Daniel F Gudbjartsson

List of Publications by Year
in descending order

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244 papers	58,287 citations	1530 106 h-index	1216 227 g-index
269 all docs	269 docs citations	269 times ranked	66059 citing authors

#	Article	IF	Citations
1	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	13.7	1,880
2	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
3	Large recurrent microdeletions associated with schizophrenia. Nature, 2008, 455, 232-236.	13.7	1,619
4	A high-resolution recombination map of the human genome. Nature Genetics, 2002, 31, 241-247.	9.4	1,571
5	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	2.6	1,550
6	A Common Variant on Chromosome 9p21 Affects the Risk of Myocardial Infarction. Science, 2007, 316, 1491-1493.	6.0	1,485
7	A mutation in APP protects against Alzheimerâ€™s disease and age-related cognitive decline. Nature, 2012, 488, 96-99.	13.7	1,442
8	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	13.7	1,399
9	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
10	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	9.4	1,247
11	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
12	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	13.9	1,093
13	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	13.7	853
14	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	13.9	845
15	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. Nature Genetics, 2007, 39, 631-637.	9.4	818
16	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	9.4	774
17	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
18	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	9.4	738

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19	Allegro, a new computer program for multipoint linkage analysis. Nature Genetics, 2000, 25, 12-13.	9.4	737
20	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	6.0	720
21	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	9.4	709
22	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
23	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
24	Genetic determinants of hair, eye and skin pigmentation in Europeans. Nature Genetics, 2007, 39, 1443-1452.	9.4	659
25	Common Sequence Variants in the LOXL1 Gene Confer Susceptibility to Exfoliation Glaucoma. Science, 2007, 317, 1397-1400.	6.0	657
26	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	9.4	649
27	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615
28	A Genetic Risk Factor for Periodic Limb Movements in Sleep. New England Journal of Medicine, 2007, 357, 639-647.	13.9	582
29	Multiple Genetic Loci for Bone Mineral Density and Fractures. New England Journal of Medicine, 2008, 358, 2355-2365.	13.9	582
30	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. Blood, 2017, 130, 742-752.	0.6	582
31	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	9.4	572
32	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	13.7	559
33	The gene encoding phosphodiesterase 4D confers risk of ischemic stroke. Nature Genetics, 2003, 35, 131-138.	9.4	555
34	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	9.4	549
35	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	13.7	548
36	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	9.4	547

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37	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	13.7	521
38	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. Nature Genetics, 2011, 43, 1131-1138.	9.4	501
39	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. Nature Communications, 2020, 11, 163.	5.8	466
40	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	9.4	445
41	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	9.4	434
42	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
43	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	9.4	426
44	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	13.7	410
45	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	9.4	409
46	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	9.4	377
47	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. Nature Genetics, 2008, 40, 281-283.	9.4	357
48	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. Nature Genetics, 2009, 41, 460-464.	9.4	353
49	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
50	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. Nature Neuroscience, 2015, 18, 953-955.	7.1	351
51	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	9.4	342
52	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
53	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. Nature Genetics, 2006, 38, 68-74.	9.4	339
54	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	9.4	338

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55	Two newly identified genetic determinants of pigmentation in Europeans. Nature Genetics, 2008, 40, 835-837.	9.4	331
56	New sequence variants associated with bone mineral density. Nature Genetics, 2009, 41, 15-17.	9.4	328
57	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. Nature Genetics, 2009, 41, 1122-1126.	9.4	313
58	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. Nature Genetics, 2008, 40, 886-891.	9.4	306
59	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	9.4	303
60	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	9.4	303
61	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	9.4	294
62	Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631.	9.4	282
63	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. Nature Genetics, 2014, 46, 826-836.	9.4	281
64	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	9.4	275
65	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7119-7124.	3.3	258
66	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	6.0	252
67	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	9.4	251
68	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	9.4	251
69	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	9.4	248
70	Cancer as a Complex Phenotype: Pattern of Cancer Distribution within and beyond the Nuclear Family. PLoS Medicine, 2004, 1, e65.	3.9	245
71	Brain age prediction using deep learning uncovers associated sequence variants. Nature Communications, 2019, 10, 5409.	5.8	238
72	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	13.7	236

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73	Inheritance of human longevity in Iceland. European Journal of Human Genetics, 2000, 8, 743-749.	1.4	230
74	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. Human Molecular Genetics, 2014, 23, 4420-4432.	1.4	227
75	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
76	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	9.4	214
77	Effects of a 5-Lipoxygenaseâ€“Activating Protein Inhibitor on Biomarkers Associated With Risk of Myocardial Infarction. JAMA - Journal of the American Medical Association, 2005, 293, 2245.	3.8	212
78	Discovery of common variants associated with low TSH levels and thyroid cancer risk. Nature Genetics, 2012, 44, 319-322.	9.4	208
79	A large-scale genome-wide association study meta-analysis of cannabis use disorder. Lancet Psychiatry,the, 2020, 7, 1032-1045.	3.7	200
80	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	9.4	199
81	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	13.7	198
82	Allegro version 2. Nature Genetics, 2005, 37, 1015-1016.	9.4	192
83	Graphtyper enables population-scale genotyping using pangenome graphs. Nature Genetics, 2017, 49, 1654-1660.	9.4	189
84	Sequence Variants in the RNF212 Gene Associate with Genome-Wide Recombination Rate. Science, 2008, 319, 1398-1401.	6.0	183
85	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. Nature Genetics, 2012, 44, 1326-1329.	9.4	178
86	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	9.4	178
87	Recombination rate and reproductive success in humans. Nature Genetics, 2004, 36, 1203-1206.	9.4	176
88	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. Nature Genetics, 2010, 42, 415-419.	9.4	169
89	Association of Variants at UMOD with Chronic Kidney Disease and Kidney Stonesâ€”Role of Age and Comorbid Diseases. PLoS Genetics, 2010, 6, e1001039.	1.5	166
90	Subclinical intestinal inflammation: an inherited abnormality in Crohnâ€™s disease relatives?. Gastroenterology, 2003, 124, 1728-1737.	0.6	165

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91	A Susceptibility Gene for Psoriatic Arthritis Maps to Chromosome 16q: Evidence for Imprinting. American Journal of Human Genetics, 2003, 72, 125-131.	2.6	165
92	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	9.4	158
93	Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. Nature Genetics, 2021, 53, 779-786.	9.4	156
94	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	9.4	155
95	Apolipoprotein(a) Genetic Sequence Variants Associated With Systemic Atherosclerosis and Coronary Atherosclerotic Burden But Not With Venous Thromboembolism. Journal of the American College of Cardiology, 2012, 60, 722-729.	1.2	149
96	Selection against variants in the genome associated with educational attainment. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E727-E732.	3.3	149
97	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	9.4	147
98	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	5.8	146
99	An Association Between the Kinship and Fertility of Human Couples. Science, 2008, 319, 813-816.	6.0	142
100	Genetic Correction of PSA Values Using Sequence Variants Associated with PSA Levels. Science Translational Medicine, 2010, 2, 62ra92.	5.8	140
101	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
102	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
103	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Human Molecular Genetics, 2011, 20, 4268-4281.	1.4	134
104	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	5.8	133
105	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
106	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. Nature Genetics, 2018, 50, 1681-1687.	9.4	131
107	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	1.2	127
108	A sequence variant on 17q21 is associated with age at onset and severity of asthma. European Journal of Human Genetics, 2010, 18, 902-908.	1.4	126

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109	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	1.5	126
110	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. Nature Genetics, 2013, 45, 1371-1374.	9.4	125
111	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
112	Common and rare variants associated with kidney stones and biochemical traits. Nature Communications, 2015, 6, 7975.	5.8	117
113	A genome-wide association study yields five novel thyroid cancer risk loci. Nature Communications, 2017, 8, 14517.	5.8	117
114	Common and low-frequency variants associated with genome-wide recombination rate. Nature Genetics, 2014, 46, 11-16.	9.4	116
115	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	1.4	114
116	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530.	1.5	112
117	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. Nature Genetics, 2008, 40, 1313-1318.	9.4	111
118	Multi-nucleotide de novo Mutations in Humans. PLoS Genetics, 2016, 12, e1006315.	1.5	111
119	Familial Risk of Lung Carcinoma in the Icelandic Population. JAMA - Journal of the American Medical Association, 2004, 292, 2977.	3.8	105
120	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
121	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. Nature Communications, 2015, 6, 7213.	5.8	101
122	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
123	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	2.4	98
124	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. Nature Communications, 2019, 10, 5402.	5.8	96
125	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	5.8	95
126	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	9.4	94

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127	Genome-wide association study implicates CHRNA2 in cannabis use disorder. Nature Neuroscience, 2019, 22, 1066-1074.	7.1	94
128	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
129	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
130	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. Addiction Biology, 2018, 23, 485-492.	1.4	90
131	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	1.0	89
132	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	9.4	89
133	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
134	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	9.4	85
135	Genome-Wide Meta-Analysis for Serum Calcium Identifies Significantly Associated SNPs near the Calcium-Sensing Receptor (CASR) Gene. PLoS Genetics, 2010, 6, e1001035.	1.5	84
136	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	5.8	84
137	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	9.4	83
138	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	9.4	83
139	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. PLoS Genetics, 2010, 6, e1001029.	1.5	82
140	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	13.7	81
141	European Bone Mineral Density Loci Are Also Associated with BMD in East-Asian Populations. PLoS ONE, 2010, 5, e13217.	1.1	81
142	Genome-wide association study across European and African American ancestries identifies a SNP in DNMT3B contributing to nicotine dependence. Molecular Psychiatry, 2018, 23, 1911-1919.	4.1	80
143	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. Nature Genetics, 2017, 49, 801-805.	9.4	75
144	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. Translational Psychiatry, 2019, 9, 258.	2.4	75

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145	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
146	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	5.8	74
147	A Missense Variant in PLEC Increases RiskÂof Atrial Fibrillation. Journal of the American College of Cardiology, 2017, 70, 2157-2168.	1.2	73
148	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	5.8	73
149	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
150	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. Nature Communications, 2018, 9, 2904.	5.8	71
151	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. Nature, 2020, 582, 78-83.	13.7	71
152	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	9.4	70
153	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. Translational Psychiatry, 2017, 7, e1109-e1109.	2.4	67
154	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. Nature Communications, 2017, 8, 15789.	5.8	67
155	Truncating mutations in RBM12 are associated with psychosis. Nature Genetics, 2017, 49, 1251-1254.	9.4	63
156	Nationwide Study on Hypertrophic Cardiomyopathy in Iceland. Circulation, 2014, 130, 1158-1167.	1.6	62
157	The inheritance of rheumatoid arthritis in Iceland. Arthritis and Rheumatism, 2001, 44, 2247-2254.	6.7	61
158	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
159	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	2.4	59
160	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	5.8	59
161	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	5.8	59
162	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	5.8	59

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163	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. European Heart Journal, 2018, 39, 3243-3249.	1.0	57
164	A common variant at 8q24.21 is associated with renal cell cancer. Nature Communications, 2013, 4, 2776.	5.8	56
165	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. European Heart Journal, 2018, 39, 2172-2178.	1.0	53
166	Rare mutations associating with serum creatinine and chronic kidney disease. Human Molecular Genetics, 2014, 23, 6935-6943.	1.4	52
167	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	5.8	52
168	Rare and Common Variants Conferring Risk of Tooth Agenesis. Journal of Dental Research, 2018, 97, 515-522.	2.5	52
169	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. Nature Communications, 2016, 7, 12342.	5.8	50
170	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. Human Molecular Genetics, 2014, 23, 3045-3053.	1.4	48
171	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	5.8	48
172	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. BMC Medical Genetics, 2017, 18, 129.	2.1	47
173	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	5.8	44
174	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	2.0	42
175	Distinction between the effects of parental and fetal genomes on fetal growth. Nature Genetics, 2021, 53, 1135-1142.	9.4	41
176	Composition of the founding population of Iceland: Biological distance and morphological variation in early historic Atlantic Europe. American Journal of Physical Anthropology, 2004, 124, 257-274.	2.1	37
177	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	5.8	32
178	Reproductive fitness and genetic risk of psychiatric disorders in the general population. Nature Communications, 2017, 8, 15833.	5.8	30
179	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. Communications Biology, 2020, 3, 189.	2.0	30
180	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30

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181	Association of BRCA2 K3326* With Small Cell Lung Cancer and Squamous Cell Cancer of the Skin. Journal of the National Cancer Institute, 2018, 110, 967-974.	3.0	29
182	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. JAMA Cardiology, 2020, 5, 13.	3.0	29
183	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. BMC Medical Genetics, 2017, 18, 103.	2.1	28
184	Sequence variants with large effects on cardiac electrophysiology and disease. Nature Communications, 2019, 10, 4803.	5.8	28
185	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
186	Evaluation of Association of HNF1B Variants with Diverse Cancers: Collaborative Analysis of Data from 19 Genome-Wide Association Studies. PLoS ONE, 2010, 5, e10858.	1.1	28
187	Variants inNKX2-5andFLNCCause Dilated Cardiomyopathy and Sudden Cardiac Death. Circulation Genomic and Precision Medicine, 2018, 11, e002151.	1.6	27
188	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
189	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Largeâ€Scale Proteomics Scan in Iceland. Arthritis and Rheumatology, 2021, 73, 2025-2034.	2.9	27
190	Genome-Wide Significant Association Between a Sequence Variant at 15q15.2 and Lung Cancer Risk. Cancer Research, 2011, 71, 1356-1361.	0.4	26
191	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. Molecular Psychiatry, 2016, 21, 594-600.	4.1	26
192	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.5	26
193	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005379.	1.5	24
194	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at CCND2 Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. Diabetes, 2015, 64, 2279-2285.	0.3	24
195	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. Nature Communications, 2019, 10, 1284.	5.8	24
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