Daniel F Gudbjartsson

List of Publications by Citations

246 papers	44,265 citations	96 h-index	210 g-index
269 ext. papers	52,521 ext. citations	22.3 avg, IF	6.1 L-index

#	Paper	IF	Citations
246	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
245	Large recurrent microdeletions associated with schizophrenia. *Nature*, **2008**, 455, 232-6	50.4	1427
244	Rate of de novo mutations and the importance of father's age to disease risk. *Nature*, **2012**, 488, 471-5	50.4	1417
243	A high-resolution recombination map of the human genome. *Nature Genetics*, **2002**, 31, 241-7	36.3	1381
242	Neuregulin 1 and susceptibility to schizophrenia. *American Journal of Human Genetics*, **2002**, 71, 877-92	11	1371
241	A common variant on chromosome 9p21 affects the risk of myocardial infarction. *Science*, **2007**, 316, 1491-3	33.3	1322
240	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. *Nature*, **2008**, 452, 638-642	50.4	1239
239	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. *Nature*, **2012**, 488, 96-9	50.4	1194
238	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. *Nature Genetics*, **2009**, 41, 18-24	36.3	1085
237	Genetics of gene expression and its effect on disease. *Nature*, **2008**, 452, 423-8	50.4	1058
236	Spread of SARS-CoV-2 in the Icelandic Population. *New England Journal of Medicine*, **2020**, 382, 2302-2315	59.2	842
235	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. *Nature Genetics*, **2007**, 39, 631-7	36.3	739
234	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2007**, 39, 865-9	36.3	715
233	Variants conferring risk of atrial fibrillation on chromosome 4q25. *Nature*, **2007**, 448, 353-7	50.4	702
232	Allegro, a new computer program for multipoint linkage analysis. *Nature Genetics*, **2000**, 25, 12-3	36.3	692
231	A common variant associated with prostate cancer in European and African populations. *Nature Genetics*, **2006**, 38, 652-8	36.3	661
230	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nature Genetics*, **2009**, 41, 342-7	36.3	627

229	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. *Nature Genetics*, **2007**, 39, 977-83	36.3	616
228	A common inversion under selection in Europeans. *Nature Genetics*, **2005**, 37, 129-37	36.3	599
227	Humoral Immune Response to SARS-CoV-2 in Iceland. *New England Journal of Medicine*, **2020**, 383, 1724-1734	59.2	593
226	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
225	Common sequence variants in the LOXL1 gene confer susceptibility to exfoliation glaucoma. *Science*, **2007**, 317, 1397-400	33.3	558
224	Genetic determinants of hair, eye and skin pigmentation in Europeans. *Nature Genetics*, **2007**, 39, 1443-52	36.3	545
223	Many sequence variants affecting diversity of adult human height. *Nature Genetics*, **2008**, 40, 609-15	36.3	522
222	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
221	Multiple genetic loci for bone mineral density and fractures. *New England Journal of Medicine*, **2008**, 358, 2355-65	59.2	511
220	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. *Nature Genetics*, **2009**, 41, 221-7	36.3	509
219	The gene encoding phosphodiesterase 4D confers risk of ischemic stroke. *Nature Genetics*, **2003**, 35, 131-8	36.3	496
218	A genetic risk factor for periodic limb movements in sleep. *New England Journal of Medicine*, **2007**, 357, 639-47	59.2	491
217	Large-scale whole-genome sequencing of the Icelandic population. *Nature Genetics*, **2015**, 47, 435-44	36.3	486
216	Parental origin of sequence variants associated with complex diseases. *Nature*, **2009**, 462, 868-74	50.4	459
215	Fine-scale recombination rate differences between sexes, populations and individuals. *Nature*, **2010**, 467, 1099-103	50.4	428
214	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
213	The nature of nurture: Effects of parental genotypes. *Science*, **2018**, 359, 424-428	33.3	409
212	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401

211	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. *Nature Genetics*, **2010**, 42, 1077-85	36.3	372
210	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. *Blood* , **2017**, 130, 742-752	2.2	365
209	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. *Nature Genetics*, **2009**, 41, 876-8	36.3	365
208	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
207	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2008**, 40, 1307-12	36.3	332
206	Detection of sharing by descent, long-range phasing and haplotype imputation. *Nature Genetics*, **2008**, 40, 1068-75	36.3	329
205	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. *Nature Genetics*, **2008**, 40, 281-3	36.3	327
204	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. *Nature Genetics*, **2009**, 41, 460-4	36.3	308
203	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. *Nature Genetics*, **2006**, 38, 68-74	36.3	304
202	Several common variants modulate heart rate, PR interval and QRS duration. *Nature Genetics*, **2010**, 42, 117-22	36.3	293
201	New sequence variants associated with bone mineral density. *Nature Genetics*, **2009**, 41, 15-7	36.3	287
200	Mutations in BRIP1 confer high risk of ovarian cancer. *Nature Genetics*, **2011**, 43, 1104-7	36.3	285
199	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. *Nature Genetics*, **2009**, 41, 1122-6	36.3	281
198	Two newly identified genetic determinants of pigmentation in Europeans. *Nature Genetics*, **2008**, 40, 835-7	36.3	281
197	New common variants affecting susceptibility to basal cell carcinoma. *Nature Genetics*, **2009**, 41, 909-14	36.3	275
196	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. *Nature Genetics*, **2008**, 40, 886-91	36.3	265
195	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. *Nature Neuroscience*, **2015**, 18, 953-5	25.5	264
194	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254

193	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
192	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nature Genetics*, **2012**, 44, 260-8	36.3	243
191	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. *Nature Genetics*, **2014**, 46, 294-8	36.3	241
190	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. *Nature Genetics*, **2011**, 43, 316-20	36.3	228
189	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. *Nature*, **2017**, 549, 519-522	50.4	223
188	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
187	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, 7119-24	11.5	218
186	A catalog of genetic loci associated with kidney function from analyses of a million individuals. *Nature Genetics*, **2019**, 51, 957-972	36.3	217
185	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. *Nature Genetics*, **2009**, 41, 926-30	36.3	213
184	Cancer as a complex phenotype: pattern of cancer distribution within and beyond the nuclear family. *PLoS Medicine*, **2004**, 1, e65	11.6	210
183	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. *Nature Genetics*, **2011**, 43, 1098-103	36.3	203
182	Inheritance of human longevity in Iceland. *European Journal of Human Genetics*, **2000**, 8, 743-9	5.3	200
181	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
180	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. *Nature*, **2013**, 497, 517-20	50.4	192
179	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. *Human Molecular Genetics*, **2014**, 23, 4420-32	5.6	188
178	Effects of a 5-lipoxygenase-activating protein inhibitor on biomarkers associated with risk of myocardial infarction: a randomized trial. *JAMA - Journal of the American Medical Association*, **2005**, 293, 2245-56	27.4	187
177	Allegro version 2. *Nature Genetics*, **2005**, 37, 1015-6	36.3	178
176	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. *Nature Genetics*, **2009**, 41, 734-8	36.3	169

175	Discovery of common variants associated with low TSH levels and thyroid cancer risk. *Nature Genetics*, **2012**, 44, 319-22	36.3	167
174	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. *Nature Genetics*, **2016**, 48, 634-9	36.3	162
173	Identification of a large set of rare complete human knockouts. *Nature Genetics*, **2015**, 47, 448-52	36.3	158
172	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. *Nature Genetics*, **2012**, 44, 1326-9	36.3	151
171	Subclinical intestinal inflammation: an inherited abnormality in Crohn‚ disease relatives?. *Gastroenterology*, **2003**, 124, 1728-37	13.3	151
170	Recombination rate and reproductive success in humans. *Nature Genetics*, **2004**, 36, 1203-6	36.3	148
169	Sequence variants in the RNF212 gene associate with genome-wide recombination rate. *Science*, **2008**, 319, 1398-401	33.3	147
168	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
167	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2010** , 42, 415-9	36.3	138
166	Association of variants at UMOD with chronic kidney disease and kidney stones-role of age and comorbid diseases. *PLoS Genetics*, **2010**, 6, e1001039	6	138
165	A susceptibility gene for psoriatic arthritis maps to chromosome 16q: evidence for imprinting. *American Journal of Human Genetics*, **2003**, 72, 125-31	11	137
164	Genetic correction of PSA values using sequence variants associated with PSA levels. *Science Translational Medicine*, **2010**, 2, 62ra92	17.5	125
163	Weighting sequence variants based on their annotation increases power of whole-genome association studies. *Nature Genetics*, **2016**, 48, 314-7	36.3	123
162	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
161	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, 722-9	15.1	118
160	Physical and neurobehavioral determinants of reproductive onset and success. *Nature Genetics*, **2016**, 48, 617-623	36.3	118
159	Identification of low-frequency variants associated with gout and serum uric acid levels. *Nature Genetics*, **2011**, 43, 1127-30	36.3	117
158	Graphtyper enables population-scale genotyping using pangenome graphs. *Nature Genetics*, **2017**, 49, 1654-1660	36.3	115

157	A sequence variant on 17q21 is associated with age at onset and severity of asthma. *European Journal of Human Genetics*, **2010**, 18, 902-8	5.3	114
156	An association between the kinship and fertility of human couples. *Science*, **2008**, 319, 813-6	33.3	111
155	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. *Human Molecular Genetics*, **2011**, 20, 4268-81	5.6	105
154	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. *Nature Genetics*, **2013**, 45, 1371-4	36.3	104
153	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. *Nature Communications*, **2016**, 7, 12050	17.4	101
152	Loss-of-function variants in ATM confer risk of gastric cancer. *Nature Genetics*, **2015**, 47, 906-10	36.3	100
151	Characterizing mutagenic effects of recombination through a sequence-level genetic map. *Science*, **2019**, 363,	33.3	97
150	Common and rare variants associated with kidney stones and biochemical traits. *Nature Communications*, **2015**, 6, 7975	17.4	95
149	Sequence variants at CYP1A1-CYP1A2 and AHR associate with coffee consumption. *Human Molecular Genetics*, **2011**, 20, 2071-7	5.6	95
148	Variant ASGR1 Associated with a Reduced Risk of Coronary Artery Disease. *New England Journal of Medicine*, **2016**, 374, 2131-41	59.2	94
147	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. *Nature Genetics*, **2008**, 40, 1313-8	36.3	93
146	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. *Nature Genetics*, **2016**, 48, 318-22	36.3	92
145	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
144	Familial risk of lung carcinoma in the Icelandic population. *JAMA - Journal of the American Medical Association*, **2004**, 292, 2977-83	27.4	87
143	Common and low-frequency variants associated with genome-wide recombination rate. *Nature Genetics*, **2014**, 46, 11-6	36.3	86
142	Brain age prediction using deep learning uncovers associated sequence variants. *Nature Communications*, **2019**, 10, 5409	17.4	86
141	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	11.5	84
140	Relatedness disequilibrium regression estimates heritability without environmental bias. *Nature Genetics*, **2018**, 50, 1304-1310	36.3	84

139	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
138	A genome-wide association study yields five novel thyroid cancer risk loci. *Nature Communications*, **2017**, 8, 14517	17.4	80
137	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. *PLoS Genetics*, **2017**, 13, e1006659	6	79
136	Multi-nucleotide de novo Mutations in Humans. *PLoS Genetics*, **2016**, 12, e1006315	6	77
135	Genome-wide meta-analysis for serum calcium identifies significantly associated SNPs near the calcium-sensing receptor (CASR) gene. *PLoS Genetics*, **2010**, 6, e1001035	6	74
134	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. *PLoS Genetics*, **2013**, 9, e1003530	6	72
133	Ancestry-shift refinement mapping of the C6orf97-ESR1 breast cancer susceptibility locus. *PLoS Genetics*, **2010**, 6, e1001029	6	72
132	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
131	European bone mineral density loci are also associated with BMD in East-Asian populations. *PLoS ONE*, **2010**, 5, e13217	3.7	67
130	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	36.3	67
129	Whole genome characterization of sequence diversity of 15,220 Icelanders. *Scientific Data*, **2017**, 4, 170184	8.5	64
128	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. *Journal of the American College of Cardiology*, **2019**, 74, 2982-2994	15.1	61
127	Genome-wide association study implicates CHRNA2 in cannabis use disorder. *Nature Neuroscience*, **2019**, 22, 1066-1074	25.5	60
126	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. *Addiction Biology*, **2018**, 23, 485-492	4.6	58
125	Identification of sequence variants influencing immunoglobulin levels. *Nature Genetics*, **2017**, 49, 1182-1191	36.3	57
124	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. *Nature Communications*, **2018**, 9, 3707	17.4	57
123	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. *Nature Genetics*, **2017**, 49, 801-805	36.3	56
122	Genome-wide analysis yields new loci associating with aortic valve stenosis. *Nature Communications* , **2018**, 9, 987	17.4	56

121	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. *Nature Genetics*, **2018**, 50, 1542-1552	36.3	56
120	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. *Nature Communications*, **2015**, 6, 7213	17.4	54
119	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. *Nature Communications*, **2018**, 9, 4447	17.4	54
118	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. *Translational Psychiatry*, **2017**, 7, e1109	8.6	52
117	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	15.1	52
116	The inheritance of rheumatoid arthritis in Iceland. *Arthritis and Rheumatism*, **2001**, 44, 2247-54		52
115	Sequence variants from whole genome sequencing a large group of Icelanders. *Scientific Data*, **2015**, 2, 150011	8.2	51
114	Multiple transmissions of de novo mutations in families. *Nature Genetics*, **2018**, 50, 1674-1680	36.3	50
113	New basal cell carcinoma susceptibility loci. *Nature Communications*, **2015**, 6, 6825	17.4	49
112	A common variant at 8q24.21 is associated with renal cell cancer. *Nature Communications*, **2013**, 4, 2776	17.4	48
111	A frameshift deletion in the sarcomere gene MYL4 causes early-onset familial atrial fibrillation. *European Heart Journal*, **2017**, 38, 27-34	9.5	47
110	Truncating mutations in RBM12 are associated with psychosis. *Nature Genetics*, **2017**, 49, 1251-1254	36.3	45
109	Nationwide study on hypertrophic cardiomyopathy in Iceland: evidence of a MYBPC3 founder mutation. *Circulation*, **2014**, 130, 1158-67	16.7	44
108	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	36.3	44
107	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. *Nature Genetics*, **2019**, 51, 267-276	36.3	44
106	A Missense Variant in PLEC Increases Risk of Atrial Fibrillation. *Journal of the American College of Cardiology*, **2017**, 70, 2157-2168	15.1	43
105	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
104	A large-scale genome-wide association study meta-analysis of cannabis use disorder. *Lancet Psychiatry,the*, **2020**, 7, 1032-1045	23.3	43

103	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. *Nature Communications*, **2019**, 10, 5402	17.4	43
102	Diversity in non-repetitive human sequences not found in the reference genome. *Nature Genetics*, **2017**, 49, 588-593	36.3	42
101	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. *European Heart Journal*, **2018**, 39, 2172-2178	9.5	42
100	The rate of meiotic gene conversion varies by sex and age. *Nature Genetics*, **2016**, 48, 1377-1384	36.3	42
99	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. *Nature Communications*, **2016**, 7, 12342	17.4	41
98	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
97	Epigenetic and genetic components of height regulation. *Nature Communications*, **2016**, 7, 13490	17.4	39
96	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. *Nature Communications*, **2018**, 9, 2904	17.4	39
95	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. *Translational Psychiatry*, **2019**, 9, 258	8.6	39
94	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. *Human Molecular Genetics*, **2014**, 23, 3045-53	5.6	39
93	Rare mutations associating with serum creatinine and chronic kidney disease. *Human Molecular Genetics*, **2014**, 23, 6935-43	5.6	39
92	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. *Nature Communications*, **2017**, 8, 15789	17.4	37
91	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. *Nature Communications*, **2019**, 10, 2054	17.4	36
90	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. *BMC Medical Genetics*, **2017**, 18, 129	2.1	36
89	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. *Nature*, **2020**, 582, 78-83	50.4	33
88	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. *Nature Communications*, **2018**, 9, 3636	17.4	31
87	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. *Nature Communications*, **2020**, 11, 5976	17.4	30
86	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. *Nature Communications*, **2020**, 11, 393	17.4	29

85	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. *European Heart Journal*, **2018**, 39, 3243-3249	9.5	29
84	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. *Nature Communications*, **2018**, 9, 5101	17.4	29
83	Composition of the founding population of Iceland: biological distance and morphological variation in early historic Atlantic Europe. *American Journal of Physical Anthropology*, **2004**, 124, 257-74	2.5	26
82	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. *European Heart Journal*, **2020**, 41, 2618-2628	9.5	26
81	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
80	Evaluation of association of HNF1B variants with diverse cancers: collaborative analysis of data from 19 genome-wide association studies. *PLoS ONE*, **2010**, 5, e10858	3.7	24
79	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. *Nature Communications*, **2018**, 9, 4568	17.4	24
78	Differences between germline genomes of monozygotic twins. *Nature Genetics*, **2021**, 53, 27-34	36.3	24
77	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. *Nature*, **2020**, 584, 619-623	50.4	23
76	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
75	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. *Nature Communications*, **2017**, 8, 14265	17.4	22
74	Long read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits		22
73	Coding variants in and increase risk of atrial fibrillation. *Communications Biology*, **2018**, 1, 68	6.7	21
72	Addictions and their familiality in Iceland. *Annals of the New York Academy of Sciences*, **2010**, 1187, 208-17	6.5	21
71	Genome-wide significant association between a sequence variant at 15q15.2 and lung cancer risk. *Cancer Research*, **2011**, 71, 1356-61	10.1	21
70	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, 2279-85	0.9	20
69	Reproductive fitness and genetic risk of psychiatric disorders in the general population. *Nature Communications*, **2017**, 8, 15833	17.4	19
68	Rare and Common Variants Conferring Risk of Tooth Agenesis. *Journal of Dental Research*, **2018**, 97, 515-522	5.2	19

67	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. *Molecular Psychiatry*, **2016**, 21, 594-600	15.1	19
66	Variants in NKX2-5 and FLNC Cause Dilated Cardiomyopathy and Sudden Cardiac Death. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002151	5.2	19
65	Insertion of an SVA-E retrotransposon into the CASP8 gene is associated with protection against prostate cancer. *Human Molecular Genetics*, **2016**, 25, 1008-18	5.6	18
64	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. *PLoS Genetics*, **2015**, 11, e1005379	6	17
63	Large-scale integration of the plasma proteome with genetics and disease. *Nature Genetics*, **2021**, 53, 1712-1721	36.3	17
62	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
61	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	9.7	16
60	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. *BMC Medical Genetics*, **2017**, 18, 103	2.1	15
59	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. *JAMA Cardiology*, **2020**, 5, 13-20	16.2	15
58	MAP1B mutations cause intellectual disability and extensive white matter deficit. *Nature Communications*, **2018**, 9, 3456	17.4	15
57	Common sequence variants associated with coronary artery disease correlate with the extent of coronary atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1526-31	9.4	14
56	Age and Influenza-Specific Pre-Vaccination Antibodies Strongly Affect Influenza Vaccine Responses in the Icelandic Population whereas Disease and Medication Have Small Effects. *Frontiers in Immunology*, **2017**, 8, 1872	8.4	14
55	GPC5 rs2352028 variant and risk of lung cancer in never smokers. *Lancet Oncology, The*, **2010**, 11, 714-6; author reply 716	21.7	14
54	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. *Nature Communications*, **2019**, 10, 1284	17.4	13
53	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. *Nature Genetics*, **2017**, 49, 1398-1402	36.3	13
52	Sequence variants associating with urinary biomarkers. *Human Molecular Genetics*, **2019**, 28, 1199-1211	5.6	13
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