

Daniel F Gudbjartsson

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Response by Björnsson et al to Letter Regarding Article, "Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland".. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2022 , 42, e46-e47	9.4	
245	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. <i>Nature Communications</i> , 2022 , 13, 634	17.4	3
244	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene.. <i>Nature Communications</i> , 2022 , 13, 705	17.4	0
243	Reconstruction of a large-scale outbreak of SARS-CoV-2 infection in Iceland informs vaccination strategies.. <i>Clinical Microbiology and Infection</i> , 2022 ,	9.5	2
242	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome.. <i>Nature Communications</i> , 2022 , 13, 1598	17.4	1
241	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
240	The power of genetic diversity in genome-wide association studies of lipids. <i>Nature</i> , 2021 ,	50.4	24
239	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021 , 53, 1712-1721	36.3	17
238	Comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". <i>Science Translational Medicine</i> , 2021 , 13, eabe8497	17.5	1
237	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. <i>Communications Biology</i> , 2021 , 4, 1148	6.7	3
236	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. <i>European Journal of Human Genetics</i> , 2021 , 29, 1061-1070	5.3	1
235	Long-read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits. <i>Nature Genetics</i> , 2021 , 53, 779-786	36.3	44
234	Eleven genomic loci affect plasma levels of chronic inflammation marker soluble urokinase-type plasminogen activator receptor. <i>Communications Biology</i> , 2021 , 4, 655	6.7	3
233	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. <i>Communications Biology</i> , 2021 , 4, 706	6.7	4
232	Predicting the probability of death using proteomics. <i>Communications Biology</i> , 2021 , 4, 758	6.7	2
231	Molecular benchmarks of a SARS-CoV-2 epidemic. <i>Nature Communications</i> , 2021 , 12, 3633	17.4	0
230	Distinction between the effects of parental and fetal genomes on fetal growth. <i>Nature Genetics</i> , 2021 , 53, 1135-1142	36.3	5

229	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in. <i>Circulation Genomic and Precision Medicine</i> , 2021 , 14, e003029	5.2	5
228	Loss-of-Function Variants in the Tumor-Suppressor Gene Confer Increased Cancer Risk. <i>Cancer Research</i> , 2021 , 81, 1954-1964	10.1	2
227	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. <i>Communications Biology</i> , 2021 , 4, 156	6.7	11
226	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021 , 42, 1959-1971	9.5	7
225	Genetic variants associated with platelet count are predictive of human disease and physiological markers. <i>Communications Biology</i> , 2021 , 4, 1132	6.7	0
224	The genomics of heart failure: design and rationale of the HERMES consortium. <i>ESC Heart Failure</i> , 2021 ,	3.7	1
223	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Large-Scale Proteomics Scan in Iceland. <i>Arthritis and Rheumatology</i> , 2021 , 73, 2025-2034	9.5	6
222	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. <i>Intelligence</i> , 2021 , 88, 101565	3	0
221	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021 , 41, 2616-2628	9.4	4
220	Differences between germline genomes of monozygotic twins. <i>Nature Genetics</i> , 2021 , 53, 27-34	36.3	24
219	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. <i>BMJ Open</i> , 2021 , 11, e049709	3	0
218	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. <i>Nature Communications</i> , 2020 , 11, 5976	17.4	30
217	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
216	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. <i>Nature</i> , 2020 , 584, 619-623	50.4	23
215	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. <i>Communications Biology</i> , 2020 , 3, 129	6.7	7
214	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. <i>Nature Communications</i> , 2020 , 11, 393	17.4	29
213	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. <i>Communications Biology</i> , 2020 , 3, 189	6.7	8
212	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. <i>Nature Communications</i> , 2020 , 11, 163	17.4	140

211	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. <i>JAMA Cardiology</i> , 2020 , 5, 13-20	16.2	15
210	A large-scale genome-wide association study meta-analysis of cannabis use disorder. <i>Lancet Psychiatry</i> , 2020 , 7, 1032-1045	23.3	43
209	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. <i>Current Biology</i> , 2020 , 30, 4643-4653.e3	6.3	10
208	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020 , 41, 2618-2628	9.5	26
207	MEPE loss-of-function variant associates with decreased bone mineral density and increased fracture risk. <i>Nature Communications</i> , 2020 , 11, 4093	17.4	4
206	Humoral Immune Response to SARS-CoV-2 in Iceland. <i>New England Journal of Medicine</i> , 2020 , 383, 1724-1734	59.34	593
205	Common and Rare Sequence Variants Influencing Tumor Biomarkers in Blood. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 225-235	4	3
204	The nature of Neanderthal introgression revealed by 27,566 Icelandic genomes. <i>Nature</i> , 2020 , 582, 78-83	30.4	33
203	Spread of SARS-CoV-2 in the Icelandic Population. <i>New England Journal of Medicine</i> , 2020 , 382, 2302-2315	59.2	842
202	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019 , 10, 4130	17.4	43
201	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122
200	Characterizing mutagenic effects of recombination through a sequence-level genetic map. <i>Science</i> , 2019 , 363,	33.3	97
199	Genome-wide association study implicates CHRNA2 in cannabis use disorder. <i>Nature Neuroscience</i> , 2019 , 22, 1066-1074	25.5	60
198	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019 , 51, 957-972	36.3	217
197	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. <i>Nature Communications</i> , 2019 , 10, 1777	17.4	3
196	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. <i>Nature Communications</i> , 2019 , 10, 2054	17.4	36
195	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. <i>Nature Communications</i> , 2019 , 10, 1284	17.4	13
194	Sequence variants with large effects on cardiac electrophysiology and disease. <i>Nature Communications</i> , 2019 , 10, 4803	17.4	12

193	Attention-deficit hyperactivity disorder shares copy number variant risk with schizophrenia and autism spectrum disorder. <i>Translational Psychiatry</i> , 2019 , 9, 258	8.6	39
192	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
191	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019 , 575, 652-657	50.4	83
190	Brain age prediction using deep learning uncovers associated sequence variants. <i>Nature Communications</i> , 2019 , 10, 5409	17.4	86
189	GraphTyper2 enables population-scale genotyping of structural variation using pangenome graphs. <i>Nature Communications</i> , 2019 , 10, 5402	17.4	43
188	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. <i>Journal of the American College of Cardiology</i> , 2019 , 74, 2982-2994	15.1	61
187	Association studies of up to 1.2 million individuals yield new insights into the genetic etiology of tobacco and alcohol use. <i>Nature Genetics</i> , 2019 , 51, 237-244	36.3	516
186	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. <i>Nature Genetics</i> , 2019 , 51, 267-276	36.3	44
185	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019 , 28, 1199-1211	5.6	13
184	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , 2018 , 9, 987	17.4	56
183	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. <i>European Heart Journal</i> , 2018 , 39, 2172-2178	9.5	42
182	A rare missense variant in associates with lower cholesterol levels. <i>Communications Biology</i> , 2018 , 1, 14	6.7	5
181	The nature of nurture: Effects of parental genotypes. <i>Science</i> , 2018 , 359, 424-428	33.3	409
180	Rare and Common Variants Conferring Risk of Tooth Agenesis. <i>Journal of Dental Research</i> , 2018 , 97, 5155-522	19	
179	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018 , 50, 42-53	36.3	246
178	Polygenic risk scores for schizophrenia and bipolar disorder associate with addiction. <i>Addiction Biology</i> , 2018 , 23, 485-492	4.6	58
177	Genome-wide association study across European and African American ancestries identifies a SNP in DNMT3B contributing to nicotine dependence. <i>Molecular Psychiatry</i> , 2018 , 23, 1911-1919	15.1	52
176	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018 , 50, 1234-1239	36.3	254

175	PR interval genome-wide association meta-analysis identifies 50 loci associated with atrial and atrioventricular electrical activity. <i>Nature Communications</i> , 2018 , 9, 2904	17.4	39
174	Coding variants in and increase risk of atrial fibrillation. <i>Communications Biology</i> , 2018 , 1, 68	6.7	21
173	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. <i>European Heart Journal</i> , 2018 , 39, 3243-3249	9.5	29
172	Relatedness disequilibrium regression estimates heritability without environmental bias. <i>Nature Genetics</i> , 2018 , 50, 1304-1310	36.3	84
171	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. <i>Communications Biology</i> , 2018 , 1, 49	6.7	8
170	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018 , 9, 2252	17.4	71
169	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. <i>Nature Communications</i> , 2018 , 9, 4568	17.4	24
168	Multiple transmissions of de novo mutations in families. <i>Nature Genetics</i> , 2018 , 50, 1674-1680	36.3	50
167	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. <i>Nature Communications</i> , 2018 , 9, 5101	17.4	29
166	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. <i>Nature Communications</i> , 2018 , 9, 4447	17.4	54
165	Variants in NKX2-5 and FLNC Cause Dilated Cardiomyopathy and Sudden Cardiac Death. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e002151	5.2	19
164	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. <i>Nature Genetics</i> , 2018 , 50, 1681-1687	36.3	67
163	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. <i>Nature Genetics</i> , 2018 , 50, 1542-1552	36.3	56
162	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018 , 9, 3707	17.4	57
161	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. <i>Nature Communications</i> , 2018 , 9, 3636	17.4	31
160	MAP1B mutations cause intellectual disability and extensive white matter deficit. <i>Nature Communications</i> , 2018 , 9, 3456	17.4	15
159	Association of BRCA2 K3326* With Small Cell Lung Cancer and Squamous Cell Cancer of the Skin. <i>Journal of the National Cancer Institute</i> , 2018 , 110, 967-974	9.7	16
158	Selection against variants in the genome associated with educational attainment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, E727-E732	11.5	84

157	A genome-wide association study yields five novel thyroid cancer risk loci. <i>Nature Communications</i> , 2017 , 8, 14517	17.4	80
156	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. <i>Nature Communications</i> , 2017 , 8, 14265	17.4	22
155	Diversity in non-repetitive human sequences not found in the reference genome. <i>Nature Genetics</i> , 2017 , 49, 588-593	36.3	42
154	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. <i>Blood</i> , 2017 , 130, 742-752	2.2	365
153	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. <i>Translational Psychiatry</i> , 2017 , 7, e1109	8.6	52
152	Truncating mutations in RBM12 are associated with psychosis. <i>Nature Genetics</i> , 2017 , 49, 1251-1254	36.3	45
151	Identification of sequence variants influencing immunoglobulin levels. <i>Nature Genetics</i> , 2017 , 49, 1182-1193	36.3	57
150	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. <i>Nature Communications</i> , 2017 , 8, 15789	17.4	37
149	Reproductive fitness and genetic risk of psychiatric disorders in the general population. <i>Nature Communications</i> , 2017 , 8, 15833	17.4	19
148	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. <i>Human Molecular Genetics</i> , 2017 , 26, 2364-2376	5.6	11
147	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. <i>Nature Genetics</i> , 2017 , 49, 801-805	36.3	56
146	Whole genome characterization of sequence diversity of 15,220 Icelanders. <i>Scientific Data</i> , 2017 , 4, 17018-17019	17.4	64
145	GraphTyper enables population-scale genotyping using pangenome graphs. <i>Nature Genetics</i> , 2017 , 49, 1654-1660	36.3	115
144	A Missense Variant in PLEC Increases Risk of Atrial Fibrillation. <i>Journal of the American College of Cardiology</i> , 2017 , 70, 2157-2168	15.1	43
143	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. <i>BMC Medical Genetics</i> , 2017 , 18, 103	2.1	15
142	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. <i>BMC Medical Genetics</i> , 2017 , 18, 129	2.1	36
141	Age and Influenza-Specific Pre-Vaccination Antibodies Strongly Affect Influenza Vaccine Responses in the Icelandic Population whereas Disease and Medication Have Small Effects. <i>Frontiers in Immunology</i> , 2017 , 8, 1872	8.4	14
140	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. <i>Nature</i> , 2017 , 549, 519-522	50.4	223

139	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. <i>Npj Genomic Medicine</i> , 2017 , 2, 24	6.2	8
138	Sequence variant at 4q25 near PITX2 associates with appendicitis. <i>Scientific Reports</i> , 2017 , 7, 3119	4.9	10
137	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. <i>Nature Genetics</i> , 2017 , 49, 1398-1402	36.3	13
136	A frameshift deletion in the sarcomere gene MYL4 causes early-onset familial atrial fibrillation. <i>European Heart Journal</i> , 2017 , 38, 27-34	9.5	47
135	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. <i>PLoS Genetics</i> , 2017 , 13, e1006659	6	79
134	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. <i>Nature Communications</i> , 2016 , 7, 12342	17.4	41
133	The rate of meiotic gene conversion varies by sex and age. <i>Nature Genetics</i> , 2016 , 48, 1377-1384	36.3	42
132	Epigenetic and genetic components of height regulation. <i>Nature Communications</i> , 2016 , 7, 13490	17.4	39
131	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , 2016 , 7, 12050	17.4	101
130	Identification of genomic loci associated with resting heart rate and shared genetic predictors with all-cause mortality. <i>Nature Genetics</i> , 2016 , 48, 1557-1563	36.3	91
129	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. <i>Molecular Psychiatry</i> , 2016 , 21, 594-600	15.1	19
128	Insertion of an SVA-E retrotransposon into the CASP8 gene is associated with protection against prostate cancer. <i>Human Molecular Genetics</i> , 2016 , 25, 1008-18	5.6	18
127	Weighting sequence variants based on their annotation increases power of whole-genome association studies. <i>Nature Genetics</i> , 2016 , 48, 314-7	36.3	123
126	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. <i>Nature Genetics</i> , 2016 , 48, 318-22	36.3	92
125	Multi-nucleotide de novo Mutations in Humans. <i>PLoS Genetics</i> , 2016 , 12, e1006315	6	77
124	Variant ASGR1 Associated with a Reduced Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 2131-41	59.2	94
123	Physical and neurobehavioral determinants of reproductive onset and success. <i>Nature Genetics</i> , 2016 , 48, 617-623	36.3	118
122	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. <i>Nature Genetics</i> , 2016 , 48, 634-9	36.3	162

121	Common sequence variants associated with coronary artery disease correlate with the extent of coronary atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015 , 35, 1526-31	9.4	14
120	Loss-of-function variants in ATM confer risk of gastric cancer. <i>Nature Genetics</i> , 2015 , 47, 906-10	36.3	100
119	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. <i>Diabetes</i> , 2015 , 64, 2279-85	0.9	20
118	Identification of a large set of rare complete human knockouts. <i>Nature Genetics</i> , 2015 , 47, 448-52	36.3	158
117	Large-scale whole-genome sequencing of the Icelandic population. <i>Nature Genetics</i> , 2015 , 47, 435-44	36.3	486
116	Common and rare variants associated with kidney stones and biochemical traits. <i>Nature Communications</i> , 2015 , 6, 7975	17.4	95
115	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. <i>Nature Communications</i> , 2015 , 6, 7213	17.4	54
114	New basal cell carcinoma susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 6825	17.4	49
113	Predicting facial characteristics from complex polygenic variations. <i>Forensic Science International: Genetics</i> , 2015 , 19, 263-268	4.3	7
112	Sequence variants from whole genome sequencing a large group of Icelanders. <i>Scientific Data</i> , 2015 , 2, 150011	8.2	51
111	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. <i>PLoS Genetics</i> , 2015 , 11, e1005379	6	17
110	Polygenic risk scores for schizophrenia and bipolar disorder predict creativity. <i>Nature Neuroscience</i> , 2015 , 18, 953-5	25.5	264
109	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015 , 6, 7756	17.4	23
108	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. <i>Nature Genetics</i> , 2014 , 46, 294-8	36.3	241
107	Common and low-frequency variants associated with genome-wide recombination rate. <i>Nature Genetics</i> , 2014 , 46, 11-6	36.3	86
106	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
105	Genome-wide association meta-analysis of human longevity identifies a novel locus conferring survival beyond 90 years of age. <i>Human Molecular Genetics</i> , 2014 , 23, 4420-32	5.6	188
104	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014 , 46, 826-36	36.3	199

103	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014 , 46, 357-63	36.3	351
102	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. <i>Human Molecular Genetics</i> , 2014 , 23, 3045-53	5.6	39
101	Nationwide study on hypertrophic cardiomyopathy in Iceland: evidence of a MYBPC3 founder mutation. <i>Circulation</i> , 2014 , 130, 1158-67	16.7	44
100	Rare mutations associating with serum creatinine and chronic kidney disease. <i>Human Molecular Genetics</i> , 2014 , 23, 6935-43	5.6	39
99	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. <i>Nature</i> , 2013 , 497, 517-20	50.4	192
98	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. <i>Nature Genetics</i> , 2013 , 45, 621-31	36.3	219
97	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. <i>PLoS Genetics</i> , 2013 , 9, e1003530	6	72
96	A common variant at 8q24.21 is associated with renal cell cancer. <i>Nature Communications</i> , 2013 , 4, 2776	17.4	48
95	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. <i>Nature Genetics</i> , 2013 , 45, 1371-4	36.3	104
94	Apolipoprotein(a) genetic sequence variants associated with systemic atherosclerosis and coronary atherosclerotic burden but not with venous thromboembolism. <i>Journal of the American College of Cardiology</i> , 2012 , 60, 722-9	15.1	118
93	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. <i>Nature Genetics</i> , 2012 , 44, 1326-9	36.3	151
92	Rate of de novo mutations and the importance of father's age to disease risk. <i>Nature</i> , 2012 , 488, 471-5	50.4	1417
91	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012 , 44, 260-8	36.3	243
90	Discovery of common variants associated with low TSH levels and thyroid cancer risk. <i>Nature Genetics</i> , 2012 , 44, 319-22	36.3	167
89	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. <i>Nature</i> , 2012 , 488, 96-9	50.4	1194
88	Mutations in BRIP1 confer high risk of ovarian cancer. <i>Nature Genetics</i> , 2011 , 43, 1104-7	36.3	285
87	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. <i>Nature Genetics</i> , 2011 , 43, 1098-103	36.3	203
86	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011 , 43, 1131-8	36.3	415

85	Identification of low-frequency variants associated with gout and serum uric acid levels. <i>Nature Genetics</i> , 2011 , 43, 1127-30	36.3	117
84	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. <i>Nature Genetics</i> , 2011 , 43, 316-20	36.3	228
83	Sequence variants at CYP1A1-CYP1A2 and AHR associate with coffee consumption. <i>Human Molecular Genetics</i> , 2011 , 20, 2071-7	5.6	95
82	Genome-wide significant association between a sequence variant at 15q15.2 and lung cancer risk. <i>Cancer Research</i> , 2011 , 71, 1356-61	10.1	21
81	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 7119-24	11.5	218
80	An algorithm for detecting high frequency copy number polymorphisms using SNP arrays. <i>Journal of Computational Biology</i> , 2011 , 18, 955-66	1.7	2
79	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. <i>Human Molecular Genetics</i> , 2011 , 20, 4268-81	5.6	105
78	Evaluating differences in linkage disequilibrium between populations. <i>Annals of Human Genetics</i> , 2010 , 74, 233-47	2.2	2
77	A sequence variant on 17q21 is associated with age at onset and severity of asthma. <i>European Journal of Human Genetics</i> , 2010 , 18, 902-8	5.3	114
76	Hundreds of variants clustered in genomic loci and biological pathways affect human height. <i>Nature</i> , 2010 , 467, 832-8	50.4	1514
75	Fine-scale recombination rate differences between sexes, populations and individuals. <i>Nature</i> , 2010 , 467, 1099-103	50.4	428
74	Several common variants modulate heart rate, PR interval and QRS duration. <i>Nature Genetics</i> , 2010 , 42, 117-22	36.3	293
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7	Estimating heritability without environmental bias		3
6	The nature of nurture: effects of parental genotypes		6
5	Recurrence of de novo mutations in families		2
4	Mutations in RPL3L and MYZAP increase risk of atrial fibrillation		1
3	Deep learning based brain age prediction uncovers associated sequence variants		2
2	CCR5-del32 is not deleterious in the homozygous state in humans		2
1	Long read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits		22