Jennifer E Huffman

List of Publications by Year in descending order

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IENNIEED F HILEEMAN

#	Article	IF	CITATIONS
1	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
2	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
3	Genome-wide association analyses identify 18 new loci associated with serum urate concentrations. Nature Genetics, 2013, 45, 145-154.	21.4	675
4	Meta-analysis and imputation refines the association of 15q25 with smoking quantity. Nature Genetics, 2010, 42, 436-440.	21.4	581
5	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	21.4	578
6	A General Approach for Haplotype Phasing across the Full Spectrum of Relatedness. PLoS Genetics, 2014, 10, e1004234.	3.5	553
7	Multi-ethnic genome-wide association study for atrial fibrillation. Nature Genetics, 2018, 50, 1225-1233.	21.4	552
8	Genome-wide association study identifies five loci associated with lung function. Nature Genetics, 2010, 42, 36-44.	21.4	518
9	Genetics of blood lipids among ~300,000 multi-ethnic participants of the Million Veteran Program. Nature Genetics, 2018, 50, 1514-1523.	21.4	497
10	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	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. Nature Genetics, 2020, 52, 680-691.	21.4	445
12	The Polygenic and Monogenic Basis of Blood Traits and Diseases. Cell, 2020, 182, 1214-1231.e11.	28.9	388
13	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	27.8	383
14	Genome-wide association and large-scale follow up identifies 16 new loci influencing lung function. Nature Genetics, 2011, 43, 1082-1090.	21.4	367
15	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. Nature Genetics, 2015, 47, 1294-1303.	21.4	357
16	Trans-ethnic and Ancestry-Specific Blood-Cell Genetics in 746,667 Individuals from 5 Global Populations. Cell, 2020, 182, 1198-1213.e14.	28.9	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). Molecular Psychiatry, 2015, 20, 183-192.	7.9	344
18	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.	3.5	331

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19	Loci Associated with N-Glycosylation of Human Immunoglobulin G Show Pleiotropy with Autoimmune Diseases and Haematological Cancers. PLoS Genetics, 2013, 9, e1003225.	3.5	323
20	Association of vitamin D status with arterial blood pressure and hypertension risk: a mendelian randomisation study. Lancet Diabetes and Endocrinology,the, 2014, 2, 719-729.	11.4	319
21	Meta-analysis of Genome-wide Association Studies for Neuroticism, and the Polygenic Association With Major Depressive Disorder. JAMA Psychiatry, 2015, 72, 642.	11.0	289
22	Association of Low-Frequency and Rare Coding-Sequence Variants with Blood Lipids and Coronary Heart Disease in 56,000 Whites and Blacks. American Journal of Human Genetics, 2014, 94, 223-232.	6.2	287
23	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
24	Large-scale analyses of common and rare variants identify 12 new loci associated with atrial fibrillation. Nature Genetics, 2017, 49, 946-952.	21.4	279
25	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
26	Genome-wide association meta-analysis highlights light-induced signaling as a driver for refractive error. Nature Genetics, 2018, 50, 834-848.	21.4	239
27	Genomics Meets Glycomics—The First GWAS Study of Human N-Glycome Identifies HNF1α as a Master Regulator of Plasma Protein Fucosylation. PLoS Genetics, 2010, 6, e1001256.	3.5	213
28	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
29	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, 940-947.	21.4	191
30	Genome-Wide Association Study Identifies Novel Loci Associated with Circulating Phospho- and Sphingolipid Concentrations. PLoS Genetics, 2012, 8, e1002490.	3.5	181
31	Meta-analysis of Genome-Wide Association Studies for Extraversion: Findings from the Genetics of Personality Consortium. Behavior Genetics, 2016, 46, 170-182.	2.1	178
32	Genome-wide association study of peripheral artery disease in the Million Veteran Program. Nature Medicine, 2019, 25, 1274-1279.	30.7	177
33	Low-frequency and rare exome chip variants associate with fasting glucose and type 2 diabetes susceptibility. Nature Communications, 2015, 6, 5897.	12.8	173
34	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	27.8	173
35	Comparative Performance of Four Methods for High-throughput Glycosylation Analysis of Immunoglobulin G in Genetic and Epidemiological Research. Molecular and Cellular Proteomics, 2014, 13, 1598-1610.	3.8	169
36	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169

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37	Genomic and transcriptomic association studies identify 16 novel susceptibility loci for venous thromboembolism. Blood, 2019, 134, 1645-1657.	1.4	162
38	Genome-wide physical activity interactions in adiposity ― A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	3.5	158
39	Genome-wide association analysis of venous thromboembolism identifies new risk loci and genetic overlap with arterial vascular disease. Nature Genetics, 2019, 51, 1574-1579.	21.4	152
40	New loci associated with central cornea thickness include COL5A1, AKAP13 and AVGR8. Human Molecular Genetics, 2010, 19, 4304-4311.	2.9	136
41	Genome-wide association analysis identifies six new loci associated with forced vital capacity. Nature Genetics, 2014, 46, 669-677.	21.4	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. Circulation, 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. Hypertension, 2017, 70, .	2.7	123
44	Actionable druggable genome-wide Mendelian randomization identifies repurposing opportunities for COVID-19. Nature Medicine, 2021, 27, 668-676.	30.7	120
45	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.	21.4	112
46	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	7.1	110
47	Exploration of haplotype research consortium imputation for genome-wide association studies in 20,032 Generation Scotland participants. Genome Medicine, 2017, 9, 23.	8.2	110
48	Sixteen new lung function signals identified through 1000 Genomes Project reference panel imputation. Nature Communications, 2015, 6, 8658.	12.8	108
49	Genome Wide Association Identifies Common Variants at the SERPINA6/SERPINA1 Locus Influencing Plasma Cortisol and Corticosteroid Binding Globulin. PLoS Genetics, 2014, 10, e1004474.	3.5	105
50	Harmonization of Neuroticism and Extraversion phenotypes across inventories and cohorts in the Genetics of Personality Consortium: an application of Item Response Theory. Behavior Genetics, 2014, 44, 295-313.	2.1	103
51	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.	6.2	103
52	Genome-Wide Association Transethnic Meta-Analyses Identifies Novel Associations Regulating Coagulation Factor VIII and von Willebrand Factor Plasma Levels. Circulation, 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. Circulation: Cardiovascular Genetics, 2012, 5, 100-112.	5.1	98
54	Mutations in <i>HNF1A</i> Result in Marked Alterations of Plasma Glycan Profile. Diabetes, 2013, 62, 1329-1337.	0.6	97

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55	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563.	21.4	93
56	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
57	Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054.	3.4	85
58	Novel Approach Identifies SNPs in SLC2A10 and KCNK9 with Evidence for Parent-of-Origin Effect on Body Mass Index. PLoS Genetics, 2014, 10, e1004508.	3.5	80
59	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
60	Genetic influences on plasma CFH and CFHR1 concentrations and their role in susceptibility to age-related macular degeneration. Human Molecular Genetics, 2013, 22, 4857-4869.	2.9	77
61	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. Nature Genetics, 2022, 54, 125-127.	21.4	75
62	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, 5000-5011.	2.9	74
63	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
64	A meta-analysis of 120 246 individuals identifies 18 new loci for fibrinogen concentration. Human Molecular Genetics, 2016, 25, 358-370.	2.9	73
65	Pedigree- and SNP-Associated Genetics and Recent Environment are the Major Contributors to Anthropometric and Cardiometabolic Trait Variation. PLoS Genetics, 2016, 12, e1005804.	3.5	72
66	High-throughput multimodal automated phenotyping (MAP) with application to PheWAS. Journal of the American Medical Informatics Association: JAMIA, 2019, 26, 1255-1262.	4.4	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. Nature Genetics, 2022, 54, 761-771.	21.4	68
68	Modulation of Genetic Associations with Serum Urate Levels by Body-Mass-Index in Humans. PLoS ONE, 2015, 10, e0119752.	2.5	64
69	Genetic Predictors of Fibrin D-Dimer Levels in Healthy Adults. Circulation, 2011, 123, 1864-1872.	1.6	60
70	A Comprehensive Evaluation of Potential Lung Function Associated Genes in the SpiroMeta General Population Sample. PLoS ONE, 2011, 6, e19382.	2.5	56
71	Rare and low-frequency variants and their association with plasma levels of fibrinogen, FVII, FVIII, and vWF. Blood, 2015, 126, e19-e29.	1.4	55
72	The association between galactosylation of immunoglobulin G and body mass index. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2014, 48, 20-25.	4.8	52

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73	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
74	Genome-wide association studies identify genetic loci for low von Willebrand factor levels. European Journal of Human Genetics, 2016, 24, 1035-1040.	2.8	45
75	Causal and Synthetic Associations of Variants in the SERPINA Gene Cluster with Alpha1-antitrypsin Serum Levels. PLoS Genetics, 2013, 9, e1003585.	3.5	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> . Arteriosclerosis, Thrombosis, and Vascular Biology, 2014, 34, 1093-1101.	2.4	43
77	The choline transporter Slc44a2 controls platelet activation and thrombosis by regulating mitochondrial function. Nature Communications, 2020, 11, 3479.	12.8	43
78	Use of the modified Atkins diet for adolescents with chronic daily headache. Cephalalgia, 2010, 30, 1014-6.	3.9	41
79	SOS2 and ACP1 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.	6.1	39
80	Rare coding variants pinpoint genes that control human hematological traits. PLoS Genetics, 2017, 13, e1006925.	3.5	39
81	Epigenetic silencing of <i>HNF1A</i> associates with changes in the composition of the human plasma <i>N</i> -glycome. Epigenetics, 2012, 7, 164-172.	2.7	37
82	Examining the current standards for genetic discovery and replication in the era of mega-biobanks. Nature Communications, 2018, 9, 5054.	12.8	37
83	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	1.9	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. Molecular Psychiatry, 2022, 27, 2264-2272.	7.9	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. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
86	A genome-wide association study identifies new loci for factor VII and implicates factor VII in ischemic stroke etiology. Blood, 2019, 133, 967-977.	1.4	34
87	The <i>TCF7L2</i> Diabetes Risk Variant is Associated with HbA _{1C} Levels: a Genomeâ€Wide Association Metaâ€Analysis. Annals of Human Genetics, 2010, 74, 471-478.	0.8	33
88	Genome-wide analysis of epistasis in body mass index using multiple human populations. European Journal of Human Genetics, 2012, 20, 857-862.	2.8	33
89	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
90	Association of <i>APOL1</i> Risk Alleles With Cardiovascular Disease in Blacks in the Million Veteran Program. Circulation, 2019, 140, 1031-1040.	1.6	31

6

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91	Association of Medication with the Human Plasma <i>N</i> Glycome. Journal of Proteome Research, 2012, 11, 1821-1831.	3.7	30
92	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	12.8	30
93	Integrative pathway genomics of lung function and airflow obstruction. Human Molecular Genetics, 2015, 24, 6836-6848.	2.9	28
94	Genome-wide Association Study of Anthropometric Traits in KorÄula Island, Croatia. Croatian Medical Journal, 2009, 50, 7-16.	0.7	27
95	Genetic variants in RBFOX3 are associated with sleep latency. European Journal of Human Genetics, 2016, 24, 1488-1495.	2.8	27
96	Genomic prediction of complex human traits: relatedness, trait architecture and predictive meta-models. Human Molecular Genetics, 2015, 24, 4167-4182.	2.9	24
97	Glycomics meets lipidomics—associations of N-glycans with classical lipids, glycerophospholipids, and sphingolipids in three European populations. Molecular BioSystems, 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. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140117.	2.6	19
99	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	1.8	19
100	An Empirical Comparison of Joint and Stratified Frameworks for Studying G × E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Gene‣ifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415.	1.3	18
101	Mendelian randomization evaluation of causal effects of fibrinogen on incident coronary heart disease. PLoS ONE, 2019, 14, e0216222.	2.5	17
102	Phenome-wide association of 1809 phenotypes and COVID-19 disease progression in the Veterans Health Administration Million Veteran Program. PLoS ONE, 2021, 16, e0251651.	2.5	17
103	Immunoglobulin isotypes of lactating Holstein cows classified as high, average, and low type-1 or -2 immune responders. Veterinary Immunology and Immunopathology, 2011, 144, 259-269.	1.2	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. PLoS Genetics, 2022, 18, e1010113.	3.5	16
105	Exome-chip meta-analysis identifies association between variation in ANKRD26 and platelet aggregation. Platelets, 2019, 30, 164-173.	2.3	15
106	Characterisation of Genome-Wide Association Epistasis Signals for Serum Uric Acid in Human Population Isolates. PLoS ONE, 2011, 6, e23836.	2.5	15
107	Mendelian Randomization Analysis of Hemostatic Factors and Their Contribution to Peripheral Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2020, 41, 380-386.	2.4	14
108	Meta-GWAS Reveals Novel Genetic Variants Associated with Urinary Excretion of Uromodulin. Journal of the American Society of Nephrology: JASN, 2022, 33, 511-529.	6.1	14

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109	Effects of Thyroid Function on Hemostasis, Coagulation, and Fibrinolysis: A Mendelian Randomization Study. Thyroid, 2021, 31, 1305-1315.	4.5	13
110	Local Exome Sequences Facilitate Imputation of Less Common Variants and Increase Power of Genome Wide Association Studies. PLoS ONE, 2013, 8, e68604.	2.5	13
111	Multiâ€phenotype analyses of hemostatic traits with cardiovascular events reveal novel genetic associations. Journal of Thrombosis and Haemostasis, 2022, 20, 1331-1349.	3.8	12
112	A multi-population phenome-wide association study of genetically-predicted height in the Million Veteran Program. PLoS Genetics, 2022, 18, e1010193.	3.5	12
113	PCSK9 loss of function is protective against extra-coronary atherosclerotic cardiovascular disease in a large multi-ethnic cohort. PLoS ONE, 2020, 15, e0239752.	2.5	9
114	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.	2.3	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. PLoS ONE, 2014, 9, e111156.	2.5	8
116	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 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. European Journal of Medical Genetics, 2011, 54, e548-52.	1.3	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. Nature Precedings, 2009, , .	0.1	6
119	Transcriptome-wide association study in UK Biobank Europeans identifies associations with blood cell traits. Human Molecular Genetics, 2022, 31, 2333-2347.	2.9	6
120	Platelet Reactivity in Individuals Over 65 Years Old Is Not Modulated by Age. Circulation Research, 2020, 127, 394-396.	4.5	3
121	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	2.5	3
122	Genome-wide and phenome-wide analysis of ideal cardiovascular health in the VA Million Veteran Program. PLoS ONE, 2022, 17, e0267900.	2.5	2
123	General Framework for Metaâ€Analysis of Haplotype Association Tests. Genetic Epidemiology, 2016, 40, 244-252	1.3	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. BMC Genetics, 2016, 17, 116.	2.7	0