

Patrick Sulem

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.

167
papers

24,447
citations

70
h-index

156
g-index

180
ext. papers

29,355
ext. citations

21.5
avg, IF

5.55
L-index

#	Paper	IF	Citations
167	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	
166	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
165	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene.. <i>Nature Communications</i> , 2022 , 13, 705	17.4	0
164	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome.. <i>Nature Communications</i> , 2022 , 13, 1598	17.4	1
163	Germline variants in tumor suppressor FBXW7 lead to impaired ubiquitination and a neurodevelopmental syndrome.. <i>American Journal of Human Genetics</i> , 2022 , 109, 601-617	11	0
162	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. <i>Communications Biology</i> , 2022 , 5,	6.7	1
161	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021 , 53, 1712-1721	36.3	17
160	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
159	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. <i>Communications Biology</i> , 2021 , 4, 1148	6.7	3
158	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. <i>European Journal of Human Genetics</i> , 2021 , 29, 1061-1070	5.3	1
157	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
156	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. <i>Communications Biology</i> , 2021 , 4, 706	6.7	4
155	Predicting the probability of death using proteomics. <i>Communications Biology</i> , 2021 , 4, 758	6.7	2
154	Molecular benchmarks of a SARS-CoV-2 epidemic. <i>Nature Communications</i> , 2021 , 12, 3633	17.4	0
153	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
152	Loss-of-Function Variants in the Tumor-Suppressor Gene Confer Increased Cancer Risk. <i>Cancer Research</i> , 2021 , 81, 1954-1964	10.1	2
151	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. <i>Nature Communications</i> , 2021 , 12, 730	17.4	4

150	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
149	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021 , 42, 1959-1971	9.5	7
148	Sequence variants in malignant hyperthermia genes in Iceland: classification and actionable findings in a population database. <i>European Journal of Human Genetics</i> , 2021 , 29, 1819-1824	5.3	0
147	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
146	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
145	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
144	Differences between germline genomes of monozygotic twins. <i>Nature Genetics</i> , 2021 , 53, 27-34	36.3	24
143	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020 , 11, 2542	17.4	16
142	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. <i>Nature</i> , 2020 , 584, 619-623	50.4	23
141	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
140	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
139	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. <i>Communications Biology</i> , 2020 , 3, 189	6.7	8
138	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
137	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
136	Humoral Immune Response to SARS-CoV-2 in Iceland. <i>New England Journal of Medicine</i> , 2020 , 383, 1724-1734	57.34	593
135	Common and Rare Sequence Variants Influencing Tumor Biomarkers in Blood. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2020 , 29, 225-235	4	3
134	Spread of SARS-CoV-2 in the Icelandic Population. <i>New England Journal of Medicine</i> , 2020 , 382, 2302-2315	59.2	842
133	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019 , 51, 1459-1474	36.3	122

132	Characterizing mutagenic effects of recombination through a sequence-level genetic map. <i>Science</i> , 2019 , 363,	33.3	97
131	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
130	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
129	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
128	Sequence variants with large effects on cardiac electrophysiology and disease. <i>Nature Communications</i> , 2019 , 10, 4803	17.4	12
127	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019 , 10, 4957	17.4	40
126	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019 , 575, 652-657	50.4	83
125	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
124	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
123	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019 , 28, 1199-1211	5.6	13
122	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
121	A rare missense variant in associates with lower cholesterol levels. <i>Communications Biology</i> , 2018 , 1, 14	6.7	5
120	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018 , 50, 1234-1239	36.3	254
119	Coding variants in and increase risk of atrial fibrillation. <i>Communications Biology</i> , 2018 , 1, 68	6.7	21
118	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
117	Relatedness disequilibrium regression estimates heritability without environmental bias. <i>Nature Genetics</i> , 2018 , 50, 1304-1310	36.3	84
116	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. <i>Communications Biology</i> , 2018 , 1, 49	6.7	8
115	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

114	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
113	Multiple transmissions of de novo mutations in families. <i>Nature Genetics</i> , 2018 , 50, 1674-1680	36.3	50
112	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. <i>Nature Communications</i> , 2018 , 9, 5101	17.4	29
111	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. <i>Nature Communications</i> , 2018 , 9, 4447	17.4	54
110	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
109	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
108	Identification of Lynch syndrome risk variants in the Romanian population. <i>Journal of Cellular and Molecular Medicine</i> , 2018 , 22, 6068-6076	5.6	4
107	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
106	MAP1B mutations cause intellectual disability and extensive white matter deficit. <i>Nature Communications</i> , 2018 , 9, 3456	17.4	15
105	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
104	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
103	A genome-wide association study yields five novel thyroid cancer risk loci. <i>Nature Communications</i> , 2017 , 8, 14517	17.4	80
102	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. <i>Nature Communications</i> , 2017 , 8, 14265	17.4	22
101	Diversity in non-repetitive human sequences not found in the reference genome. <i>Nature Genetics</i> , 2017 , 49, 588-593	36.3	42
100	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017 , 49, 834-841	36.3	257
99	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. <i>Blood</i> , 2017 , 130, 742-752	2.2	365
98	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in MSH6 and PMS2. <i>Nature Communications</i> , 2017 , 8, 14755	17.4	56
97	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. <i>Translational Psychiatry</i> , 2017 , 7, e1109	8.6	52

96	Identification of sequence variants influencing immunoglobulin levels. <i>Nature Genetics</i> , 2017 , 49, 1182-1193	10.1	57
95	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. <i>Nature Communications</i> , 2017 , 8, 15789	17.4	37
94	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. <i>Nature Genetics</i> , 2017 , 49, 674-679	36.3	70
93	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
92	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
91	Whole genome characterization of sequence diversity of 15,220 Icelanders. <i>Scientific Data</i> , 2017 , 4, 17018.5	18.5	64
90	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
89	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. <i>BMC Medical Genetics</i> , 2017 , 18, 103	2.1	15
88	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
87	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. <i>Nature</i> , 2017 , 549, 519-522	50.4	223
86	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
85	Sequence variant at 4q25 near PITX2 associates with appendicitis. <i>Scientific Reports</i> , 2017 , 7, 3119	4.9	10
84	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
83	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
82	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. <i>PLoS Genetics</i> , 2017 , 13, e1006659	6	79
81	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. <i>Nature Communications</i> , 2016 , 7, 12342	17.4	41
80	The rate of meiotic gene conversion varies by sex and age. <i>Nature Genetics</i> , 2016 , 48, 1377-1384	36.3	42
79	Epigenetic and genetic components of height regulation. <i>Nature Communications</i> , 2016 , 7, 13490	17.4	39

78	A rare missense mutation in <i>CHRNA4</i> associates with smoking behavior and its consequences. <i>Molecular Psychiatry</i> , 2016 , 21, 594-600	15.1	19
77	Insertion of an SVA-E retrotransposon into the <i>CASP8</i> gene is associated with protection against prostate cancer. <i>Human Molecular Genetics</i> , 2016 , 25, 1008-18	5.6	18
76	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. <i>Nature Communications</i> , 2016 , 7, 10572	17.4	42
75	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
74	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. <i>Nature Genetics</i> , 2016 , 48, 318-22	36.3	92
73	Identification of a novel susceptibility locus at 13q34 and refinement of the 20p12.2 region as a multi-signal locus associated with bladder cancer risk in individuals of European ancestry. <i>Human Molecular Genetics</i> , 2016 , 25, 1203-14	5.6	20
72	Comprehensive population-wide detection of Lynch syndrome in Iceland.. <i>Journal of Clinical Oncology</i> , 2016 , 34, 1542-1542	2.2	2
71	Multi-nucleotide de novo Mutations in Humans. <i>PLoS Genetics</i> , 2016 , 12, e1006315	6	77
70	A sequence variant associating with educational attainment also affects childhood cognition. <i>Scientific Reports</i> , 2016 , 6, 36189	4.9	
69	Variant <i>ASGR1</i> Associated with a Reduced Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016 , 374, 2131-41	59.2	94
68	Physical and neurobehavioral determinants of reproductive onset and success. <i>Nature Genetics</i> , 2016 , 48, 617-623	36.3	118
67	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
66	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016 , 76, 5103-14	10.1	66
65	Loss-of-function variants in <i>ATM</i> confer risk of gastric cancer. <i>Nature Genetics</i> , 2015 , 47, 906-10	36.3	100
64	Loss-of-function variants in <i>ABCA7</i> confer risk of Alzheimer's disease. <i>Nature Genetics</i> , 2015 , 47, 445-7	36.3	222
63	Identification of a large set of rare complete human knockouts. <i>Nature Genetics</i> , 2015 , 47, 448-52	36.3	158
62	Large-scale whole-genome sequencing of the Icelandic population. <i>Nature Genetics</i> , 2015 , 47, 435-44	36.3	486
61	Common and rare variants associated with kidney stones and biochemical traits. <i>Nature Communications</i> , 2015 , 6, 7975	17.4	95

60	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015 , 6, 8464	17.4	203
59	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. <i>Nature Communications</i> , 2015 , 6, 7213	17.4	54
58	New basal cell carcinoma susceptibility loci. <i>Nature Communications</i> , 2015 , 6, 6825	17.4	49
57	Sequence variants from whole genome sequencing a large group of Icelanders. <i>Scientific Data</i> , 2015 , 2, 150011	8.2	51
56	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
55	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015 , 6, 7756	17.4	23
54	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
53	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014 , 514, 92-97	50.4	401
52	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014 , 46, 736-41	36.3	228
51	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014 , 46, 357-63	36.3	351
50	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. <i>Leukemia</i> , 2014 , 28, 1371-4	10.7	72
49	Rare mutations associating with serum creatinine and chronic kidney disease. <i>Human Molecular Genetics</i> , 2014 , 23, 6935-43	5.6	39
48	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
47	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. <i>PLoS Genetics</i> , 2013 , 9, e1003530	6	72
46	A common variant at 8q24.21 is associated with renal cell cancer. <i>Nature Communications</i> , 2013 , 4, 2776	17.4	48
45	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
44	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
43	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012 , 492, 369-75	50.4	257

42	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
41	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
40	Discovery of common variants associated with low TSH levels and thyroid cancer risk. <i>Nature Genetics</i> , 2012 , 44, 319-22	36.3	167
39	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. <i>Nature</i> , 2012 , 488, 96-9	50.4	1194
38	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012 , 17, 1116-29	15.1	93
37	Mutations in BRIP1 confer high risk of ovarian cancer. <i>Nature Genetics</i> , 2011 , 43, 1104-7	36.3	285
36	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. <i>Nature Genetics</i> , 2011 , 43, 1098-103	36.3	203
35	Identification of low-frequency variants associated with gout and serum uric acid levels. <i>Nature Genetics</i> , 2011 , 43, 1127-30	36.3	117
34	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
33	Sequence variants at CYP1A1-CYP1A2 and AHR associate with coffee consumption. <i>Human Molecular Genetics</i> , 2011 , 20, 2071-7	5.6	95
32	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
31	Sequence variants at CHRN3-CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010 , 42, 448-53	36.3	582
30	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010 , 42, 1077-85	36.3	372
29	Genetic correction of PSA values using sequence variants associated with PSA levels. <i>Science Translational Medicine</i> , 2010 , 2, 62ra92	17.5	125
28	Ancestry-shift refinement mapping of the C6orf97-ESR1 breast cancer susceptibility locus. <i>PLoS Genetics</i> , 2010 , 6, e1001029	6	72
27	Parental origin of sequence variants associated with complex diseases. <i>Nature</i> , 2009 , 462, 868-74	50.4	459
26	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. <i>Nature Genetics</i> , 2009 , 41, 18-24	36.3	1085
25	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. <i>Nature Genetics</i> , 2009 , 41, 221-7	36.3	509

24	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. <i>Nature Genetics</i> , 2009 , 41, 342-7	36.3	627
23	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. <i>Nature Genetics</i> , 2009 , 41, 460-4	36.3	308
22	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. <i>Nature Genetics</i> , 2009 , 41, 734-8	36.3	169
21	A genome-wide association study of lung cancer identifies a region of chromosome 5p15 associated with risk for adenocarcinoma. <i>American Journal of Human Genetics</i> , 2009 , 85, 679-91	11	442
20	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. <i>Nature</i> , 2008 , 452, 638-642	50.4	1239
19	Many sequence variants affecting diversity of adult human height. <i>Nature Genetics</i> , 2008 , 40, 609-15	36.3	522
18	Two newly identified genetic determinants of pigmentation in Europeans. <i>Nature Genetics</i> , 2008 , 40, 835-7	36.3	281
17	Detection of sharing by descent, long-range phasing and haplotype imputation. <i>Nature Genetics</i> , 2008 , 40, 1068-75	36.3	329
16	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. <i>Nature Genetics</i> , 2008 , 40, 1307-12	36.3	332
15	Genetic determinants of hair, eye and skin pigmentation in Europeans. <i>Nature Genetics</i> , 2007 , 39, 1443-53	36.3	545
14	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. <i>Nature Genetics</i> , 2007 , 39, 977-83	36.3	616
13	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. <i>Nature Genetics</i> , 2007 , 39, 865-9	36.3	715
12	Variants conferring risk of atrial fibrillation on chromosome 4q25. <i>Nature</i> , 2007 , 448, 353-7	50.4	702
11	A common variant associated with prostate cancer in European and African populations. <i>Nature Genetics</i> , 2006 , 38, 652-8	36.3	661
10	Cancer as a complex phenotype: pattern of cancer distribution within and beyond the nuclear family. <i>PLoS Medicine</i> , 2004 , 1, e65	11.6	210
9	Cancer incidence among Icelandic deck officers in a population-based study. <i>Scandinavian Journal of Work, Environment and Health</i> , 2003 , 29, 100-5	4.3	8
8	The sequences of 150,119 genomes in the UK biobank		5
7	A rare missense mutation in MYH6 confers high risk of coarctation of the aorta		3

6	Estimating heritability without environmental bias	3
5	Recurrence of de novo mutations in families	2
4	Mutations in RPL3L and MYZAP increase risk of atrial fibrillation	1
3	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation	4
2	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers	5
1	Long read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits	22