David A Hinds

List of Publications by Year
in descending order

129 papers	35,121 citations	15001 68 h-index	14386 132 g-index
147 all docs	147 docs citations	147 times ranked	47553 citing authors

#	Article	IF	Citations
1	Multitrait genetic association analysis identifies 50 new risk loci for gastro-oesophageal reflux, seven new loci for Barrettâ€™s oesophagus and provides insights into clinical heterogeneity in reflux diagnosis. Gut, 2022, 71, 1053-1061.	6.1	74
2	Prevalence of Alpha-1 Antitrypsin Deficiency, Self-Reported Behavior Change, and Health Care Engagement Among Direct-to-Consumer Recipients of a Personalized Genetic Risk Report. Chest, 2022, 161, 373-381.	0.4	13
3	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.3	11
4	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	9.4	215
5	Characterizing mood disorders in the AFFECT study: a large, longitudinal, and phenotypically rich genetic cohort in the US. Translational Psychiatry, 2022, 12, 121.	2.4	6
6	Genome-wide association analysis and replication in 810,625 individuals with varicose veins. Nature Communications, 2022, 13, .	5.8	8
7	Genome-wide association study of musical beat synchronization demonstrates high polygenicity. Nature Human Behaviour, 2022, 6, 1292-1309.	6.2	33
8	The genetic architecture of pneumonia susceptibility implicates mucin biology and a relationship with psychiatric illness. Nature Communications, 2022, 13, .	5.8	7
9	Genome-wide meta-analysis of insomnia prioritizes genes associated with metabolic and psychiatric pathways. Nature Genetics, 2022, 54, 1125-1132.	9.4	61
10	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
11	Genome-wide association study in almost 195,000 individuals identifies 50 previously unidentified genetic loci for eye color. Science Advances, 2021, 7, .	4.7	36
12	Nuclear genome-wide associations with mitochondrial heteroplasmy. Science Advances, 2021, 7, .	4.7	16
13	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
14	Resource profile and user guide of the Polygenic Index Repository. Nature Human Behaviour, 2021, 5, 1744-1758.	6.2	63
15	FUT6 deficiency compromises basophil function by selectively abrogating their sialyl-Lewis x expression. Communications Biology, 2021, 4, 832.	2.0	7
16	Genome-wide association study of problematic opioid prescription use in 132,113 23andMe research participants of European ancestry. Molecular Psychiatry, 2021, 26, 6209-6217.	4.1	26
17	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	1.4	26
18	Genome-wide association studies of antidepressant class response and treatment-resistant depression. Translational Psychiatry, 2020, 10, 360.	2.4	33

#	Article	IF	Citations
19	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
20	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
21	Cross-trait analyses with migraine reveal widespread pleiotropy and suggest a vascular component to migraine headache. International Journal of Epidemiology, 2020, 49, 1022-1031.	0.9	34
22	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. PLoS ONE, 2020, 15, e0241552.	1.1	7
23	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.	2.6	79
24	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
25	Social and non-social autism symptoms and trait domains are genetically dissociable. Communications Biology, 2019, 2, 328.	2.0	57
26	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	5.8	417
27	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participantsâ€™ perspective. Psychiatry Research, 2019, 278, 173-179.	1.7	6
28	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. American Journal of Human Genetics, 2019, 104, 665-684.	2.6	183
29	Genome-wide analysis of insomnia in 1,331,010 individuals identifies new risk loci and functional pathways. Nature Genetics, 2019, 51, 394-403.	9.4	593
30	Association of Whole-Genome and NETRIN1 Signaling Pathwayâ€“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.	1.1	16
31	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
32	Genetic association and differential expression of PITX2 with acute appendicitis. Human Genetics, 2019, 138, 37-47.	1.8	14
33	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.	9.4	1,307
34	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.	9.4	536
35	Eleven loci with new reproducible genetic associations with allergic disease risk. Journal of Allergy and Clinical Immunology, 2019, 143, 691-699.	1.5	49
36	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.	7.1	1,589

#	Article	IF	Citations
37	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.	9.4	86
38	Genome-wide association analyses identify 44 risk variants and refine the genetic architecture of major depression. Nature Genetics, 2018, 50, 668-681.	9.4	2,224
39	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa. Translational Psychiatry, 2018, 8, 35.	2.4	95
40	Genome-wide meta-analysis of cognitive empathy: heritability, and correlates with sex, neuropsychiatric conditions and cognition. Molecular Psychiatry, 2018, 23, 1402-1409.	4.1	102
41	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	5.8	134
42	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. Nature Communications, 2018, 9, 4264.	5.8	21
43	Genome-wide association and HLA fine-mapping studies identify risk loci and genetic pathways underlying allergic rhinitis. Nature Genetics, 2018, 50, 1072-1080.	9.4	106
44	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. PLoS Genetics, 2018, 14, e1007394.	1.5	35
45	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.	1.4	29
46	Meta-analysis identifies novel risk loci and yields systematic insights into the biology of male-pattern baldness. Nature Communications, 2017, 8, 14694.	5.8	58
47	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
48	Genome-wide analyses for personality traits identify six genomic loci and show correlations with psychiatric disorders. Nature Genetics, 2017, 49, 152-156.	9.4	350
49	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
50	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.	4.9	191
51	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	1.8	39
52	A meta-analysis of genome-wide association studies identifies 17 new Parkinson's disease risk loci. Nature Genetics, 2017, 49, 1511-1516.	9.4	944
53	Genome-wide association and HLA region fine-mapping studies identify susceptibility loci for multiple common infections. Nature Communications, 2017, 8, 599.	5.8	298
54	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. New England Journal of Medicine, 2017, 377, 1156-1167.	13.9	309

#	Article	IF	Citations
55	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	2.6	29
56	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.	1.5	72
57	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.	1.4	32
58	Two-stage genome-wide association study identifies a novel susceptibility locus associated with melanoma. Oncotarget, 2017, 8, 17586-17592.	0.8	61
59	Phenome-wide association study using research participantsâ€™ self-reported data provides insight into the Th17 and IL-17 pathway. PLoS ONE, 2017, 12, e0186405.	1.1	16
60	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.	2.0	36
61	Detection and interpretation of shared genetic influences on 42 human traits. Nature Genetics, 2016, 48, 709-717.	9.4	990
62	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. Nature Genetics, 2016, 48, 624-633.	9.4	870
63	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
64	Identification of 15 genetic loci associated with risk of major depression in individuals of European descent. Nature Genetics, 2016, 48, 1031-1036.	9.4	655
65	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2016, 7, 12048.	5.8	117
66	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. Nature Communications, 2016, 7, 12510.	5.8	94
67	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. Nature Genetics, 2016, 48, 1557-1563.	9.4	131
68	Genetic variants linked to education predict longevity. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 13366-13371.	3.3	110
69	Chronic gastroesophageal reflux disease shares genetic background with esophageal adenocarcinoma and Barrett's esophagus. Human Molecular Genetics, 2016, 25, 828-835.	1.4	31
70	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, 1867-1874.	1.4	103
71	GWAS of 89,283 individuals identifies genetic variants associated with self-reporting of being a morning person. Nature Communications, 2016, 7, 10448.	5.8	263
72	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308

#	Article	IF	Citations
73	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. Nature Communications, 2015, 6, 8842.	5.8	100
74	Genetic variants associated with motion sickness point to roles for inner ear development, neurological processes and glucose homeostasis. Human Molecular Genetics, 2015, 24, 2700-2708.	1.4	70
75	A genome-wide association study identifies four novel susceptibility loci underlying inguinal hernia. Nature Communications, 2015, 6, 10130.	5.8	68
76	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
77	minimac2: faster genotype imputation. Bioinformatics, 2015, 31, 782-784.	1.8	444
78	Assessment of the Genetic Basis of Rosacea by Genome-Wide Association Study. Journal of Investigative Dermatology, 2015, 135, 1548-1555.	0.3	129
79	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
80	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.	9.4	529
81	Genome-wide association analysis identifies 11 risk variants associated with the asthma with hay fever phenotype. Journal of Allergy and Clinical Immunology, 2014, 133, 1564-1571.	1.5	195
82	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
83	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, 203-217.	1.0	10
84	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. Genes and Immunity, 2013, 14, 441-446.	2.2	27
85	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, 1489-1496.	0.3	83
86	A genome-wide association meta-analysis of self-reported allergy identifies shared and allergy-specific susceptibility loci. Nature Genetics, 2013, 45, 907-911.	9.4	232
87	Genome-Wide Analysis Points to Roles for Extracellular Matrix Remodeling, the Visual Cycle, and Neuronal Development in Myopia. PLoS Genetics, 2013, 9, e1003299.	1.5	263
88	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	1.5	92
89	Varenicline for smoking cessation: nausea severity and variation in nicotinic receptor genes. Pharmacogenomics Journal, 2012, 12, 349-358.	0.9	34
90	Genetic variants associated with breast size also influence breast cancer risk. BMC Medical Genetics, 2012, 13, 53.	2.1	65

#	Article	IF	Citations
91	A genetic variant near olfactory receptor genes influences cilantro preference. Flavour, 2012, 1, .	2.3	72
92	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. PLoS ONE, 2012, 7, e34442.	1.1	128
93	Genetic variants in the MRPS30 region and postmenopausal breast cancer risk. Genome Medicine, 2011, 3, 42.	3.6	19
94	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. PLoS ONE, 2011, 6, e23473.	1.1	117
95	Pooled versus individual genotyping in a breast cancer genomeâ€wide association study. Genetic Epidemiology, 2010, 34, 603-612.	0.6	11
96	Variant in PNPLA3 is associated with alcoholic liver disease. Nature Genetics, 2010, 42, 21-23.	9.4	388
97	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, 74-79.	1.1	18
98	Resequencing of Nicotinic Acetylcholine Receptor Genes and Association of Common and Rare Variants with the FagerstrÃ¶m Test for Nicotine Dependence. Neuropsychopharmacology, 2010, 35, 2392-2402.	2.8	62
99	Assessment of Clinical Validity of a Breast Cancer Risk Model Combining Genetic and Clinical Information. Journal of the National Cancer Institute, 2010, 102, 1618-1627.	3.0	151
100	Variation in PNPLA3 is associated with outcomes in alcoholic liver disease. Nature Precedings, 2009, , .	0.1	0
101	Variation in PNPLA3 is associated with outcomes in alcoholic liver disease. Nature Precedings, 2009, , .	0.1	0
102	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, 173-181.	5.1	170
103	Variation in the FGFR2 Gene and the Effects of Postmenopausal Hormone Therapy on Invasive Breast Cancer. Cancer Epidemiology Biomarkers and Prevention, 2009, 18, 3079-3085.	1.1	54
104	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. Nature Genetics, 2008, 40, 149-151.	9.4	303
105	A Genomewide Single-Nucleotideâ€“Polymorphism Panel for Mexican American Admixture Mapping. American Journal of Human Genetics, 2007, 80, 1014-1023.	2.6	119
106	A Genomewide Association Study of Skin Pigmentation in a South Asian Population. American Journal of Human Genetics, 2007, 81, 1119-1132.	2.6	261
107	A Common Allele on Chromosome 9 Associated with Coronary Heart Disease. Science, 2007, 316, 1488-1491.	6.0	1,591
108	Common Sequence Polymorphisms Shaping Genetic Diversity in Arabidopsis thaliana. Science, 2007, 317, 338-342.	6.0	689

#	Article	IF	Citations
109	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Nature, 2007, 448, 1050-1053.	13.7	406
110	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
111	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
112	A Genomewide Single-Nucleotideâ€“Polymorphism Panel with High Ancestry Information for African American Admixture Mapping. American Journal of Human Genetics, 2006, 79, 640-649.	2.6	157
113	Common deletions and SNPs are in linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 82-85.	9.4	338
114	Fine-scale recombination patterns differ between chimpanzees and humans. Nature Genetics, 2005, 37, 429-434.	9.4	263
115	Genome-wide definitive haplotypes determined using a collection of complete hydatidiform moles. Genome Research, 2005, 15, 1511-1518.	2.4	16
116	Whole-Genome Patterns of Common DNA Variation in Three Human Populations. Science, 2005, 307, 1072-1079.	6.0	1,074
117	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, 1493-1500.	2.4	78
118	Matching Strategies for Genetic Association Studies in Structured Populations. American Journal of Human Genetics, 2004, 74, 317-325.	2.6	98
119	Application of pooled genotyping to scan candidate regions for association with HDL cholesterol levels. Human Genomics, 2004, 1, 421.	1.4	83
120	Genomic DNA Insertions and Deletions Occur Frequently Between Humans and Nonhuman Primates. Genome Research, 2003, 13, 341-346.	2.4	81
121	Blocks of Limited Haplotype Diversity Revealed by High-Resolution Scanning of Human Chromosome 21. Science, 2001, 294, 1719-1723.	6.0	1,082
122	Exclusion of linkage to the HLA region in ninety multiplex sibships with autism. Journal of Autism and Developmental Disorders, 1999, 29, 195-201.	1.7	35
123	Sibâ€pair analysis of the collaborative study on the genetics of alcoholism data set. Genetic Epidemiology, 1999, 17, S187-91.	0.6	2
124	A second-generation screen of the human genome for susceptibility to insulin-dependent diabetes mellitus. Nature Genetics, 1998, 19, 292-296.	9.4	330
125	From Structure to Sequence and Back Again. Journal of Molecular Biology, 1996, 258, 201-209.	2.0	34
126	A full genome search in multiple sclerosis. Nature Genetics, 1996, 13, 472-476.	9.4	638

#	Article	IF	Citations
127	Simulation of protein-folding pathways: lost in (conformational) space?. Trends in Biotechnology, 1995, 13, 23-27.	4.9	11
128	Exploring conformational space with a simple lattice model for protein structure. Journal of Molecular Biology, 1994, 243, 668-682.	2.0	153
129	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, 2536-2540.	3.3	207