> , 2016, 315, 1129.	7.4	220
30	Sleep characteristics across the lifespan in 1.1 million people from the Netherlands, United Kingdom and United States: a systematic review and meta-analysis. <i>Nature Human Behaviour</i> , 2021, 5, 113-122.	12.0	193
31	Genetic studies of accelerometer-based sleep measures yield new insights into human sleep behaviour. <i>Nature Communications</i> , 2019, 10, 1585.	12.8	189
32	Development and Standardization of an Improved Type 1 Diabetes Genetic Risk Score for Use in Newborn Screening and Incident Diagnosis. <i>Diabetes Care</i> , 2019, 42, 200-207.	8.6	187
33	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	27.8	183
34	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	27.8	173
35	Gene-environment interactions in the UK Biobank study. <i>International Journal of Epidemiology</i> , 2017, 46, dyw337.	1.9	159
36	Assessing the Pathogenicity, Penetrance, and Expressivity of Putative Disease-Causing Variants in a Population Setting. <i>American Journal of Human Genetics</i> , 2019, 104, 275-286.	6.2	158

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37	Genome-wide association study of offspring birth weight in 86,577 women identifies five novel loci and highlights maternal genetic effects that are independent of fetal genetics. <i>Human Molecular Genetics</i> , 2018, 27, 742-756.	2.9	156
38	Using genetics to understand the causal influence of higher BMI on depression. <i>International Journal of Epidemiology</i> , 2019, 48, 834-848.	1.9	156
39	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. <i>Nature Communications</i> , 2016, 7, 10494.	12.8	153
40	Evidence of a causal relationship between body mass index and psoriasis: A mendelian randomization study. <i>PLoS Medicine</i> , 2019, 16, e1002739.	8.4	144
41	Genetic determinants of daytime napping and effects on cardiometabolic health. <i>Nature Communications</i> , 2021, 12, 900.	12.8	136
42	Genetic Evidence for a Link Between Favorable Adiposity and Lower Risk of Type 2 Diabetes, Hypertension, and Heart Disease. <i>Diabetes</i> , 2016, 65, 2448-2460.	0.6	122
43	Common conditions associated with hereditary haemochromatosis genetic variants: cohort study in UK Biobank. <i>BMJ: British Medical Journal</i> , 2019, 364, k5222.	2.3	119
44	Genome-wide association analysis of self-reported daytime sleepiness identifies 42 loci that suggest biological subtypes. <i>Nature Communications</i> , 2019, 10, 3503.	12.8	117
45	Another explanation for apparent epistasis. <i>Nature</i> , 2014, 514, E3-E5.	27.8	116
46	Cell Specific eQTL Analysis without Sorting Cells. <i>PLoS Genetics</i> , 2015, 11, e1005223.	3.5	115
47	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. <i>Aging</i> , 2016, 8, 547-560.	3.1	113
48	Genetic predictors of participation in optional components of UK Biobank. <i>Nature Communications</i> , 2021, 12, 886.	12.8	106
49	A Genome-Wide Association Study of IVGTT-Based Measures of First-Phase Insulin Secretion Refines the Underlying Physiology of Type 2 Diabetes Variants. <i>Diabetes</i> , 2017, 66, 2296-2309.	0.6	102
50	Telomere length and risk of idiopathic pulmonary fibrosis and chronic obstructive pulmonary disease: a mendelian randomisation study. <i>Lancet Respiratory Medicine</i> , 2021, 9, 285-294.	10.7	94
51	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
52	Mosaic Turner syndrome shows reduced penetrance in an adult population study. <i>Genetics in Medicine</i> , 2019, 21, 877-886.	2.4	88
53	Genome-wide association analysis of diverticular disease points towards neuromuscular, connective tissue and epithelial pathomechanisms. <i>Gut</i> , 2019, 68, 854-865.	12.1	84
54	Investigating causal relations between sleep traits and risk of breast cancer in women: mendelian randomisation study. <i>BMJ: British Medical Journal</i> , 2019, 365, l2327.	2.3	79

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55	A Common Allele in FGF21 Associated with Sugar Intake Is Associated with Body Shape, Lower Total Body-Fat Percentage, and Higher Blood Pressure. <i>Cell Reports</i> , 2018, 23, 327-336.	6.4	76
56	Genome-Wide and Abdominal MRI Data Provide Evidence That a Genetically Determined Favorable Adiposity Phenotype Is Characterized by Lower Ectopic Liver Fat and Lower Risk of Type 2 Diabetes, Heart Disease, and Hypertension. <i>Diabetes</i> , 2019, 68, 207-219.	0.6	72
57	Prosaposin is a regulator of progranulin levels and oligomerization. <i>Nature Communications</i> , 2016, 7, 11992.	12.8	68
58	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. <i>BMC Proceedings</i> , 2014, 8, S2.	1.6	65
59	Variants in the FTO and CDKAL1 loci have recessive effects on risk of obesity and type 2 diabetes, respectively. <i>Diabetologia</i> , 2016, 59, 1214-1221.	6.3	65
60	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017, 8, 744.	12.8	64
61	Allelic heterogeneity and more detailed analyses of known loci explain additional phenotypic variation and reveal complex patterns of association. <i>Human Molecular Genetics</i> , 2011, 20, 4082-4092.	2.9	61
62	Imputation of Variants from the 1000 Genomes Project Modestly Improves Known Associations and Can Identify Low-frequency Variant - Phenotype Associations Undetected by HapMap Based Imputation. <i>PLoS ONE</i> , 2013, 8, e64343.	2.5	61
63	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	12.8	61
64	GWAS Identifies Risk Locus for Erectile Dysfunction and Implicates Hypothalamic Neurobiology and Diabetes in Etiology. <i>American Journal of Human Genetics</i> , 2019, 104, 157-163.	6.2	55
65	Genetic evidence that lower circulating FSH levels lengthen menstrual cycle, increase age at menopause and impact female reproductive health. <i>Human Reproduction</i> , 2016, 31, 473-481.	0.9	51
66	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. <i>PLoS ONE</i> , 2017, 12, e0185083.	2.5	49
67	A Low-Frequency Inactivating <i>AKT2</i> Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , 2017, 66, 2019-2032.	0.6	47
68	DNA methylation and inflammation marker profiles associated with a history of depression. <i>Human Molecular Genetics</i> , 2018, 27, 2840-2850.	2.9	46
69	Effects of body mass index on relationship status, social contact and socio-economic position: Mendelian randomization and within-sibling study in UK Biobank. <i>International Journal of Epidemiology</i> , 2020, 49, 1173-1184.	1.9	42
70	Genetic Evidence for Different Adiposity Phenotypes and Their Opposing Influences on Ectopic Fat and Risk of Cardiometabolic Disease. <i>Diabetes</i> , 2021, 70, 1843-1856.	0.6	42
71	Quantifying the extent to which index event biases influence large genetic association studies. <i>Human Molecular Genetics</i> , 2017, 26, ddw433.	2.9	40
72	Does Obesity Cause Thyroid Cancer? A Mendelian Randomization Study. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2020, 105, e2398-e2407.	3.6	40

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73	Association of maternal circulating 25(OH)D and calcium with birth weight: A mendelian randomisation analysis. <i>PLoS Medicine</i> , 2019, 16, e1002828.	8.4	39
74	Mitochondrial genetic variation is enriched in G-quadruplex regions that stall DNA synthesis in vitro. <i>Human Molecular Genetics</i> , 2020, 29, 1292-1309.	2.9	36
75	Genome-Wide Association Study of Microscopic Colitis in the UK Biobank Confirms Immune-Related Pathogenesis. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 1578-1582.	1.3	32
76	Targeted Allelic Expression Profiling in Human Islets Identifies <i>cis</i> -Regulatory Effects for Multiple Variants Identified by Type 2 Diabetes Genome-Wide Association Studies. <i>Diabetes</i> , 2015, 64, 1484-1491.	0.6	31
77	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	5.3	31
78	Is disrupted sleep a risk factor for Alzheimer's disease? Evidence from a two-sample Mendelian randomization analysis. <i>International Journal of Epidemiology</i> , 2021, 50, 817-828.	1.9	31
79	Quantification of the overall contribution of gene-environment interaction for obesity-related traits. <i>Nature Communications</i> , 2020, 11, 1385.	12.8	31
80	Higher adiposity and mental health: causal inference using Mendelian randomization. <i>Human Molecular Genetics</i> , 2021, 30, 2371-2382.	2.9	29
81	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 379-384.	7.1	28
82	Influence of cell distribution and diabetes status on the association between mitochondrial DNA copy number and aging phenotypes in the InCHIANTI study. <i>Aging Cell</i> , 2018, 17, e12683.	6.7	26
83	Using Mendelian Randomisation methods to understand whether diurnal preference is causally related to mental health. <i>Molecular Psychiatry</i> , 2021, 26, 6305-6316.	7.9	26
84	Assessing the Causal Role of Sleep Traits on Glycated Hemoglobin: A Mendelian Randomization Study. <i>Diabetes Care</i> , 2022, 45, 772-781.	8.6	25
85	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at <i>CCND2</i> Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. <i>Diabetes</i> , 2015, 64, 2279-2285.	0.6	24
86	A genome-wide association study identifies 5 loci associated with frozen shoulder and implicates diabetes as a causal risk factor. <i>PLoS Genetics</i> , 2021, 17, e1009577.	3.5	23
87	Genetic evidence that higher central adiposity causes gastro-oesophageal reflux disease: a Mendelian randomization study. <i>International Journal of Epidemiology</i> , 2020, 49, 1270-1281.	1.9	20
88	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2017, 25, 137-146.	2.8	18
89	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. <i>BMC Proceedings</i> , 2016, 10, 71-77.	1.6	17
90	A single nucleotide polymorphism genetic risk score to aid diagnosis of coeliac disease: a pilot study in clinical care. <i>Alimentary Pharmacology and Therapeutics</i> , 2020, 52, 1165-1173.	3.7	17

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91	A genome-wide association study implicates multiple mechanisms influencing raised urinary albumin-to-creatinine ratio. <i>Human Molecular Genetics</i> , 2019, 28, 4197-4207.	2.9	16
92	Common maternal and fetal genetic variants show expected polygenic effects on risk of small- or large-for-gestational-age (SGA or LGA), except in the smallest 3% of babies. <i>PLoS Genetics</i> , 2020, 16, e1009191.	3.5	13
93	The Common <i>HNF1A</i> Variant I27L Is a Modifier of Age at Diabetes Diagnosis in Individuals With HNF1A-MODY. <i>Diabetes</i> , 2018, 67, 1903-1907.	0.6	12
94	Assessment of MTNR1B Type 2 Diabetes Genetic Risk Modification by Shift Work and Morningness-Eveningness Preference in the UK Biobank. <i>Diabetes</i> , 2020, 69, 259-266.	0.6	11
95	A Mendelian Randomization Study Provides Evidence That Adiposity and Dyslipidemia Lead to Lower Urinary Albumin-to-Creatinine Ratio, a Marker of Microvascular Function. <i>Diabetes</i> , 2020, 69, 1072-1082.	0.6	10
96	Disease consequences of higher adiposity uncoupled from its adverse metabolic effects using Mendelian randomisation. <i>ELife</i> , 2022, 11, .	6.0	10
97	Clinical Features and Genetic Risk of Demyelination Following Anti-TNF Treatment. <i>Journal of Crohn's and Colitis</i> , 2020, 14, 1653-1661.	1.3	9
98	Higher maternal adiposity reduces offspring birthweight if associated with a metabolically favourable profile. <i>Diabetologia</i> , 2021, 64, 2790-2802.	6.3	9
99	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. <i>Human Molecular Genetics</i> , 2015, 24, 1504-1512.	2.9	8
100	Methods for quick, accurate and cost-effective determination of the type 1 diabetes genetic risk score (T1D-GRS). <i>Clinical Chemistry and Laboratory Medicine</i> , 2020, 58, e102-e104.	2.3	8
101	Understanding Factors That Cause Tinnitus: A Mendelian Randomization Study in the UK Biobank. <i>Ear and Hearing</i> , 2022, 43, 70-80.	2.1	7
102	Large Copy-Number Variants in UK Biobank Caused by Clonal Hematopoiesis May Confound Penetrance Estimates. <i>American Journal of Human Genetics</i> , 2020, 107, 325-329.	6.2	6
103	Mendelian randomization supports a causative effect of TSH on thyroid carcinoma. <i>Endocrine-Related Cancer</i> , 2020, 27, 551-559.	3.1	6
104	Response to Prakash et al.. <i>Genetics in Medicine</i> , 2019, 21, 1884-1885.	2.4	5
105	Genome-Wide Association Analysis of Pancreatic Beta-Cell Glucose Sensitivity. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2021, 106, 80-90.	3.6	5
106	Babies of South Asian and European Ancestry Show Similar Associations With Genetic Risk Score for Birth Weight Despite the Smaller Size of South Asian Newborns. <i>Diabetes</i> , 2022, 71, 821-836.	0.6	3
107	Simulated distributions from negative experiments highlight the importance of the body mass index distribution in explaining depression-to-body mass index genetic risk score interactions. <i>International Journal of Epidemiology</i> , 2022, 51, 1581-1592.	1.9	2
108	Fetal alleles predisposing to metabolically favorable adiposity are associated with higher birth weight. <i>Human Molecular Genetics</i> , 2022, 31, 1762-1775.	2.9	2

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109	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.6	1
110	Genetically defined favourable adiposity is not associated with a clinically meaningful difference in clinical course in people with type 2 diabetes but does associate with a favourable metabolic profile. Diabetic Medicine, 2021, 38, e14531.	2.3	1
111	OWE-16 Development and clinical validation of a genetic risk score for coeliac disease. , 2019, , .		0
112	Mendelian randomization to investigate the link between TSH and thyroid cancer. Endocrine-Related Cancer, 2021, 28, L11-L14.	3.1	0
113	Mendelian randomization supports a causative effect of TSH on thyroid carcinoma. Endocrine-Related Cancer, 2020, 27, Z1.	3.1	0
114	Does visual imagery vividness have a genetic basis? A genome-wide association study of 1019 individuals. Journal of Neurology, Neurosurgery and Psychiatry, 2022, 93, A51.1-A51.	1.9	0