

# Jennifer E Huffman

## List of Publications by Year in descending order

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Version: 2024-02-01

124  
papers

18,359  
citations

19608

61  
h-index

16605

123  
g-index

146  
all docs

146  
docs citations

146  
times ranked

29182  
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	13.7	1,204
2	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
3	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , 2013, 45, 145-154.	9.4	675
4	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , 2010, 42, 436-440.	9.4	581
5	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , 2013, 45, 501-512.	9.4	578
6	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. <i>PLoS Genetics</i> , 2014, 10, e1004234.	1.5	553
7	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
8	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , 2010, 42, 36-44.	9.4	518
9	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , 2018, 50, 1514-1523.	9.4	497
10	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , 2017, 49, 1758-1766.	9.4	470
11	Discovery of 318 new risk loci for type 2 diabetes and related vascular outcomes among 1.4 million participants in a multi-ancestry meta-analysis. <i>Nature Genetics</i> , 2020, 52, 680-691.	9.4	445
12	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , 2020, 182, 1214-1231.e11.	13.5	388
13	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , 2012, 490, 267-272.	13.7	383
14	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , 2011, 43, 1082-1090.	9.4	367
15	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , 2015, 47, 1294-1303.	9.4	357
16	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , 2020, 182, 1198-1213.e14.	13.5	353
17	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53,949). <i>Molecular Psychiatry</i> , 2015, 20, 183-192.	4.1	344
18	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

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19	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. <i>PLoS Genetics</i> , 2013, 9, e1003225.	1.5	323
20	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , 2014, 2, 719-729.	5.5	319
21	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , 2015, 72, 642.	6.0	289
22	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. <i>American Journal of Human Genetics</i> , 2014, 94, 223-232.	2.6	287
23	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
24	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , 2017, 49, 946-952.	9.4	279
25	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
26	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , 2018, 50, 834-848.	9.4	239
27	Genomics Meets Glycomics—The First GWAS Study of Human N-Glycome Identifies HNF1 $\alpha$ as a Master Regulator of Plasma Protein Fucosylation. <i>PLoS Genetics</i> , 2010, 6, e1001256.	1.5	213
28	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
29	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. <i>Nature Genetics</i> , 2011, 43, 940-947.	9.4	191
30	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. <i>PLoS Genetics</i> , 2012, 8, e1002490.	1.5	181
31	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , 2016, 46, 170-182.	1.4	178
32	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , 2019, 25, 1274-1279.	15.2	177
33	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , 2015, 6, 5897.	5.8	173
34	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , 2015, 523, 459-462.	13.7	173
35	Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1598-1610.	2.5	169
36	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

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37	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , 2019, 134, 1645-1657.	0.6	162
38	Genome-wide physical activity interactions in adiposity – A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , 2017, 13, e1006528.	1.5	158
39	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. <i>Nature Genetics</i> , 2019, 51, 1574-1579.	9.4	152
40	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. <i>Human Molecular Genetics</i> , 2010, 19, 4304-4311.	1.4	136
41	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , 2014, 46, 669-677.	9.4	131
42	Multiethnic Meta-Analysis of Genome-Wide Association Studies in >100 000 Subjects Identifies 23 Fibrinogen-Associated Loci but No Strong Evidence of a Causal Association Between Circulating Fibrinogen and Cardiovascular Disease. <i>Circulation</i> , 2013, 128, 1310-1324.	1.6	128
43	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
44	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. <i>Nature Medicine</i> , 2021, 27, 668-676.	15.2	120
45	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
46	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 13366-13371.	3.3	110
47	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , 2017, 9, 23.	3.6	110
48	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , 2015, 6, 8658.	5.8	108
49	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. <i>PLoS Genetics</i> , 2014, 10, e1004474.	1.5	105
50	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. <i>Behavior Genetics</i> , 2014, 44, 295-313.	1.4	103
51	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. <i>American Journal of Human Genetics</i> , 2019, 104, 260-274.	2.6	103
52	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , 2019, 139, 620-635.	1.6	102
53	Association Between Chromosome 9p21 Variants and the Ankle-Brachial Index Identified by a Meta-Analysis of 21 Genome-Wide Association Studies. <i>Circulation: Cardiovascular Genetics</i> , 2012, 5, 100-112.	5.1	98
54	Mutations in <i>HNF1A</i> Result in Marked Alterations of Plasma Glycan Profile. <i>Diabetes</i> , 2013, 62, 1329-1337.	0.3	97

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55	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 2017, 49, 1560-1563.	9.4	93
56	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	9.4	91
57	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
58	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. <i>PLoS Genetics</i> , 2014, 10, e1004508.	1.5	80
59	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	6.2	79
60	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. <i>Human Molecular Genetics</i> , 2013, 22, 4857-4869.	1.4	77
61	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. <i>Nature Genetics</i> , 2022, 54, 125-127.	9.4	75
62	Polymorphisms in B3GAT1, SLC9A9 and MGAT5 are associated with variation within the human plasma N-glycome of 3533 European adults. <i>Human Molecular Genetics</i> , 2011, 20, 5000-5011.	1.4	74
63	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
64	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , 2016, 25, 358-370.	1.4	73
65	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. <i>PLoS Genetics</i> , 2016, 12, e1005804.	1.5	72
66	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2019, 26, 1255-1262.	2.2	69
67	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
68	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. <i>PLoS ONE</i> , 2015, 10, e0119752.	1.1	64
69	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. <i>Circulation</i> , 2011, 123, 1864-1872.	1.6	60
70	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. <i>PLoS ONE</i> , 2011, 6, e19382.	1.1	56
71	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , 2015, 126, e19-e29.	0.6	55
72	The association between galactosylation of immunoglobulin G and body mass index. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , 2014, 48, 20-25.	2.5	52

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73	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , 2015, 6, 6065.	5.8	45
74	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. <i>European Journal of Human Genetics</i> , 2016, 24, 1035-1040.	1.4	45
75	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. <i>PLoS Genetics</i> , 2013, 9, e1003585.	1.5	43
76	Genome-Wide Association Study for Circulating Tissue Plasminogen Activator Levels and Functional Follow-Up Implicates Endothelial <i>STXBP5</i> and <i>STX2</i> . <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2014, 34, 1093-1101.	1.1	43
77	The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. <i>Nature Communications</i> , 2020, 11, 3479.	5.8	43
78	Use of the modified Atkins diet for adolescents with chronic daily headache. <i>Cephalalgia</i> , 2010, 30, 1014-6.	1.8	41
79	SOS2 and ACP1 Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , 2017, 28, 981-994.	3.0	39
80	Rare coding variants pinpoint genes that control human hematological traits. <i>PLoS Genetics</i> , 2017, 13, e1006925.	1.5	39
81	Epigenetic silencing of <i>HNF1A</i> associates with changes in the composition of the human plasma N-glycome. <i>Epigenetics</i> , 2012, 7, 164-172.	1.3	37
82	Examining the current standards for genetic discovery and replication in the era of mega-biobanks. <i>Nature Communications</i> , 2018, 9, 5054.	5.8	37
83	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , 2017, 46, dyw318.	0.9	36
84	A genome-wide association study of suicide attempts in the million veterans program identifies evidence of pan-ancestry and ancestry-specific risk loci. <i>Molecular Psychiatry</i> , 2022, 27, 2264-2272.	4.1	35
85	Meta-analysis of 49â€¦549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in <i>ANGPTL4</i> determining fasting TG levels. <i>Journal of Medical Genetics</i> , 2016, 53, 441-449.	1.5	34
86	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , 2019, 133, 967-977.	0.6	34
87	The <i>TCF7L2</i> Diabetes Risk Variant is Associated with HbA <sub>1C</sub> Levels: a Genome-Wide Association Meta-Analysis. <i>Annals of Human Genetics</i> , 2010, 74, 471-478.	0.3	33
88	Genome-wide analysis of epistasis in body mass index using multiple human populations. <i>European Journal of Human Genetics</i> , 2012, 20, 857-862.	1.4	33
89	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015, 6, 7756.	5.8	32
90	Association of <i>APOL1</i> Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. <i>Circulation</i> , 2019, 140, 1031-1040.	1.6	31

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91	Association of Medication with the Human Plasma N-Glycome. <i>Journal of Proteome Research</i> , 2012, 11, 1821-1831.	1.8	30
92	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. <i>Nature Communications</i> , 2019, 10, 357.	5.8	30
93	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , 2015, 24, 6836-6848.	1.4	28
94	Genome-wide Association Study of Anthropometric Traits in Korčula Island, Croatia. <i>Croatian Medical Journal</i> , 2009, 50, 7-16.	0.2	27
95	Genetic variants in RBF3X are associated with sleep latency. <i>European Journal of Human Genetics</i> , 2016, 24, 1488-1495.	1.4	27
96	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , 2015, 24, 4167-4182.	1.4	24
97	Glycomics meets lipidomics—associations of N-glycans with classical lipids, glycerophospholipids, and sphingolipids in three European populations. <i>Molecular BioSystems</i> , 2011, 7, 1852.	2.9	19
98	The total burden of rare, non-synonymous exome genetic variants is not associated with childhood or late-life cognitive ability. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20140117.	1.2	19
99	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , 2018, 3, 4.	0.9	19
100	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene–Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , 2016, 40, 404-415.	0.6	18
101	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , 2019, 14, e0216222.	1.1	17
102	Phenome-wide association of 1809 phenotypes and COVID-19 disease progression in the Veterans Health Administration Million Veteran Program. <i>PLoS ONE</i> , 2021, 16, e0251651.	1.1	17
103	Immunoglobulin isotypes of lactating Holstein cows classified as high, average, and low type-1 or -2 immune responders. <i>Veterinary Immunology and Immunopathology</i> , 2011, 144, 259-269.	0.5	16
104	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program. <i>PLoS Genetics</i> , 2022, 18, e1010113.	1.5	16
105	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. <i>Platelets</i> , 2019, 30, 164-173.	1.1	15
106	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. <i>PLoS ONE</i> , 2011, 6, e23836.	1.1	15
107	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2020, 41, 380-386.	1.1	14
108	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. <i>Journal of the American Society of Nephrology: JASN</i> , 2022, 33, 511-529.	3.0	14

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109	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. <i>Thyroid</i> , 2021, 31, 1305-1315.	2.4	13
110	Local Exome Sequences Facilitate Imputation of Less Common Variants and Increase Power of Genome Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e68604.	1.1	13
111	Multi-phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. <i>Journal of Thrombosis and Haemostasis</i> , 2022, 20, 1331-1349.	1.9	12
112	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. <i>PLoS Genetics</i> , 2022, 18, e1010193.	1.5	12
113	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. <i>PLoS ONE</i> , 2020, 15, e0239752.	1.1	9
114	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program. <i>Frontiers in Genetics</i> , 2021, 12, 777076.	1.1	9
115	No Evidence for Genome-Wide Interactions on Plasma Fibrinogen by Smoking, Alcohol Consumption and Body Mass Index: Results from Meta-Analyses of 80,607 Subjects. <i>PLoS ONE</i> , 2014, 9, e111156.	1.1	8
116	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. <i>Npj Aging and Mechanisms of Disease</i> , 2015, 1, 15011.	4.5	8
117	Leprosy epidemics during history increased protective allele frequency of PARK2/PACRG genes in the population of the Mljet Island, Croatia. <i>European Journal of Medical Genetics</i> , 2011, 54, e548-52.	0.7	7
118	Genome-wide association study identifies FUT8 and ESR2 as co-regulators of a bi-antennary N-linked glycan A2 (GlcNAc-2-Man-3-GlcNAc-2-) in human plasma proteins. <i>Nature Precedings</i> , 2009, , .	0.1	6
119	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. <i>Human Molecular Genetics</i> , 2022, 31, 2333-2347.	1.4	6
120	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. <i>Circulation Research</i> , 2020, 127, 394-396.	2.0	3
121	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. <i>PLoS ONE</i> , 2012, 7, e31369.	1.1	3
122	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. <i>PLoS ONE</i> , 2022, 17, e0267900.	1.1	2
123	General Framework for Meta-Analysis of Haplotype Association Tests. <i>Genetic Epidemiology</i> , 2016, 40, 244-252.	0.6	0
124	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. <i>BMC Genetics</i> , 2016, 17, 116.	2.7	0