

# Jennifer E Huffman

## List of Publications by Citations

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127  
papers

11,854  
citations

54  
h-index

108  
g-index

146  
ext. papers

15,816  
ext. citations

15.4  
avg, IF

4.4  
L-index

#	Paper	IF	Citations
127	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , <b>2016</b> , 533, 539-42	50.4	850
126	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. <i>Nature Genetics</i> , <b>2010</b> , 42, 436-40	36.3	521
125	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. <i>Nature Genetics</i> , <b>2013</b> , 45, 145-54	36.3	505
124	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. <i>Nature Genetics</i> , <b>2013</b> , 45, 501-12	36.3	437
123	Genome-wide association study identifies five loci associated with lung function. <i>Nature Genetics</i> , <b>2010</b> , 42, 36-44	36.3	430
122	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , <b>2018</b> , 50, 1412-1425	36.3	386
121	A general approach for haplotype phasing across the full spectrum of relatedness. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004234	6	377
120	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. <i>Nature Genetics</i> , <b>2011</b> , 43, 1082-90	36.3	313
119	Exome-wide association study of plasma lipids in >300,000 individuals. <i>Nature Genetics</i> , <b>2017</b> , 49, 1758-1766	36.3	310
118	FTO genotype is associated with phenotypic variability of body mass index. <i>Nature</i> , <b>2012</b> , 490, 267-72	50.4	304
117	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , <b>2018</b> , 50, 1225-1233	36.3	277
116	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. <i>Nature Genetics</i> , <b>2018</b> , 50, 1514-1523	36.3	260
115	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). <i>Molecular Psychiatry</i> , <b>2015</b> , 20, 183-92	15.1	250
114	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. <i>Lancet Diabetes and Endocrinology</i> , <b>2014</b> , 2, 719-29	18.1	250
113	Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003225	6	242
112	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> , <b>2014</b> , 94, 223-32	11	233
111	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. <i>Nature Genetics</i> , <b>2015</b> , 47, 1294-1303	36.3	226

110	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. <i>JAMA Psychiatry</i> , <b>2015</b> , 72, 642-50	14.5	222
109	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> , <b>2015</b> , 11, e1005378	6	220
108	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , <b>2018</b> , 50, 26-41	36.3	186
107	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. <i>Nature Genetics</i> , <b>2016</b> , 48, 1151-1161	36.3	181
106	Genomics meets glycomics-the first GWAS study of human N-Glycome identifies HNF1 $\alpha$ s a master regulator of plasma protein fucosylation. <i>PLoS Genetics</i> , <b>2010</b> , 6, e1001256	6	177
105	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. <i>Nature Genetics</i> , <b>2017</b> , 49, 946-952	36.3	176
104	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. <i>American Journal of Human Genetics</i> , <b>2014</b> , 94, 233-45	11	170
103	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> , <b>2011</b> , 43, 940-7	36.3	168
102	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. <i>Nature Communications</i> , <b>2015</b> , 6, 5897	17.4	147
101	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. <i>PLoS Genetics</i> , <b>2012</b> , 8, e1002490	6	145
100	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> , <b>2020</b> , 52, 680-691	36.3	140
99	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. <i>Nature Genetics</i> , <b>2018</b> , 50, 834-848	36.3	135
98	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. <i>Human Molecular Genetics</i> , <b>2010</b> , 19, 4304-11	5.6	125
97	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. <i>Behavior Genetics</i> , <b>2016</b> , 46, 170-82	3.2	122
96	Comparative performance of four methods for high-throughput glycosylation analysis of immunoglobulin G in genetic and epidemiological research. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 1598-610	7.6	120
95	Directional dominance on stature and cognition in diverse human populations. <i>Nature</i> , <b>2015</b> , 523, 459-463	30.4	119
94	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> , <b>2013</b> , 128, 1310-24	16.7	107
93	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. <i>Nature Communications</i> , <b>2017</b> , 8, 14977	17.4	105

92	Genome-wide association analysis identifies six new loci associated with forced vital capacity. <i>Nature Genetics</i> , <b>2014</b> , 46, 669-77	36.3	104
91	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006528	6	103
90	The Polygenic and Monogenic Basis of Blood Traits and Diseases. <i>Cell</i> , <b>2020</b> , 182, 1214-1231.e11	56.2	96
89	Genetic variants linked to education predict longevity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2016</b> , 113, 13366-13371	11.5	90
88	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. <i>Cell</i> , <b>2020</b> , 182, 1198-1213.e14	56.2	88
87	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. <i>Genome Medicine</i> , <b>2017</b> , 9, 23	14.4	85
86	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. <i>Hypertension</i> , <b>2017</b> ,	8.5	85
85	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> , <b>2012</b> , 5, 100-12		84
84	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> , <b>2014</b> , 44, 295-313	3.2	80
83	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. <i>Nature Communications</i> , <b>2015</b> , 6, 8658	17.4	79
82	Mutations in HNF1A result in marked alterations of plasma glycan profile. <i>Diabetes</i> , <b>2013</b> , 62, 1329-37	0.9	74
81	Genome-wide association study of peripheral artery disease in the Million Veteran Program. <i>Nature Medicine</i> , <b>2019</b> , 25, 1274-1279	50.5	73
80	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004474	6	71
79	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , <b>2017</b> , 49, 1560-1563	36.3	68
78	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. <i>Blood</i> , <b>2019</b> , 134, 1645-1657	2.2	63
77	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. <i>Human Molecular Genetics</i> , <b>2013</b> , 22, 4857-69	5.6	62
76	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> , <b>2011</b> , 20, 5000-11	5.6	61
75	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. <i>Nature Genetics</i> , <b>2019</b> , 51, 636-648	36.3	59

74	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. <i>Nature Genetics</i> , <b>2019</b> , 51, 1574-1579	36.3	56
73	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. <i>Human Molecular Genetics</i> , <b>2016</b> , 25, 358-70	5.6	54
72	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. <i>Circulation</i> , <b>2019</b> , 139, 620-635	16.7	51
71	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. <i>PLoS Genetics</i> , <b>2016</b> , 12, e1005804	6	50
70	Genetic predictors of fibrin D-dimer levels in healthy adults. <i>Circulation</i> , <b>2011</b> , 123, 1864-72	16.7	47
69	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , <b>2016</b> , 7, 13357	17.4	46
68	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. <i>Blood</i> , <b>2015</b> , 126, e19-29	2.2	45
67	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004508	6	45
66	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> , <b>2019</b> , 104, 260-274	11	43
65	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. <i>PLoS ONE</i> , <b>2011</b> , 6, e19382	3.7	41
64	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. <i>American Journal of Epidemiology</i> , <b>2019</b> , 188, 1033-1054	3.8	39
63	Causal and synthetic associations of variants in the SERPINA gene cluster with alpha1-antitrypsin serum levels. <i>PLoS Genetics</i> , <b>2013</b> , 9, e1003585	6	37
62	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. <i>European Journal of Human Genetics</i> , <b>2016</b> , 24, 1035-40	5.3	34
61	The association between galactosylation of immunoglobulin G and body mass index. <i>Progress in Neuro-Psychopharmacology and Biological Psychiatry</i> , <b>2014</b> , 48, 20-5	5.5	33
60	Genome-wide association study for circulating tissue plasminogen activator levels and functional follow-up implicates endothelial STXBP5 and STX2. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2014</b> , 34, 1093-101	9.4	33
59	Use of the modified Atkins diet for adolescents with chronic daily headache. <i>Cephalgia</i> , <b>2010</b> , 30, 1014-61	6.1	33
58	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , <b>2021</b> , 5, 59-70	12.8	33
57	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. <i>Nature Communications</i> , <b>2015</b> , 6, 6065	17.4	32

56	Epigenetic silencing of HNF1A associates with changes in the composition of the human plasma N-glycome. <i>Epigenetics</i> , <b>2012</b> , 7, 164-72	5.7	31
55	Modulation of genetic associations with serum urate levels by body-mass-index in humans. <i>PLoS ONE</i> , <b>2015</b> , 10, e0119752	3.7	31
54	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2017</b> , 28, 981-994	12.7	30
53	Association of medication with the human plasma N-glycome. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 1821-31	5.6	29
52	The TCF7L2 diabetes risk variant is associated with HbA <sub>1c</sub> levels: a genome-wide association meta-analysis. <i>Annals of Human Genetics</i> , <b>2010</b> , 74, 471-8	2.2	29
51	Rare coding variants pinpoint genes that control human hematological traits. <i>PLoS Genetics</i> , <b>2017</b> , 13, e1006925	6	28
50	Genome-wide association study of anthropometric traits in Korcula Island, Croatia. <i>Croatian Medical Journal</i> , <b>2009</b> , 50, 7-16	1.6	27
49	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. <i>Journal of Medical Genetics</i> , <b>2016</b> , 53, 441-9 <sup>5.8</sup>	5.8	27
48	Genome-wide analysis of epistasis in body mass index using multiple human populations. <i>European Journal of Human Genetics</i> , <b>2012</b> , 20, 857-62	5.3	26
47	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , <b>2020</b> , 52, 1314-1332	36.3	26
46	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. <i>International Journal of Epidemiology</i> , <b>2017</b> , 46, 894-904	7.8	25
45	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2019</b> , 26, 1255-1262	8.6	23
44	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , <b>2015</b> , 6, 7756	17.4	23
43	Examining the current standards for genetic discovery and replication in the era of mega-biobanks. <i>Nature Communications</i> , <b>2018</b> , 9, 5054	17.4	22
42	Integrative pathway genomics of lung function and airflow obstruction. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 6836-48	5.6	20
41	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. <i>Human Molecular Genetics</i> , <b>2015</b> , 24, 4167-82	5.6	19
40	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. <i>Nature Medicine</i> , <b>2021</b> , 27, 668-676	50.5	19
39	Association of Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. <i>Circulation</i> , <b>2019</b> , 140, 1031-1040	16.7	18

38	Genetic variants in RBF0X3 are associated with sleep latency. <i>European Journal of Human Genetics</i> , <b>2016</b> , 24, 1488-95	5.3	18
37	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> , <b>2014</b> , 281, 20140117	4.4	17
36	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. <i>Blood</i> , <b>2019</b> , 133, 967-977	2.2	17
35	Glycomics meets lipidomics--associations of N-glycans with classical lipids, glycerophospholipids, and sphingolipids in three European populations. <i>Molecular BioSystems</i> , <b>2011</b> , 7, 1852-62		16
34	Meta-analysis of exome array data identifies six novel genetic loci for lung function. <i>Wellcome Open Research</i> , <b>2018</b> , 3, 4	4.8	16
33	Characterisation of genome-wide association epistasis signals for serum uric acid in human population isolates. <i>PLoS ONE</i> , <b>2011</b> , 6, e23836	3.7	15
32	An Empirical Comparison of Joint and Stratified Frameworks for Studying G x E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene-Lifestyle Interactions Working Group. <i>Genetic Epidemiology</i> , <b>2016</b> , 40, 404-15	2.6	15
31	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. <i>Nature Communications</i> , <b>2019</b> , 10, 357	17.4	12
30	Immunoglobulin isotypes of lactating Holstein cows classified as high, average, and low type-1 or -2 immune responders. <i>Veterinary Immunology and Immunopathology</i> , <b>2011</b> , 144, 259-69	2	12
29	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. <i>PLoS ONE</i> , <b>2019</b> , 14, e0216222	3.7	11
28	The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. <i>Nature Communications</i> , <b>2020</b> , 11, 3479	17.4	11
27	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. <i>Platelets</i> , <b>2019</b> , 30, 164-173	3.6	9
26	Local exome sequences facilitate imputation of less common variants and increase power of genome wide association studies. <i>PLoS ONE</i> , <b>2013</b> , 8, e68604	3.7	8
25	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19.. <i>Nature Genetics</i> , <b>2022</b> ,	36.3	7
24	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> , <b>2009</b> ,		6
23	Fine mapping the region reveals a common intronic insertion associated to HDL-C. <i>Npj Aging and Mechanisms of Disease</i> , <b>2015</b> , 1, 15011	5.5	5
22	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> , <b>2014</b> , 9, e111156	3.7	5
21	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> , <b>2011</b> , 54, e548-52	2.6	5

20	Alternative splicing of alters the risk for severe COVID-19 <b>2021</b> ,		5
19	A trans-ancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation		5
18	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
17	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease-Brief Report. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2021</b> , 41, 380-386	9.4	4
16	Phenome-wide association of 1809 phenotypes and COVID-19 disease progression in the Veterans Health Administration Million Veteran Program. <i>PLoS ONE</i> , <b>2021</b> , 16, e0251651	3.7	4
15	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
14	Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. <i>PLoS ONE</i> , <b>2012</b> , 7, e31369	3.7	2
13	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239752	3.7	2
12	Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies		2
11	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. <i>Thyroid</i> , <b>2021</b> , 31, 1305-1315	6.2	2
10	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin.. <i>Journal of the American Society of Nephrology: JASN</i> , <b>2022</b> , 33, 511-529	12.7	2
9	A multi-ancestry 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> ,	36.3	2
8	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. <i>Circulation Research</i> , <b>2020</b> , 127, 394-396	15.7	1
7	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> , <b>2021</b> , 12, 777076	4.5	1
6	A MUC5B gene polymorphism, rs35705950-T, confers protective effects in COVID-19 infection		1
5	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> , <b>2022</b> , 18, e1010113	6	0
4	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. <i>PLoS Genetics</i> , <b>2022</b> , 18, e1010193	6	0
3	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> , <b>2016</b> , 17, 116	2.6	



- 2 General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52 2.6
- 1 Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. *PLoS ONE*, **2022**, 17, e0267900 3.7