

Anne U Jackson

List of Publications by Year in descending order

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Version: 2024-02-01

76
papers

41,547
citations

24978

57
h-index

54797

84
g-index

90
all docs

90
docs citations

90
times ranked

39005
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
2	ACE2 expression in adipose tissue is associated with cardio-metabolic risk factors and cell type composition—implications for COVID-19. <i>International Journal of Obesity</i> , 2022, 46, 1478-1486.	1.6	18
3	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	5.8	87
4	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15
5	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353
6	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. <i>PLoS Genetics</i> , 2020, 16, e1009019.	1.5	11
7	New alcohol-related genes suggest shared genetic mechanisms with neuropsychiatric disorders. <i>Nature Human Behaviour</i> , 2019, 3, 950-961.	6.2	75
8	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	13.7	161
9	Colocalization of GWAS and eQTL signals at loci with multiple signals identifies additional candidate genes for body fat distribution. <i>Human Molecular Genetics</i> , 2019, 28, 4161-4172.	1.4	41
10	Adipose Tissue Gene Expression Associations Reveal Hundreds of Candidate Genes for Cardiometabolic Traits. <i>American Journal of Human Genetics</i> , 2019, 105, 773-787.	2.6	45
11	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , 2019, 188, 1033-1054.	1.6	85
12	Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. <i>Nature Communications</i> , 2019, 10, 376.	5.8	64
13	Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , 2019, 570, 71-76.	13.7	248
14	Integrative analysis of gene expression, DNA methylation, physiological traits, and genetic variation in human skeletal muscle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 10883-10888.	3.3	114
15	A multi-ancestry genome-wide study incorporating gene-smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. <i>Human Molecular Genetics</i> , 2019, 28, 2615-2633.	1.4	31
16	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , 2019, 51, 636-648.	9.4	112
17	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	9.4	89
18	Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , 2018, 27, 1664-1674.	1.4	30

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19	A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. <i>American Journal of Human Genetics</i> , 2018, 102, 375-400.	2.6	123
20	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	9.4	924
21	Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. <i>PLoS ONE</i> , 2018, 13, e0198166.	1.1	94
22	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.	9.4	286
23	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
24	Genetic Regulation of Adipose Gene Expression and Cardio-Metabolic Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 428-443.	2.6	141
25	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.	0.3	102
26	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , 2017, 8, 14977.	5.8	169
27	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.3	615
28	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.	0.3	47
29	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
30	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , 2017, 70, .	1.3	123
31	A Type 2 Diabetes-Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the <i>ADCY5</i> Locus. <i>Diabetes</i> , 2017, 66, 2521-2530.	0.3	54
32	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
33	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. <i>PLoS Medicine</i> , 2017, 14, e1002383.	3.9	341
34	Novel association of TM6SF2 rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns. <i>Journal of Lipid Research</i> , 2017, 58, 1471-1481.	2.0	49
35	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
36	Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. <i>PLoS Genetics</i> , 2017, 13, e1007079.	1.5	49

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37	The genetic architecture of type 2 diabetes. <i>Nature</i> , 2016, 536, 41-47.	13.7	952
38	The genetic regulatory signature of type 2 diabetes in human skeletal muscle. <i>Nature Communications</i> , 2016, 7, 11764.	5.8	114
39	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	5.8	74
40	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , 2016, 48, 1151-1161.	9.4	261
41	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. <i>Nature Genetics</i> , 2016, 48, 1171-1184.	9.4	362
42	Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies <i>BCL2</i> and <i>FAM19A2</i> as Novel Insulin Sensitivity Loci. <i>Diabetes</i> , 2016, 65, 3200-3211.	0.3	67
43	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
44	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	1.5	331
45	Multiple Hepatic Regulatory Variants at the <i>GALNT2</i> GWAS Locus Associated with High-Density Lipoprotein Cholesterol. <i>American Journal of Human Genetics</i> , 2015, 97, 801-815.	2.6	49
46	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
47	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
48	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
49	Identification and Functional Characterization of <i>G6PC2</i> Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the <i>G6PC2-ABCB11</i> Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
50	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. <i>Nature Genetics</i> , 2015, 47, 1415-1425.	9.4	365
51	Impact of Type 2 Diabetes Susceptibility Variants on Quantitative Glycemic Traits Reveals Mechanistic Heterogeneity. <i>Diabetes</i> , 2014, 63, 2158-2171.	0.3	297
52	A Central Role for <i>GRB10</i> in Regulation of Islet Function in Man. <i>PLoS Genetics</i> , 2014, 10, e1004235.	1.5	164
53	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	9.4	1,818
54	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.	9.4	959

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55	Discovery and refinement of loci associated with lipid levels. <i>Nature Genetics</i> , 2013, 45, 1274-1283.	9.4	2,641
56	Common variants associated with plasma triglycerides and risk for coronary artery disease. <i>Nature Genetics</i> , 2013, 45, 1345-1352.	9.4	754
57	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013, 45, 621-631.	9.4	282
58	Trans-Ethnic Fine-Mapping of Lipid Loci Identifies Population-Specific Signals and Allelic Heterogeneity That Increases the Trait Variance Explained. <i>PLoS Genetics</i> , 2013, 9, e1003379.	1.5	112
59	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	1.5	371
60	The Metabochip, a Custom Genotyping Array for Genetic Studies of Metabolic, Cardiovascular, and Anthropometric Traits. <i>PLoS Genetics</i> , 2012, 8, e1002793.	1.5	448
61	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. <i>PLoS Genetics</i> , 2012, 8, e1002607.	1.5	419
62	Large-scale association analyses identify new loci influencing glycemic traits and provide insight into the underlying biological pathways. <i>Nature Genetics</i> , 2012, 44, 991-1005.	9.4	746
63	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. <i>Nature Genetics</i> , 2012, 44, 981-990.	9.4	1,748
64	A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. <i>Nature Genetics</i> , 2012, 44, 659-669.	9.4	762
65	Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , 2011, 478, 103-109.	13.7	1,855
66	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. <i>Nature Genetics</i> , 2011, 43, 1005-1011.	9.4	403
67	Fine Mapping of Five Loci Associated with Low-Density Lipoprotein Cholesterol Detects Variants That Double the Explained Heritability. <i>PLoS Genetics</i> , 2011, 7, e1002198.	1.5	134
68	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010, 467, 832-838.	13.7	1,789
69	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. <i>Nature Genetics</i> , 2010, 42, 579-589.	9.4	1,631
70	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. <i>Nature Genetics</i> , 2010, 42, 949-960.	9.4	836
71	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. <i>Nature Genetics</i> , 2010, 42, 937-948.	9.4	2,634
72	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. <i>Nature Genetics</i> , 2010, 42, 105-116.	9.4	1,982

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73	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662
74	Common variants at 30 loci contribute to polygenic dyslipidemia. Nature Genetics, 2009, 41, 56-65.	9.4	1,234
75	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
76	Newly identified loci that influence lipid concentrations and risk of coronary artery disease. Nature Genetics, 2008, 40, 161-169.	9.4	1,488