

Adam E Locke

List of Publications by Year in descending order

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Version: 2024-02-01

65
papers

18,627
citations

87843

38
h-index

88593

70
g-index

85
all docs

85
docs citations

85
times ranked

29044
citing authors

#	ARTICLE	IF	CITATIONS
1	Heterozygous variants of <i>CLPB</i> are a cause of severe congenital neutropenia. <i>Blood</i> , 2022, 139, 779-791.	0.6	25
2	Genome-wide analysis provides genetic evidence that ACE2 influences COVID-19 risk and yields risk scores associated with severe disease. <i>Nature Genetics</i> , 2022, 54, 382-392.	9.4	97
3	Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci. <i>Nature Communications</i> , 2022, 13, 1644.	5.8	63
4	Exome sequencing in bipolar disorder identifies AKAP11 as a risk gene shared with schizophrenia. <i>Nature Genetics</i> , 2022, 54, 541-547.	9.4	65
5	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	9.4	250
6	High heritability of ascending aortic diameter and trans-ancestry prediction of thoracic aortic disease. <i>Nature Genetics</i> , 2022, 54, 772-782.	9.4	29
7	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. <i>Nature Genetics</i> , 2022, 54, 761-771.	9.4	68
8	Whole Exome Sequencing Enhanced Imputation Identifies 85 Metabolite Associations in the Alpine CHRIS Cohort. <i>Metabolites</i> , 2022, 12, 604.	1.3	6
9	Association of structural variation with cardiometabolic traits in Finns. <i>American Journal of Human Genetics</i> , 2021, 108, 583-596.	2.6	22
10	Mitochondrial genome copy number measured by DNA sequencing in human blood is strongly associated with metabolic traits via cell-type composition differences. <i>Human Genomics</i> , 2021, 15, 34.	1.4	7
11	Pan-ancestry exome-wide association analyses of COVID-19 outcomes in 586,157 individuals. <i>American Journal of Human Genetics</i> , 2021, 108, 1350-1355.	2.6	72
12	Sequencing of 640,000 exomes identifies <i>GPR75</i> variants associated with protection from obesity. <i>Science</i> , 2021, 373, .	6.0	130
13	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. <i>Cell</i> , 2021, 184, 4784-4818.e17.	13.5	188
14	Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. <i>Molecular Psychiatry</i> , 2021, 26, 5239-5250.	4.1	15
15	Exome sequencing and analysis of 454,787 UK Biobank participants. <i>Nature</i> , 2021, 599, 628-634.	13.7	377
16	Gene-level analysis of rare variants in 379,066 whole exome sequences identifies an association of GIGYF1 loss of function with type 2 diabetes. <i>Scientific Reports</i> , 2021, 11, 21565.	1.6	25
17	Genetic and functional evidence links a missense variant in <i>B4GALT1</i> to lower LDL and fibrinogen. <i>Science</i> , 2021, 374, 1221-1227.	6.0	14
18	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021, 600, 675-679.	13.7	353

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19	Adiponectin GWAS loci harboring extensive allelic heterogeneity exhibit distinct molecular consequences. <i>PLoS Genetics</i> , 2020, 16, e1009019.	1.5	11
20	Exome sequencing of Finnish isolates enhances rare-variant association power. <i>Nature</i> , 2019, 572, 323-328.	13.7	161
21	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
22	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
23	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
24	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
25	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.	3.3	28
26	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	9.4	1,331
27	Extremely rare variants reveal patterns of germline mutation rate heterogeneity in humans. <i>Nature Communications</i> , 2018, 9, 3753.	5.8	121
28	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. <i>American Journal of Human Genetics</i> , 2018, 102, 1204-1211.	2.6	102
29	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
30	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	13.7	544
31	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. <i>American Journal of Human Genetics</i> , 2017, 100, 865-884.	2.6	131
32	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
33	Interaction between the <i>FTO</i> gene, body mass index and depression: meta-analysis of 13701 individuals. <i>British Journal of Psychiatry</i> , 2017, 211, 70-76.	1.7	49
34	Across-cohort QC analyses of GWAS summary statistics from complex traits. <i>European Journal of Human Genetics</i> , 2017, 25, 137-146.	1.4	18
35	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <i>Scientific Data</i> , 2017, 4, 170179.	2.4	31
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	Exome Sequencing of Familial Bipolar Disorder. <i>JAMA Psychiatry</i> , 2016, 73, 590.	6.0	97
39	Next-generation genotype imputation service and methods. <i>Nature Genetics</i> , 2016, 48, 1284-1287.	9.4	2,828
40	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. <i>Nature Communications</i> , 2016, 7, 10495.	5.8	245
41	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. <i>Human Molecular Genetics</i> , 2016, 25, 2070-2081.	1.4	21
42	Genome-Wide Association Study of Down Syndrome-Associated Atrioventricular Septal Defects. <i>G3: Genes, Genomes, Genetics</i> , 2015, 5, 1961-1971.	0.8	28
43	Mendelian Randomization Study of Body Mass Index and Colorectal Cancer Risk. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2015, 24, 1024-1031.	1.1	67
44	Contribution of copy-number variation to Down syndrome-associated atrioventricular septal defects. <i>Genetics in Medicine</i> , 2015, 17, 554-560.	1.1	24
45	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	13.7	1,328
46	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	13.7	3,823
47	Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. <i>PLoS Genetics</i> , 2015, 11, e1004876.	1.5	95
48	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. <i>Human Molecular Genetics</i> , 2015, 24, 6849-6860.	1.4	55
49	Population genetic differentiation of height and body mass index across Europe. <i>Nature Genetics</i> , 2015, 47, 1357-1362.	9.4	227
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	In search of rare variants: Preliminary results from whole genome sequencing of 1,325 individuals with psychophysiological endophenotypes. <i>Psychophysiology</i> , 2014, 51, 1309-1320.	1.2	25
52	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. <i>American Journal of Human Genetics</i> , 2014, 94, 233-245.	2.6	193
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	Quality control and conduct of genome-wide association meta-analyses. <i>Nature Protocols</i> , 2014, 9, 1192-1212.	5.5	398

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55	Simulation of Finnish Population History, Guided by Empirical Genetic Data, to Assess Power of Rare-Variant Tests in Finland. <i>American Journal of Human Genetics</i> , 2014, 94, 710-720.	2.6	24
56	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
57	Abstract 050: Meta-analysis of Genetic Associations in up to 339,224 Individuals Identify 66 New Loci for Bmi, Confirming a Neuronal Contribution to Body Weight Regulation and Implicating Several Novel Pathways. <i>Circulation</i> , 2013, 127, .	1.6	0
58	An Excess of Deleterious Variants in VEGF-A Pathway Genes in Down-Syndrome-Associated Atrioventricular Septal Defects. <i>American Journal of Human Genetics</i> , 2012, 91, 646-659.	2.6	99
59	Altered patterns of multiple recombinant events are associated with nondisjunction of chromosome 21. <i>Human Genetics</i> , 2012, 131, 1039-1046.	1.8	39
60	Lack of maternal folic acid supplementation is associated with heart defects in Down syndrome: A report from the National Down Syndrome Project. <i>Birth Defects Research Part A: Clinical and Molecular Teratology</i> , 2011, 91, 885-893.	1.6	43
61	Variation in folate pathway genes contributes to risk of congenital heart defects among individuals with Down syndrome. <i>Genetic Epidemiology</i> , 2010, 34, 613-623.	0.6	66
62	Combining Microarray-based Genomic Selection (MGS) with the Illumina Genome Analyzer Platform to Sequence Diploid Target Regions. <i>Annals of Human Genetics</i> , 2009, 73, 502-513.	0.3	16
63	Validity of Self-Reported Sunscreen Use by Parents, Children, and Lifeguards. <i>American Journal of Preventive Medicine</i> , 2009, 36, 63-69.	1.6	85
64	Ethnicity, sex, and the incidence of congenital heart defects: a report from the National Down Syndrome Project. <i>Genetics in Medicine</i> , 2008, 10, 173-180.	1.1	232
65	A novel procedure for genotyping of single nucleotide polymorphisms in trisomy with genomic DNA and the invader assay. <i>Nucleic Acids Research</i> , 2008, 36, e145-e145.	6.5	14