Jennifer E Huffman

List of Publications by Year in Descending Order

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	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19.. *Nature Genetics*, **2022**,	36.3	7
126	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin.. *Journal of the American Society of Nephrology: JASN*, **2022**, 33, 511-529	12.7	2
125	A Phenome-Wide Association Study of genes associated with COVID-19 severity reveals shared genetics with complex diseases in the Million Veteran Program.. *PLoS Genetics*, **2022**, 18, e1010113	6	0
124	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. *PLoS ONE*, **2022**, 17, e0267900	3.7	
123	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. *PLoS Genetics*, **2022**, 18, e1010193	6	0
122	Genetic Loci Associated With COVID-19 Positivity and Hospitalization in White, Black, and Hispanic Veterans of the VA Million Veteran Program.. *Frontiers in Genetics*, **2021**, 12, 777076	4.5	1
121	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease-Brief Report. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 380-386	9.4	4
120	Alternative splicing of alters the risk for severe COVID-19 **2021**,		5
119	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. *Nature Medicine*, **2021**, 27, 668-676	50.5	19
118	Phenome-wide association of 1809 phenotypes and COVID-19 disease progression in the Veterans Health Administration Million Veteran Program. *PLoS ONE*, **2021**, 16, e0251651	3.7	4
117	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
116	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. *Thyroid*, **2021**, 31, 1305-1315	6.2	2
115	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. *Circulation Research*, **2020**, 127, 394-396	15.7	1
114	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. *Nature Genetics*, **2020**, 52, 680-691	36.3	140
113	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. *PLoS ONE*, **2020**, 15, e0239752	3.7	2
112	The Polygenic and Monogenic Basis of Blood Traits and Diseases. *Cell*, **2020**, 182, 1214-1231.e11	56.2	96
111	The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. *Nature Communications*, **2020**, 11, 3479	17.4	11

110	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
109	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. *Cell*, **2020**, 182, 1198-1213.e14	56.2	88
108	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
107	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. *American Journal of Epidemiology*, **2019**, 188, 1033-1054	3.8	39
106	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. *PLoS ONE*, **2019**, 14, e0216222	3.7	11
105	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
104	Association of Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. *Circulation*, **2019**, 140, 1031-1040	16.7	18
103	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. *Blood*, **2019**, 134, 1645-1657	2.2	63
102	Genome-wide association study of peripheral artery disease in the Million Veteran Program. *Nature Medicine*, **2019**, 25, 1274-1279	50.5	73
101	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. *Journal of the American Medical Informatics Association: JAMIA*, **2019**, 26, 1255-1262	8.6	23
100	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. *Nature Genetics*, **2019**, 51, 1574-1579	36.3	56
99	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. *Circulation*, **2019**, 139, 620-635	16.7	51
98	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. *American Journal of Human Genetics*, **2019**, 104, 260-274	11	43
97	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. *Blood*, **2019**, 133, 967-977	2.2	17
96	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. *Platelets*, **2019**, 30, 164-173	3.6	9
95	Multi-ethnic genome-wide association study for atrial fibrillation. *Nature Genetics*, **2018**, 50, 1225-1233	36.3	277
94	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16
93	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186

92	Examining the current standards for genetic discovery and replication in the era of mega-biobanks. *Nature Communications*, **2018**, 9, 5054	17.4	22
91	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. *Nature Genetics*, **2018**, 50, 1514-1523	36.3	260
90	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
89	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. *Nature Genetics*, **2018**, 50, 834-848	36.3	135
88	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
87	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. *Genome Medicine*, **2017**, 9, 23	14.4	85
86	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. *Nature Genetics*, **2017**, 49, 946-952	36.3	176
85	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. *Nature Communications*, **2017**, 8, 14977	17.4	105
84	and Loci Identified through Large-Scale Exome Chip Analysis Regulate Kidney Development and Function. *Journal of the American Society of Nephrology: JASN*, **2017**, 28, 981-994	12.7	30
83	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. *Nature Genetics*, **2017**, 49, 1560-1563	36.3	68
82	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
81	Rare coding variants pinpoint genes that control human hematological traits. *PLoS Genetics*, **2017**, 13, e1006925	6	28
80	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
79	Genome-wide physical activity interactions in adiposity - A meta-analysis of 200,452 adults. *PLoS Genetics*, **2017**, 13, e1006528	6	103
78	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
77	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
76	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
75	Genome-wide association study of copy number variation with lung function identifies a novel signal of association near BANP for forced vital capacity. *BMC Genetics*, **2016**, 17, 116	2.6	

74	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. *Human Molecular Genetics*, **2016**, 25, 358-70	5.6	54
73	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. *Behavior Genetics*, **2016**, 46, 170-82	3.2	122
72	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. *European Journal of Human Genetics*, **2016**, 24, 1035-40	5.3	34
71	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. *PLoS Genetics*, **2016**, 12, e1005804	6	50
70	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. *Genetic Epidemiology*, **2016**, 40, 404-15	2.6	15
69	Meta-analysis of 49 549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in ANGPTL4 determining fasting TG levels. *Journal of Medical Genetics*, **2016**, 53, 441-9	5.8	27
68	Genetic variants in RBFOX3 are associated with sleep latency. *European Journal of Human Genetics*, **2016**, 24, 1488-95	5.3	18
67	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
66	General Framework for Meta-Analysis of Haplotype Association Tests. *Genetic Epidemiology*, **2016**, 40, 244-52	2.6	
65	Genetic contributions to variation in general cognitive function: a meta-analysis of genome-wide association studies in the CHARGE consortium (N=53949). *Molecular Psychiatry*, **2015**, 20, 183-92	15.1	250
64	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
63	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
62	Integrative pathway genomics of lung function and airflow obstruction. *Human Molecular Genetics*, **2015**, 24, 6836-48	5.6	20
61	Genome of The Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. *Nature Communications*, **2015**, 6, 6065	17.4	32
60	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. *Blood*, **2015**, 126, e19-29	2.2	45
59	Fine mapping the region reveals a common intronic insertion associated to HDL-C. *Npj Aging and Mechanisms of Disease*, **2015**, 1, 15011	5.5	5
58	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. *PLoS Genetics*, **2015**, 11, e1005378	6	220
57	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. *JAMA Psychiatry*, **2015**, 72, 642-50	14.5	222

56	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. *Human Molecular Genetics*, **2015**, 24, 4167-82	5.6	19
55	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. *Nature Communications*, **2015**, 6, 8658	17.4	79
54	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
53	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. *Nature Communications*, **2015**, 6, 5897	17.4	147
52	Modulation of genetic associations with serum urate levels by body-mass-index in humans. *PLoS ONE*, **2015**, 10, e0119752	3.7	31
51	Association of low-frequency and rare coding-sequence variants with blood lipids and coronary heart disease in 56,000 whites and blacks. *American Journal of Human Genetics*, **2014**, 94, 223-32	11	233
50	Whole-exome sequencing identifies rare and low-frequency coding variants associated with LDL cholesterol. *American Journal of Human Genetics*, **2014**, 94, 233-45	11	170
49	Genome-wide association analysis identifies six new loci associated with forced vital capacity. *Nature Genetics*, **2014**, 46, 669-77	36.3	104
48	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. *Behavior Genetics*, **2014**, 44, 295-313	3.2	80
47	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. *Lancet Diabetes and Endocrinology,the*, **2014**, 2, 719-29	18.1	250
46	The association between galactosylation of immunoglobulin G and body mass index. *Progress in Neuro-Psychopharmacology and Biological Psychiatry*, **2014**, 48, 20-5	5.5	33
45	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. *PLoS ONE*, **2014**, 9, e111156	3.7	5
44	The total burden of rare, non-synonymous exome genetic variants is not associated with childhood or late-life cognitive ability. *Proceedings of the Royal Society B: Biological Sciences*, **2014**, 281, 20140117	4.4	17
43	Genome-wide association study for circulating tissue plasminogen activator levels and functional follow-up implicates endothelial STXBP5 and STX2. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2014**, 34, 1093-101	9.4	33
42	Novel approach identifies SNPs in SLC2A10 and KCNK9 with evidence for parent-of-origin effect on body mass index. *PLoS Genetics*, **2014**, 10, e1004508	6	45
41	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
40	Genome wide association identifies common variants at the SERPINA6/SERPINA1 locus influencing plasma cortisol and corticosteroid binding globulin. *PLoS Genetics*, **2014**, 10, e1004474	6	71
39	Comparative performance of four methods for high-throughput glycosylation analysis of immunoglobulin G in genetic and epidemiological research. *Molecular and Cellular Proteomics*, **2014** , 13, 1598-610	7.6	120

38	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. *Nature Genetics*, **2013**, 45, 145-54	36.3	505
37	Mutations in HNF1A result in marked alterations of plasma glycan profile. *Diabetes*, **2013**, 62, 1329-37	0.9	74
36	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
35	Loci associated with N-glycosylation of human immunoglobulin G show pleiotropy with autoimmune diseases and haematological cancers. *PLoS Genetics*, **2013**, 9, e1003225	6	242
34	Causal and synthetic associations of variants in the SERPINA gene cluster with alpha1-antitrypsin serum levels. *PLoS Genetics*, **2013**, 9, e1003585	6	37
33	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. *Human Molecular Genetics*, **2013**, 22, 4857-69	5.6	62
32	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. *Circulation*, **2013**, 128, 1310-24	16.7	107
31	Local exome sequences facilitate imputation of less common variants and increase power of genome wide association studies. *PLoS ONE*, **2013**, 8, e68604	3.7	8
30	Association between chromosome 9p21 variants and the ankle-brachial index identified by a meta-analysis of 21 genome-wide association studies. *Circulation: Cardiovascular Genetics*, **2012**, 5, 100-12		84
29	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
28	Association of medication with the human plasma N-glycome. *Journal of Proteome Research*, **2012**, 11, 1821-31	5.6	29
27	Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations. *PLoS Genetics*, **2012**, 8, e1002490	6	145
26	Epigenetic silencing of HNF1A associates with changes in the composition of the human plasma N-glycome. *Epigenetics*, **2012**, 7, 164-72	5.7	31
25	Genome-wide analysis of epistasis in body mass index using multiple human populations. *European Journal of Human Genetics*, **2012**, 20, 857-62	5.3	26
24	Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. *PLoS ONE*, **2012**, 7, e31369	3.7	2
23	Leprosy epidemics during history increased protective allele frequency of PARK2/PACRG genes in the population of the Mljet Island, Croatia. *European Journal of Medical Genetics*, **2011**, 54, e548-52	2.6	5
22	Glycomics meets lipidomics--associations of N-glycans with classical lipids, glycerophospholipids, and sphingolipids in three European populations. *Molecular BioSystems*, **2011**, 7, 1852-62		16
21	Immunoglobulin isotypes of lactating Holstein cows classified as high, average, and low type-1 or -2 immune responders. *Veterinary Immunology and Immunopathology*, **2011**, 144, 259-69	2	12

20	Polymorphisms in B3GAT1, SLC9A9 and MGAT5 are associated with variation within the human plasma N-glycome of 3533 European adults. *Human Molecular Genetics*, **2011**, 20, 5000-11	5.6	61
19	Genetic predictors of fibrin D-dimer levels in healthy adults. *Circulation*, **2011**, 123, 1864-72	16.7	47
18	Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque. *Nature Genetics*, **2011**, 43, 940-7	36.3	168
17	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. *Nature Genetics*, **2011**, 43, 1082-90	36.3	313
16	A comprehensive evaluation of potential lung function associated genes in the SpiroMeta general population sample. *PLoS ONE*, **2011**, 6, e19382	3.7	41
15	Characterisation of genome-wide association epistasis signals for serum uric acid in human population isolates. *PLoS ONE*, **2011**, 6, e23836	3.7	15
14	The TCF7L2 diabetes risk variant is associated with HbA(C) levels: a genome-wide association meta-analysis. *Annals of Human Genetics*, **2010**, 74, 471-8	2.2	29
13	Genome-wide association study identifies five loci associated with lung function. *Nature Genetics*, **2010**, 42, 36-44	36.3	430
12	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. *Nature Genetics*, **2010**, 42, 436-40	36.3	521
11	Genomics meets glycomics-the first GWAS study of human N-Glycome identifies HNF1 as a master regulator of plasma protein fucosylation. *PLoS Genetics*, **2010**, 6, e1001256	6	177
10	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. *Human Molecular Genetics*, **2010**, 19, 4304-11	5.6	125
9	Use of the modified Atkins diet for adolescents with chronic daily headache. *Cephalalgia*, **2010**, 30, 1014-61	6	33
8	Genome-wide association study of anthropometric traits in Korcula Island, Croatia. *Croatian Medical Journal*, **2009**, 50, 7-16	1.6	27
7	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. *Nature Precedings*, **2009**,		6
6	Genetic analysis of over one million people identifies 535 novel loci for blood pressure		4
5	The Polygenic and Monogenic Basis of Blood Traits and Diseases		3
4	Efficient variant set mixed model association tests for continuous and binary traits in large-scale whole genome sequencing studies		2
3	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

2	A MUC5B gene polymorphism, rs35705950-T, confers protective effects in COVID-19 infection		1
1	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. *Nature Genetics*,	36.3	2