David A Hinds

List of Publications by Year in Descending Order

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	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals.. *Nature Genetics*, **2022**,	36.3	7
129	Characterizing mood disorders in the AFFECT study: a large, longitudinal, and phenotypically rich genetic cohort in the US.. *Translational Psychiatry*, **2022**, 12, 121	8.6	0
128	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. *Science Advances*, **2021**, 7,	14.3	11
127	Nuclear genome-wide associations with mitochondrial heteroplasmy. *Science Advances*, **2021**, 7,	14.3	2
126	Genetic analyses identify widespread sex-differential participation bias. *Nature Genetics*, **2021**, 53, 663-671	36.3	20
125	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. *Gut*, **2021**,	19.2	2
124	Resource profile and user guide of the Polygenic Index Repository. *Nature Human Behaviour*, **2021**,	12.8	5
123	FUT6 deficiency compromises basophil function by selectively abrogating their sialyl-Lewis x expression. *Communications Biology*, **2021**, 4, 832	6.7	2
122	Genome-wide association study identifies 48 common genetic variants associated with handedness. *Nature Human Behaviour*, **2021**, 5, 59-70	12.8	33
121	Habitual sleep disturbances and migraine: a Mendelian randomization study. *Annals of Clinical and Translational Neurology*, **2020**, 7, 2370-2380	5.3	6
120	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. *PLoS Genetics*, **2020**, 16, e1008725	6	10
119	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. *PLoS ONE*, **2020**, 15, e0241552	3.7	1
118	Insights into the genetic basis of retinal detachment. *Human Molecular Genetics*, **2020**, 29, 689-702	5.6	9
117	Genome-wide association studies of antidepressant class response and treatment-resistant depression. *Translational Psychiatry*, **2020**, 10, 360	8.6	7
116	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. *International Journal of Epidemiology*, **2020**, 49, 1022-1031	7.8	15
115	Social and non-social autism symptoms and trait domains are genetically dissociable. *Communications Biology*, **2019**, 2, 328	6.7	30
114	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. *Nature Communications*, **2019**, 10, 343	17.4	205

113	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participants' perspective. *Psychiatry Research*, **2019**, 278, 173-179	9.9	2
112	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. *American Journal of Human Genetics*, **2019**, 104, 665-684	11	83
111	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. *Nature Genetics*, **2019**, 51, 394-403	36.3	246
110	Characterization of Prevalence and Health Consequences of Uniparental Disomy in Four Million Individuals from the General Population. *American Journal of Human Genetics*, **2019**, 105, 921-932	11	36
109	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. *Nature Communications*, **2019**, 10, 4857	17.4	34
108	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions. *Nature Neuroscience*, **2019**, 22, 343-352	25.5	639
107	Association of Whole-Genome and NETRIN1 Signaling Pathway-Derived Polygenic Risk Scores for Major Depressive Disorder and White Matter Microstructure in the UK Biobank. *Biological Psychiatry: Cognitive Neuroscience and Neuroimaging*, **2019**, 4, 91-100	3.4	12
106	An atlas of genetic influences on osteoporosis in humans and mice. *Nature Genetics*, **2019**, 51, 258-266	36.3	270
105	Genetic association and differential expression of PITX2 with acute appendicitis. *Human Genetics*, **2019**, 138, 37-47	6.3	9
104	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. *Nature Genetics*, **2019**, 51, 237-244	36.3	516
103	Genome-wide association analyses of risk tolerance and risky behaviors in over 1 million individuals identify hundreds of loci and shared genetic influences. *Nature Genetics*, **2019**, 51, 245-257	36.3	259
102	Eleven loci with new reproducible genetic associations with allergic disease risk. *Journal of Allergy and Clinical Immunology*, **2019**, 143, 691-699	11.5	28
101	Genome-wide association meta-analysis of individuals of European ancestry identifies new loci explaining a substantial fraction of hair color variation and heritability. *Nature Genetics*, **2018**, 50, 652-656	36.3	59
100	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. *Nature Genetics*, **2018**, 50, 668-681	36.3	1301
99	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa. *Translational Psychiatry*, **2018**, 8, 35	8.6	55
98	Genome-wide meta-analysis of cognitive empathy: heritability, and correlates with sex, neuropsychiatric conditions and cognition. *Molecular Psychiatry*, **2018**, 23, 1402-1409	15.1	62
97	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. *Nature Genetics*, **2018**, 50, 1072-1080	36.3	52
96	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. *PLoS Genetics*, **2018**, 14, e1007394	6	25

95	Assessment of rosacea symptom severity by genome-wide association study and expression analysis highlights immuno-inflammatory and skin pigmentation genes. *Human Molecular Genetics*, **2018**, 27, 2762-2772	5.6	15
94	Phenome-wide association studies across large population cohorts support drug target validation. *Nature Communications*, **2018**, 9, 4285	17.4	76
93	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. *Nature Communications*, **2018**, 9, 4264	17.4	14
92	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. *Nature Communications*, **2017**, 8, 14694	17.4	36
91	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. *Journal of Allergy and Clinical Immunology*, **2017**, 140, 771-781	11.5	36
90	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. *Nature Genetics*, **2017**, 49, 152-156	36.3	251
89	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. *Nature Genetics*, **2017**, 49, 1752-1757	36.3	256
88	Identification of novel risk loci for restless legs syndrome in genome-wide association studies in individuals of European ancestry: a meta-analysis. *Lancet Neurology, The*, **2017**, 16, 898-907	24.1	121
87	Two-stage genome-wide association study identifies a novel susceptibility locus associated with melanoma. *Oncotarget*, **2017**, 8, 17586-17592	3.3	42
86	A multi-stage genome-wide association study of uterine fibroids in African Americans. *Human Genetics*, **2017**, 136, 1363-1373	6.3	17
85	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. *Nature Genetics*, **2017**, 49, 1511-1516	36.3	629
84	Genome-wide association and HLA region fine-mapping studies identify susceptibility loci for multiple common infections. *Nature Communications*, **2017**, 8, 599	17.4	173
83	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. *New England Journal of Medicine*, **2017**, 377, 1156-1167	59.2	183
82	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. *American Journal of Human Genetics*, **2017**, 101, 913-924	11	17
81	Gene-based analysis of regulatory variants identifies 4 putative novel asthma risk genes related to nucleotide synthesis and signaling. *Journal of Allergy and Clinical Immunology*, **2017**, 139, 1148-1157	11.5	43
80	GWAS of self-reported mosquito bite size, itch intensity and attractiveness to mosquitoes implicates immune-related predisposition loci. *Human Molecular Genetics*, **2017**, 26, 1391-1406	5.6	17
79	Phenome-wide association study using research participants' self-reported data provides insight into the Th17 and IL-17 pathway. *PLoS ONE*, **2017**, 12, e0186405	3.7	14
78	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. *Nature Communications*, **2016**, 7, 12048	17.4	82

77	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. *Nature Communications*, **2016**, 7, 12510	17.4	65
76	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. *Nature Genetics*, **2016**, 48, 1557-1563	36.3	91
75	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
74	Chronic gastroesophageal reflux disease shares genetic background with esophageal adenocarcinoma and Barrett's esophagus. *Human Molecular Genetics*, **2016**, 25, 828-35	5.6	26
73	Genome-wide association analysis of self-reported events in 6135 individuals and 252 827 controls identifies 8 loci associated with thrombosis. *Human Molecular Genetics*, **2016**, 25, 1867-74	5.6	71
72	GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. *Nature Communications*, **2016**, 7, 10448	17.4	207
71	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. *PLoS Genetics*, **2016**, 12, e1006125	6	222
70	Genome-wide association analysis of pain severity in dysmenorrhea identifies association at chromosome 1p13.2, near the nerve growth factor locus. *Pain*, **2016**, 157, 2571-2581	8	22
69	Detection and interpretation of shared genetic influences on 42 human traits. *Nature Genetics*, **2016**, 48, 709-17	36.3	657
68	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
67	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
66	Identification of 15 genetic loci associated with risk of major depression in individuals of European descent. *Nature Genetics*, **2016**, 48, 1031-6	36.3	487
65	minimac2: faster genotype imputation. *Bioinformatics*, **2015**, 31, 782-4	7.2	264
64	Assessment of the genetic basis of rosacea by genome-wide association study. *Journal of Investigative Dermatology*, **2015**, 135, 1548-1555	4.3	97
63	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. *Nature Communications*, **2015**, 6, 8464	17.4	203
62	Multi-ancestry genome-wide association study of 21,000 cases and 95,000 controls identifies new risk loci for atopic dermatitis. *Nature Genetics*, **2015**, 47, 1449-1456	36.3	329
61	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. *Nature Communications*, **2015**, 6, 8842	17.4	75
60	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. *Human Molecular Genetics*, **2015**, 24, 2700-8	5.6	53

59	A genome-wide association study identifies four novel susceptibility loci underlying inguinal hernia. *Nature Communications*, **2015**, 6, 10130	17.4	43
58	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
57	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. *Journal of Allergy and Clinical Immunology*, **2014**, 133, 1564-71	11.5	143
56	Replicability and robustness of genome-wide-association studies for behavioral traits. *Psychological Science*, **2014**, 25, 1975-86	7.9	75
55	Economic evaluation of using a genetic test to direct breast cancer chemoprevention in white women with a previous breast biopsy. *Applied Health Economics and Health Policy*, **2014**, 12, 203-17	3.4	7
54	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. *Genes and Immunity*, **2013**, 14, 441-6	4.4	25
53	Androgenetic alopecia: identification of four genetic risk loci and evidence for the contribution of WNT signaling to its etiology. *Journal of Investigative Dermatology*, **2013**, 133, 1489-96	4.3	64
52	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. *Nature Genetics*, **2013**, 45, 907-11	36.3	191
51	Genome-wide analysis points to roles for extracellular matrix remodeling, the visual cycle, and neuronal development in myopia. *PLoS Genetics*, **2013**, 9, e1003299	6	190
50	Genetic variants associated with breast size also influence breast cancer risk. *BMC Medical Genetics*, **2012**, 13, 53	2.1	50
49	A genetic variant near olfactory receptor genes influences cilantro preference. *Flavour*, **2012**, 1,		50
48	Novel associations for hypothyroidism include known autoimmune risk loci. *PLoS ONE*, **2012**, 7, e34442	3.7	105
47	Six novel susceptibility Loci for early-onset androgenetic alopecia and their unexpected association with common diseases. *PLoS Genetics*, **2012**, 8, e1002746	6	70
46	Varenicline for smoking cessation: nausea severity and variation in nicotinic receptor genes. *Pharmacogenomics Journal*, **2012**, 12, 349-58	3.5	19
45	Genetic variants in the MRPS30 region and postmenopausal breast cancer risk. *Genome Medicine*, **2011**, 3, 42	14.4	13
44	Efficient replication of over 180 genetic associations with self-reported medical data. *PLoS ONE*, **2011**, 6, e23473	3.7	101
43	Variant in PNPLA3 is associated with alcoholic liver disease. *Nature Genetics*, **2010**, 42, 21-3	36.3	328
42	Variation in the FGFR2 gene and the effect of a low-fat dietary pattern on invasive breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2010**, 19, 74-9	4	18

41	Resequencing of nicotinic acetylcholine receptor genes and association of common and rare variants with the Fagerstr□h test for nicotine dependence. *Neuropsychopharmacology*, **2010**, 35, 2392-402	8.7	55
40	Assessment of clinical validity of a breast cancer risk model combining genetic and clinical information. *Journal of the National Cancer Institute*, **2010**, 102, 1618-27	9.7	133
39	Pooled versus individual genotyping in a breast cancer genome-wide association study. *Genetic Epidemiology*, **2010**, 34, 603-12	2.6	10
38	Comprehensive whole-genome and candidate gene analysis for response to statin therapy in the Treating to New Targets (TNT) cohort. *Circulation: Cardiovascular Genetics*, **2009**, 2, 173-81		149
37	Variation in the FGFR2 gene and the effects of postmenopausal hormone therapy on invasive breast cancer. *Cancer Epidemiology Biomarkers and Prevention*, **2009**, 18, 3079-85	4	51
36	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. *Nature Genetics*, **2008**, 40, 149-51	36.3	262
35	Common sequence polymorphisms shaping genetic diversity in Arabidopsis thaliana. *Science*, **2007**, 317, 338-42	33.3	596
34	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. *Nature*, **2007**, 448, 1050-3	50.4	352
33	Genome-wide detection and characterization of positive selection in human populations. *Nature*, **2007**, 449, 913-8	50.4	1367
32	A second generation human haplotype map of over 3.1 million SNPs. *Nature*, **2007**, 449, 851-61	50.4	3647
31	A genomewide single-nucleotide-polymorphism panel for Mexican American admixture mapping. *American Journal of Human Genetics*, **2007**, 80, 1014-23	11	113
30	A genomewide association study of skin pigmentation in a South Asian population. *American Journal of Human Genetics*, **2007**, 81, 1119-32	11	215
29	A common allele on chromosome 9 associated with coronary heart disease. *Science*, **2007**, 316, 1488-91	33.3	1415
28	A genomewide single-nucleotide-polymorphism panel with high ancestry information for African American admixture mapping. *American Journal of Human Genetics*, **2006**, 79, 640-9	11	142
27	Common deletions and SNPs are in linkage disequilibrium in the human genome. *Nature Genetics*, **2006**, 38, 82-5	36.3	303
26	Whole-genome patterns of common DNA variation in three human populations. *Science*, **2005**, 307, 1072-9	33.3	972
25	Fine-scale recombination patterns differ between chimpanzees and humans. *Nature Genetics*, **2005**, 37, 429-34	36.3	226
24	Genome-wide definitive haplotypes determined using a collection of complete hydatidiform moles. *Genome Research*, **2005**, 15, 1511-8	9.7	15

23	Segmental phylogenetic relationships of inbred mouse strains revealed by fine-scale analysis of sequence variation across 4.6 mb of mouse genome. *Genome Research*, **2004**, 14, 1493-500	9.7	71
22	Matching strategies for genetic association studies in structured populations. *American Journal of Human Genetics*, **2004**, 74, 317-25	11	88
21	Application of pooled genotyping to scan candidate regions for association with HDL cholesterol levels. *Human Genomics*, **2004**, 1, 421-34	6.8	68
20	Genomic DNA insertions and deletions occur frequently between humans and nonhuman primates. *Genome Research*, **2003**, 13, 341-6	9.7	68
19	Blocks of limited haplotype diversity revealed by high-resolution scanning of human chromosome 21. *Science*, **2001**, 294, 1719-23	33.3	948
18	Exclusion of linkage to the HLA region in ninety multiplex sibships with autism. *Journal of Autism and Developmental Disorders*, **1999**, 29, 195-201	4.6	31
17	Sib-pair analysis of the collaborative study on the genetics of alcoholism data set. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S187-91	2.6	2
16	A second-generation screen of the human genome for susceptibility to insulin-dependent diabetes mellitus. *Nature Genetics*, **1998**, 19, 292-6	36.3	296
15	From structure to sequence and back again. *Journal of Molecular Biology*, **1996**, 258, 201-9	6.5	33
14	A full genome search in multiple sclerosis. *Nature Genetics*, **1996**, 13, 472-6	36.3	572
13	Simulation of protein-folding pathways: lost in (conformational) space?. *Trends in Biotechnology*, **1995**, 13, 23-27	15.1	11
12	Exploring conformational space with a simple lattice model for protein structure. *Journal of Molecular Biology*, **1994**, 243, 668-82	6.5	137
11	A lattice model for protein structure prediction at low resolution. *Proceedings of the National Academy of Sciences of the United States of America*, **1992**, 89, 2536-40	11.5	182
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	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depressive disorder		21
7	Genome-wide Analysis of Insomnia (N=1,331,010) Identifies Novel Loci and Functional Pathways		12
6	Phenome-wide association studies (PheWAS) across large real-world data population cohorts support drug target validation		5

List of Publications

5	Social and non-social autism symptom and trait domains are genetically dissociable	1
4	Genome-wide association analyses of chronotype in 697,828 individuals provides new insights into circadian rhythms in humans and links to disease	5
3	Parkinson disease age of onset GWAS: defining heritability, genetic loci and a-synuclein mechanisms	6
2	Genome-wide meta-analysis of depression identifies 102 independent variants and highlights the importance of the prefrontal brain regions	8
1	Genome-wide association study of musical beat synchronization demonstrates high polygenicity	9