David A Hinds

List of Publications by Year
in descending order

129 papers	35,121 citations	13068 68 h-index	12558 132 g-index
147 all docs	147 docs citations	147 times ranked	43103 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	13.7	4,137
2	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
3	Genome-wide detection and characterization of positive selection in human populations. Nature, 2007, 449, 913-918.	13.7	1,788
4	A Common Allele on Chromosome 9 Associated with Coronary Heart Disease. Science, 2007, 316, 1488-1491.	6.0	1,591
5	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
6	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
7	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	13.7	1,204
8	Blocks of Limited Haplotype Diversity Revealed by High-Resolution Scanning of Human Chromosome 21. Science, 2001, 294, 1719-1723.	6.0	1,082
9	Whole-Genome Patterns of Common DNA Variation in Three Human Populations. Science, 2005, 307, 1072-1079.	6.0	1,074
10	Detection and interpretation of shared genetic influences on 42 human traits. Nature Genetics, 2016, 48, 709-717.	9.4	990
11	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
12	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
13	Common Sequence Polymorphisms Shaping Genetic Diversity in Arabidopsis thaliana. Science, 2007, 317, 338-342.	6.0	689
14	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
15	A full genome search in multiple sclerosis. Nature Genetics, 1996, 13, 472-476.	9.4	638
16	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
17	An atlas of genetic influences on osteoporosis in humans and mice. Nature Genetics, 2019, 51, 258-266.	9.4	557
18	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

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19	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
20	minimac2: faster genotype imputation. Bioinformatics, 2015, 31, 782-784.	1.8	444
21	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	9.4	432
22	Genome-wide association analyses of chronotype in 697,828 individuals provides insights into circadian rhythms. Nature Communications, 2019, 10, 343.	5.8	417
23	A sequence-based variation map of 8.27 million SNPs in inbred mouse strains. Nature, 2007, 448, 1050-1053.	13.7	406
24	Variant in PNPLA3 is associated with alcoholic liver disease. Nature Genetics, 2010, 42, 21-23.	9.4	388
25	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
26	Common deletions and SNPs are in linkage disequilibrium in the human genome. Nature Genetics, 2006, 38, 82-85.	9.4	338
27	A second-generation screen of the human genome for susceptibility to insulin-dependent diabetes mellitus. Nature Genetics, 1998, 19, 292-296.	9.4	330
28	Genetic Associations with Gestational Duration and Spontaneous Preterm Birth. New England Journal of Medicine, 2017, 377, 1156-1167.	13.9	309
29	Genome-Wide Association Analyses in 128,266 Individuals Identifies New Morningness and Sleep Duration Loci. PLoS Genetics, 2016, 12, e1006125.	1.5	308
30	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	5.8	304
31	Genome-wide scan identifies variation in MLXIPL associated with plasma triglycerides. Nature Genetics, 2008, 40, 149-151.	9.4	303
32	Genome-wide association and HLA region fine-mapping studies identify susceptibility loci for multiple common infections. Nature Communications, 2017, 8, 599.	5.8	298
33	Fine-scale recombination patterns differ between chimpanzees and humans. Nature Genetics, 2005, 37, 429-434.	9.4	263
34	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
35	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
36	A Genomewide Association Study of Skin Pigmentation in a South Asian Population. American Journal of Human Genetics, 2007, 81, 1119-1132.	2.6	261

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37	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
38	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
39	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
40	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
41	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
42	Genetic Architectures of Childhood- and Adult-Onset Asthma Are Partly Distinct. American Journal of Human Genetics, 2019, 104, 665-684.	2.6	183
43	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
44	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
45	Exploring conformational space with a simple lattice model for protein structure. Journal of Molecular Biology, 1994, 243, 668-682.	2.0	153
46	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
47	Phenome-wide association studies across large population cohorts support drug target validation. Nature Communications, 2018, 9, 4285.	5.8	134
48	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
49	Assessment of the Genetic Basis of Rosacea by Genome-Wide Association Study. Journal of Investigative Dermatology, 2015, 135, 1548-1555.	0.3	129
50	Novel Associations for Hypothyroidism Include Known Autoimmune Risk Loci. PLoS ONE, 2012, 7, e34442.	1.1	128
51	Genetic analyses identify widespread sex-differential participation bias. Nature Genetics, 2021, 53, 663-671.	9.4	124
52	A Genomewide Single-Nucleotideâ€“Polymorphism Panel for Mexican American Admixture Mapping. American Journal of Human Genetics, 2007, 80, 1014-1023.	2.6	119
53	Efficient Replication of over 180 Genetic Associations with Self-Reported Medical Data. PLoS ONE, 2011, 6, e23473.	1.1	117
54	Genome-wide association study identifies novel susceptibility loci for cutaneous squamous cell carcinoma. Nature Communications, 2016, 7, 12048.	5.8	117

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55	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
56	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
57	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
58	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
59	Shared genetic aetiology of puberty timing between sexes and with health-related outcomes. Nature Communications, 2015, 6, 8842.	5.8	100
60	Matching Strategies for Genetic Association Studies in Structured Populations. American Journal of Human Genetics, 2004, 74, 317-325.	2.6	98
61	Genome-wide analyses of self-reported empathy: correlations with autism, schizophrenia, and anorexia nervosa. Translational Psychiatry, 2018, 8, 35.	2.4	95
62	Genome-wide association study identifies 14 novel risk alleles associated with basal cell carcinoma. Nature Communications, 2016, 7, 12510.	5.8	94
63	Six Novel Susceptibility Loci for Early-Onset Androgenetic Alopecia and Their Unexpected Association with Common Diseases. PLoS Genetics, 2012, 8, e1002746.	1.5	92
64	Replicability and Robustness of Genome-Wide-Association Studies for Behavioral Traits. Psychological Science, 2014, 25, 1975-1986.	1.8	92
65	Genome-wide association and epidemiological analyses reveal common genetic origins between uterine leiomyomata and endometriosis. Nature Communications, 2019, 10, 4857.	5.8	90
66	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
67	Application of pooled genotyping to scan candidate regions for association with HDL cholesterol levels. Human Genomics, 2004, 1, 421.	1.4	83
68	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
69	Genomic DNA Insertions and Deletions Occur Frequently Between Humans and Nonhuman Primates. Genome Research, 2003, 13, 341-346.	2.4	81
70	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
71	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	6.2	79
72	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

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73	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
74	A genetic variant near olfactory receptor genes influences cilantro preference. Flavour, 2012, 1, .	2.3	72
75	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
76	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
77	A genome-wide association study identifies four novel susceptibility loci underlying inguinal hernia. Nature Communications, 2015, 6, 10130.	5.8	68
78	Genetic variants associated with breast size also influence breast cancer risk. BMC Medical Genetics, 2012, 13, 53.	2.1	65
79	Shared genetic variants suggest common pathways in allergy and autoimmune diseases. Journal of Allergy and Clinical Immunology, 2017, 140, 771-781.	1.5	63
80	Resource profile and user guide of the Polygenic Index Repository. Nature Human Behaviour, 2021, 5, 1744-1758.	6.2	63
81	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
82	Two-stage genome-wide association study identifies a novel susceptibility locus associated with melanoma. Oncotarget, 2017, 8, 17586-17592.	0.8	61
83	Genome-wide meta-analysis of insomnia prioritizes genes associated with metabolic and psychiatric pathways. Nature Genetics, 2022, 54, 1125-1132.	9.4	61
84	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
85	Social and non-social autism symptoms and trait domains are genetically dissociable. Communications Biology, 2019, 2, 328.	2.0	57
86	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
87	Eleven loci with new reproducible genetic associations with allergic disease risk. Journal of Allergy and Clinical Immunology, 2019, 143, 691-699.	1.5	49
88	A multi-stage genome-wide association study of uterine fibroids in African Americans. Human Genetics, 2017, 136, 1363-1373.	1.8	39
89	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
90	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

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91	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
92	Whole exome sequencing reveals HSPA1L as a genetic risk factor for spontaneous preterm birth. PLoS Genetics, 2018, 14, e1007394.	1.5	35
93	From Structure to Sequence and Back Again. Journal of Molecular Biology, 1996, 258, 201-209.	2.0	34
94	Varenicline for smoking cessation: nausea severity and variation in nicotinic receptor genes. Pharmacogenomics Journal, 2012, 12, 349-358.	0.9	34
95	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
96	Genome-wide association studies of antidepressant class response and treatment-resistant depression. Translational Psychiatry, 2020, 10, 360.	2.4	33
97	Genome-wide association study of musical beat synchronization demonstrates high polygenicity. Nature Human Behaviour, 2022, 6, 1292-1309.	6.2	33
98	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
99	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
100	Chronic gastroesophageal reflux disease shares genetic background with esophageal adenocarcinoma and Barrett's esophagus. Human Molecular Genetics, 2016, 25, 828-835.	1.4	31
101	Multiethnic GWAS Reveals Polygenic Architecture of Earlobe Attachment. American Journal of Human Genetics, 2017, 101, 913-924.	2.6	29
102	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
103	A new regulatory variant in the interleukin-6 receptor gene associates with asthma risk. Genes and Immunity, 2013, 14, 441-446.	2.2	27
104	Age-of-onset information helps identify 76 genetic variants associated with allergic disease. PLoS Genetics, 2020, 16, e1008725.	1.5	27
105	Insights into the genetic basis of retinal detachment. Human Molecular Genetics, 2020, 29, 689-702.	1.4	26
106	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
107	Gene expression imputation identifies candidate genes and susceptibility loci associated with cutaneous squamous cell carcinoma. Nature Communications, 2018, 9, 4264.	5.8	21
108	Genetic variants in the MRPS30 region and postmenopausal breast cancer risk. Genome Medicine, 2011, 3, 42.	3.6	19

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109	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
110	Habitual sleep disturbances and migraine: a Mendelian randomization study. Annals of Clinical and Translational Neurology, 2020, 7, 2370-2380.	1.7	18
111	Genome-wide definitive haplotypes determined using a collection of complete hydatidiform moles. Genome Research, 2005, 15, 1511-1518.	2.4	16
112	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
113	Nuclear genome-wide associations with mitochondrial heteroplasmy. Science Advances, 2021, 7, .	4.7	16
114	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
115	Genetic association and differential expression of PITX2 with acute appendicitis. Human Genetics, 2019, 138, 37-47.	1.8	14
116	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
117	Simulation of protein-folding pathways: lost in (conformational) space?. Trends in Biotechnology, 1995, 13, 23-27.	4.9	11
118	Pooled versus individual genotyping in a breast cancer genomeâ€wide association study. Genetic Epidemiology, 2010, 34, 603-612.	0.6	11
119	Multi-Trait Genetic Analysis Identifies Autoimmune Loci Associated with Cutaneous Melanoma. Journal of Investigative Dermatology, 2022, 142, 1607-1616.	0.3	11
120	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
121	Genome-wide association analysis and replication in 810,625 individuals with varicose veins. Nature Communications, 2022, 13, .	5.8	8
122	FUT6 deficiency compromises basophil function by selectively abrogating their sialyl-Lewis x expression. Communications Biology, 2021, 4, 832.	2.0	7
123	The association of clinical phenotypes to known AD/FTD genetic risk loci and their inter-relationship. PLoS ONE, 2020, 15, e0241552.	1.1	7
124	The genetic architecture of pneumonia susceptibility implicates mucin biology and a relationship with psychiatric illness. Nature Communications, 2022, 13, .	5.8	7
125	Phenotypic analysis of 23andMe survey data: Treatment-resistant depression from participantsâ€™ perspective. Psychiatry Research, 2019, 278, 173-179.	1.7	6
126	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

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127	Sibâ€pair analysis of the collaborative study on the genetics of alcoholism data set. Genetic Epidemiology, 1999, 17, S187-91.	0.6	2
128	Variation in PNPLA3 is associated with outcomes in alcoholic liver disease. Nature Precedings, 2009, , .	0.1	0
129	Variation in PNPLA3 is associated with outcomes in alcoholic liver disease. Nature Precedings, 2009, , .	0.1	0