

David A Hinds

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

130
papers

24,622
citations

63
h-index

147
g-index

147
ext. papers

30,924
ext. citations

16.7
avg, IF

6.09
L-index

#	Paper	IF	Citations
130	A second generation human haplotype map of over 3.1 million SNPs. <i>Nature</i> , 2007 , 449, 851-61	50.4	3647
129	A common allele on chromosome 9 associated with coronary heart disease. <i>Science</i> , 2007 , 316, 1488-91	33.3	1415
128	Genome-wide detection and characterization of positive selection in human populations. <i>Nature</i> , 2007 , 449, 913-8	50.4	1367
127	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. <i>Nature Genetics</i> , 2018 , 50, 668-681	36.3	1301
126	Whole-genome patterns of common DNA variation in three human populations. <i>Science</i> , 2005 , 307, 1072-9	33.3	972
125	Blocks of limited haplotype diversity revealed by high-resolution scanning of human chromosome 21. <i>Science</i> , 2001 , 294, 1719-23	33.3	948
124	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016 , 533, 539-42	50.4	850
123	Detection and interpretation of shared genetic influences on 42 human traits. <i>Nature Genetics</i> , 2016 , 48, 709-17	36.3	657
122	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. <i>Nature Neuroscience</i> , 2019 , 22, 343-352	25.5	639
121	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. <i>Nature Genetics</i> , 2017 , 49, 1511-1516	36.3	629
120	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. <i>Nature Genetics</i> , 2016 , 48, 624-33	36.3	602
119	Common sequence polymorphisms shaping genetic diversity in <i>Arabidopsis thaliana</i> . <i>Science</i> , 2007 , 317, 338-42	33.3	596
118	A full genome search in multiple sclerosis. <i>Nature Genetics</i> , 1996 , 13, 472-6	36.3	572
117	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019 , 51, 237-244	36.3	516
116	Identification of 15 genetic loci associated with risk of major depression in individuals of European descent. <i>Nature Genetics</i> , 2016 , 48, 1031-6	36.3	487
115	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. <i>Nature</i> , 2007 , 448, 1050-3	50.4	352
114	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. <i>Nature Genetics</i> , 2015 , 47, 1449-1456	36.3	329

113	Variant in PNPLA3 is associated with alcoholic liver disease. <i>Nature Genetics</i> , 2010 , 42, 21-3	36.3	328
112	Common deletions and SNPs are in linkage disequilibrium in the human genome. <i>Nature Genetics</i> , 2006 , 38, 82-5	36.3	303
111	A second-generation screen of the human genome for susceptibility to insulin-dependent diabetes mellitus. <i>Nature Genetics</i> , 1998 , 19, 292-6	36.3	296
110	An atlas of genetic influences on osteoporosis in humans and mice. <i>Nature Genetics</i> , 2019 , 51, 258-266	36.3	270
109	minimac2: faster genotype imputation. <i>Bioinformatics</i> , 2015 , 31, 782-4	7.2	264
108	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. <i>Nature Genetics</i> , 2008 , 40, 149-51	36.3	262
107	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. <i>Nature Genetics</i> , 2019 , 51, 245-257	36.3	259
106	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017 , 49, 1752-1757	36.3	256
105	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. <i>Nature Genetics</i> , 2017 , 49, 152-156	36.3	251
104	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. <i>Nature Genetics</i> , 2019 , 51, 394-403	36.3	246
103	Fine-scale recombination patterns differ between chimpanzees and humans. <i>Nature Genetics</i> , 2005 , 37, 429-34	36.3	226
102	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. <i>PLoS Genetics</i> , 2016 , 12, e1006125	6	222
101	A genomewide association study of skin pigmentation in a South Asian population. <i>American Journal of Human Genetics</i> , 2007 , 81, 1119-32	11	215
100	GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. <i>Nature Communications</i> , 2016 , 7, 10448	17.4	207
99	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. <i>Nature Communications</i> , 2019 , 10, 343	17.4	205
98	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015 , 6, 8464	17.4	203
97	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. <i>Nature Genetics</i> , 2013 , 45, 907-11	36.3	191
96	Genome-wide analysis points to roles for extracellular matrix remodeling, the visual cycle, and neuronal development in myopia. <i>PLoS Genetics</i> , 2013 , 9, e1003299	6	190

95	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. <i>New England Journal of Medicine</i> , 2017 , 377, 1156-1167	59.2	183
94	A lattice model for protein structure prediction at low resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992 , 89, 2536-40	11.5	182
93	Genome-wide association and HLA region fine-mapping studies identify susceptibility loci for multiple common infections. <i>Nature Communications</i> , 2017 , 8, 599	17.4	173
92	Comprehensive whole-genome and candidate gene analysis for response to statin therapy in the Treating to New Targets (TNT) cohort. <i>Circulation: Cardiovascular Genetics</i> , 2009 , 2, 173-81		149
91	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. <i>Journal of Allergy and Clinical Immunology</i> , 2014 , 133, 1564-71	11.5	143
90	A genomewide single-nucleotide-polymorphism panel with high ancestry information for African American admixture mapping. <i>American Journal of Human Genetics</i> , 2006 , 79, 640-9	11	142
89	Exploring conformational space with a simple lattice model for protein structure. <i>Journal of Molecular Biology</i> , 1994 , 243, 668-82	6.5	137
88	Assessment of clinical validity of a breast cancer risk model combining genetic and clinical information. <i>Journal of the National Cancer Institute</i> , 2010 , 102, 1618-27	9.7	133
87	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. <i>Lancet Neurology</i> , 2017 , 16, 898-907	24.1	121
86	A genomewide single-nucleotide-polymorphism panel for Mexican American admixture mapping. <i>American Journal of Human Genetics</i> , 2007 , 80, 1014-23	11	113
85	Novel associations for hypothyroidism include known autoimmune risk loci. <i>PLoS ONE</i> , 2012 , 7, e34442	3.7	105
84	Efficient replication of over 180 genetic associations with self-reported medical data. <i>PLoS ONE</i> , 2011 , 6, e23473	3.7	101
83	Assessment of the genetic basis of rosacea by genome-wide association study. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1548-1555	4.3	97
82	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. <i>Nature Genetics</i> , 2016 , 48, 1557-1563	36.3	91
81	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	11.5	90
80	Matching strategies for genetic association studies in structured populations. <i>American Journal of Human Genetics</i> , 2004 , 74, 317-25	11	88
79	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. <i>American Journal of Human Genetics</i> , 2019 , 104, 665-684	11	83
78	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2016 , 7, 12048	17.4	82

77	Phenome-wide association studies across large population cohorts support drug target validation. <i>Nature Communications</i> , 2018 , 9, 4285	17.4	76
76	Replicability and robustness of genome-wide-association studies for behavioral traits. <i>Psychological Science</i> , 2014 , 25, 1975-86	7.9	75
75	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. <i>Nature Communications</i> , 2015 , 6, 8842	17.4	75
74	Genome-wide association analysis of self-reported events in 6135 individuals and 252 827 controls identifies 8 loci associated with thrombosis. <i>Human Molecular Genetics</i> , 2016 , 25, 1867-74	5.6	71
73	Segmental phylogenetic relationships of inbred mouse strains revealed by fine-scale analysis of sequence variation across 4.6 mb of mouse genome. <i>Genome Research</i> , 2004 , 14, 1493-500	9.7	71
72	Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. <i>PLoS Genetics</i> , 2012 , 8, e1002746	6	70
71	Genomic DNA insertions and deletions occur frequently between humans and nonhuman primates. <i>Genome Research</i> , 2003 , 13, 341-6	9.7	68
70	Application of pooled genotyping to scan candidate regions for association with HDL cholesterol levels. <i>Human Genomics</i> , 2004 , 1, 421-34	6.8	68
69	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. <i>Nature Communications</i> , 2016 , 7, 12510	17.4	65
68	Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology. <i>Journal of Investigative Dermatology</i> , 2013 , 133, 1489-96	4.3	64
67	Genome-wide meta-analysis of cognitive empathy: heritability, and correlates with sex, neuropsychiatric conditions and cognition. <i>Molecular Psychiatry</i> , 2018 , 23, 1402-1409	15.1	62
66	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. <i>Nature Genetics</i> , 2018 , 50, 652-656	36.3	59
65	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa. <i>Translational Psychiatry</i> , 2018 , 8, 35	8.6	55
64	Resequencing of nicotinic acetylcholine receptor genes and association of common and rare variants with the Fagerström test for nicotine dependence. <i>Neuropsychopharmacology</i> , 2010 , 35, 2392-402	8.7	55
63	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. <i>Human Molecular Genetics</i> , 2015 , 24, 2700-8	5.6	53
62	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. <i>Nature Genetics</i> , 2018 , 50, 1072-1080	36.3	52
61	Variation in the FGFR2 gene and the effects of postmenopausal hormone therapy on invasive breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2009 , 18, 3079-85	4	51
60	Genetic variants associated with breast size also influence breast cancer risk. <i>BMC Medical Genetics</i> , 2012 , 13, 53	2.1	50

59	A genetic variant near olfactory receptor genes influences cilantro preference. <i>Flavour</i> , 2012 , 1,		50
58	Gene-based analysis of regulatory variants identifies 4 putative novel asthma risk genes related to nucleotide synthesis and signaling. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 139, 1148-1157	11.5	43
57	A genome-wide association study identifies four novel susceptibility loci underlying inguinal hernia. <i>Nature Communications</i> , 2015 , 6, 10130	17.4	43
56	Two-stage genome-wide association study identifies a novel susceptibility locus associated with melanoma. <i>Oncotarget</i> , 2017 , 8, 17586-17592	3.3	42
55	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. <i>Nature Communications</i> , 2017 , 8, 14694	17.4	36
54	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. <i>Journal of Allergy and Clinical Immunology</i> , 2017 , 140, 771-781	11.5	36
53	Characterization of Prevalence and Health Consequences of Uniparental Disomy in Four Million Individuals from the General Population. <i>American Journal of Human Genetics</i> , 2019 , 105, 921-932	11	36
52	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. <i>Nature Communications</i> , 2019 , 10, 4857	17.4	34
51	From structure to sequence and back again. <i>Journal of Molecular Biology</i> , 1996 , 258, 201-9	6.5	33
50	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021 , 5, 59-70	12.8	33
49	Exclusion of linkage to the HLA region in ninety multiplex sibships with autism. <i>Journal of Autism and Developmental Disorders</i> , 1999 , 29, 195-201	4.6	31
48	Social and non-social autism symptoms and trait domains are genetically dissociable. <i>Communications Biology</i> , 2019 , 2, 328	6.7	30
47	Eleven loci with new reproducible genetic associations with allergic disease risk. <i>Journal of Allergy and Clinical Immunology</i> , 2019 , 143, 691-699	11.5	28
46	Chronic gastroesophageal reflux disease shares genetic background with esophageal adenocarcinoma and Barrett's esophagus. <i>Human Molecular Genetics</i> , 2016 , 25, 828-35	5.6	26
45	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. <i>PLoS Genetics</i> , 2018 , 14, e1007394	6	25
44	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. <i>Genes and Immunity</i> , 2013 , 14, 441-6	4.4	25
43	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015 , 6, 7756	17.4	23
42	Genome-wide association analysis of pain severity in dysmenorrhea identifies association at chromosome 1p13.2, near the nerve growth factor locus. <i>Pain</i> , 2016 , 157, 2571-2581	8	22

41	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
40	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021 , 53, 663-676	6.3	20
39	Varenicline for smoking cessation: nausea severity and variation in nicotinic receptor genes. <i>Pharmacogenomics Journal</i> , 2012 , 12, 349-58	3.5	19
38	Variation in the FGFR2 gene and the effect of a low-fat dietary pattern on invasive breast cancer. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2010 , 19, 74-9	4	18
37	A multi-stage genome-wide association study of uterine fibroids in African Americans. <i>Human Genetics</i> , 2017 , 136, 1363-1373	6.3	17
36	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. <i>American Journal of Human Genetics</i> , 2017 , 101, 913-924	11	17
35	GWAS of self-reported mosquito bite size, itch intensity and attractiveness to mosquitoes implicates immune-related predisposition loci. <i>Human Molecular Genetics</i> , 2017 , 26, 1391-1406	5.6	17
34	Assessment of rosacea symptom severity by genome-wide association study and expression analysis highlights immuno-inflammatory and skin pigmentation genes. <i>Human Molecular Genetics</i> , 2018 , 27, 2762-2772	5.6	15
33	Genome-wide definitive haplotypes determined using a collection of complete hydatidiform moles. <i>Genome Research</i> , 2005 , 15, 1511-8	9.7	15
32	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. <i>International Journal of Epidemiology</i> , 2020 , 49, 1022-1031	7.8	15
31	Phenome-wide association study using research participants' self-reported data provides insight into the Th17 and IL-17 pathway. <i>PLoS ONE</i> , 2017 , 12, e0186405	3.7	14
30	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. <i>Nature Communications</i> , 2018 , 9, 4264	17.4	14
29	Genetic variants in the MRPS30 region and postmenopausal breast cancer risk. <i>Genome Medicine</i> , 2011 , 3, 42	14.4	13
28	Genome-wide Analysis of Insomnia (N=1,331,010) Identifies Novel Loci and Functional Pathways		12
27	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2019 , 4, 91-100	3.4	12
26	Simulation of protein-folding pathways: lost in (conformational) space?. <i>Trends in Biotechnology</i> , 1995 , 13, 23-27	15.1	11
25	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. <i>Science Advances</i> , 2021 , 7,	14.3	11
24	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. <i>PLoS Genetics</i> , 2020 , 16, e1008725	6	10

23	Pooled versus individual genotyping in a breast cancer genome-wide association study. <i>Genetic Epidemiology</i> , 2010 , 34, 603-12	2.6	10
22	Genome-wide association study of musical beat synchronization demonstrates high polygenicity		9
21	Insights into the genetic basis of retinal detachment. <i>Human Molecular Genetics</i> , 2020 , 29, 689-702	5.6	9
20	Genetic association and differential expression of PITX2 with acute appendicitis. <i>Human Genetics</i> , 2019 , 138, 37-47	6.3	9
19	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions		8
18	Economic evaluation of using a genetic test to direct breast cancer chemoprevention in white women with a previous breast biopsy. <i>Applied Health Economics and Health Policy</i> , 2014 , 12, 203-17	3.4	7
17	Genome-wide association studies of antidepressant class response and treatment-resistant depression. <i>Translational Psychiatry</i> , 2020 , 10, 360	8.6	7
16	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. <i>Nature Genetics</i> , 2022 ,	36.3	7
15	Habitual sleep disturbances and migraine: a Mendelian randomization study. <i>Annals of Clinical and Translational Neurology</i> , 2020 , 7, 2370-2380	5.3	6
14	Parkinson disease age of onset GWAS: defining heritability, genetic loci and a-synuclein mechanisms		6
13	Phenome-wide association studies (PheWAS) across large real-world data population cohorts support drug target validation		5
12	Genome-wide association analyses of chronotype in 697,828 individuals provides new insights into circadian rhythms in humans and links to disease		5
11	Resource profile and user guide of the Polygenic Index Repository. <i>Nature Human Behaviour</i> , 2021 ,	12.8	5
10	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa		4
9	Genome-wide meta-analysis of cognitive empathy: heritability, and correlates with sex, neuropsychiatric conditions and brain anatomy		3
8	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participants' perspective. <i>Psychiatry Research</i> , 2019 , 278, 173-179	9.9	2
7	Sib-pair analysis of the collaborative study on the genetics of alcoholism data set. <i>Genetic Epidemiology</i> , 1999 , 17 Suppl 1, S187-91	2.6	2
6	Nuclear genome-wide associations with mitochondrial heteroplasmy. <i>Science Advances</i> , 2021 , 7,	14.3	2

5	Multitrait genetic association analysis identifies 50 new risk loci for gastro-oesophageal reflux, seven new loci for Barrett's oesophagus and provides insights into clinical heterogeneity in reflux diagnosis. <i>Gut</i> , 2021 ,	19.2	2
4	FUT6 deficiency compromises basophil function by selectively abrogating their sialyl-Lewis x expression. <i>Communications Biology</i> , 2021 , 4, 832	6.7	2
3	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. <i>PLoS ONE</i> , 2020 , 15, e0241552	3.7	1
2	Social and non-social autism symptom and trait domains are genetically dissociable		1
1	Characterizing mood disorders in the AFFECT study: a large, longitudinal, and phenotypically rich genetic cohort in the US.. <i>Translational Psychiatry</i> , 2022 , 12, 121	8.6	0