Patrick Sulem

List of Publications by Citations

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	Rate of de novo mutations and the importance of father's age to disease risk. *Nature*, **2012**, 488, 471-5	50.4	1417
166	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. *Nature*, **2008**, 452, 638-642	50.4	1239
165	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. *Nature*, **2012**, 488, 96-9	50.4	1194
164	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
163	Spread of SARS-CoV-2 in the Icelandic Population. *New England Journal of Medicine*, **2020**, 382, 2302-2315	59.2	842
162	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2007**, 39, 865-9	36.3	715
161	Variants conferring risk of atrial fibrillation on chromosome 4q25. *Nature*, **2007**, 448, 353-7	50.4	702
160	A common variant associated with prostate cancer in European and African populations. *Nature Genetics*, **2006**, 38, 652-8	36.3	661
159	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nature Genetics*, **2009**, 41, 342-7	36.3	627
158	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
157	Humoral Immune Response to SARS-CoV-2 in Iceland. *New England Journal of Medicine*, **2020**, 383, 1724-1734	59.2	593
156	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
155	Genetic determinants of hair, eye and skin pigmentation in Europeans. *Nature Genetics*, **2007**, 39, 1443-52	36.3	545
154	Many sequence variants affecting diversity of adult human height. *Nature Genetics*, **2008**, 40, 609-15	36.3	522
153	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. *Nature Genetics*, **2009**, 41, 221-7	36.3	509
152	Large-scale whole-genome sequencing of the Icelandic population. *Nature Genetics*, **2015**, 47, 435-44	36.3	486
151	Parental origin of sequence variants associated with complex diseases. *Nature*, **2009**, 462, 868-74	50.4	459

150	A genome-wide association study of lung cancer identifies a region of chromosome 5p15 associated with risk for adenocarcinoma. *American Journal of Human Genetics*, **2009**, 85, 679-91	11	442
149	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
148	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
147	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. *Blood* , **2017**, 130, 742-752	2.2	365
146	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
145	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2008**, 40, 1307-12	36.3	332
144	Detection of sharing by descent, long-range phasing and haplotype imputation. *Nature Genetics*, **2008**, 40, 1068-75	36.3	329
143	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. *Nature Genetics*, **2009**, 41, 460-4	36.3	308
142	Mutations in BRIP1 confer high risk of ovarian cancer. *Nature Genetics*, **2011**, 43, 1104-7	36.3	285
141	Two newly identified genetic determinants of pigmentation in Europeans. *Nature Genetics*, **2008**, 40, 835-7	36.3	281
140	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. *Nature Genetics*, **2017**, 49, 834-841	36.3	257
139	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
138	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254
137	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
136	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
135	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. *Nature Genetics*, **2014**, 46, 736-41	36.3	228
134	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. *Nature Genetics*, **2011**, 43, 316-20	36.3	228
133	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. *Nature*, **2017**, 549, 519-522	50.4	223

132	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. *Nature Genetics*, **2015**, 47, 445-7	36.3	222
131	Cancer as a complex phenotype: pattern of cancer distribution within and beyond the nuclear family. *PLoS Medicine*, **2004**, 1, e65	11.6	210
130	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. *Nature Communications*, **2015**, 6, 8464	17.4	203
129	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. *Nature Genetics*, **2011**, 43, 1098-103	36.3	203
128	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. *Nature*, **2013**, 497, 517-20	50.4	192
127	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. *Nature Genetics*, **2009**, 41, 734-8	36.3	169
126	Discovery of common variants associated with low TSH levels and thyroid cancer risk. *Nature Genetics*, **2012**, 44, 319-22	36.3	167
125	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
124	Identification of a large set of rare complete human knockouts. *Nature Genetics*, **2015**, 47, 448-52	36.3	158
123	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
122	Genetic correction of PSA values using sequence variants associated with PSA levels. *Science Translational Medicine*, **2010**, 2, 62ra92	17.5	125
121	Weighting sequence variants based on their annotation increases power of whole-genome association studies. *Nature Genetics*, **2016**, 48, 314-7	36.3	123
120	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
119	Physical and neurobehavioral determinants of reproductive onset and success. *Nature Genetics*, **2016**, 48, 617-623	36.3	118
118	Identification of low-frequency variants associated with gout and serum uric acid levels. *Nature Genetics*, **2011**, 43, 1127-30	36.3	117
117	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
116	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
115	Loss-of-function variants in ATM confer risk of gastric cancer. *Nature Genetics*, **2015**, 47, 906-10	36.3	100

114	Characterizing mutagenic effects of recombination through a sequence-level genetic map. *Science*, **2019**, 363,	33.3	97
113	Common and rare variants associated with kidney stones and biochemical traits. *Nature Communications*, **2015**, 6, 7975	17.4	95
112	Sequence variants at CYP1A1-CYP1A2 and AHR associate with coffee consumption. *Human Molecular Genetics*, **2011**, 20, 2071-7	5.6	95
111	Variant ASGR1 Associated with a Reduced Risk of Coronary Artery Disease. *New England Journal of Medicine*, **2016**, 374, 2131-41	59.2	94
110	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. *Molecular Psychiatry*, **2012**, 17, 1116-29	15.1	93
109	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. *Nature Genetics*, **2016**, 48, 318-22	36.3	92
108	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
107	Relatedness disequilibrium regression estimates heritability without environmental bias. *Nature Genetics*, **2018**, 50, 1304-1310	36.3	84
106	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
105	A genome-wide association study yields five novel thyroid cancer risk loci. *Nature Communications*, **2017**, 8, 14517	17.4	80
104	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. *PLoS Genetics*, **2017**, 13, e1006659	6	79
103	Multi-nucleotide de novo Mutations in Humans. *PLoS Genetics*, **2016**, 12, e1006315	6	77
102	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. *Leukemia*, **2014**, 28, 1371-4	10.7	72
101	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. *PLoS Genetics*, **2013**, 9, e1003530	6	72
100	Ancestry-shift refinement mapping of the C6orf97-ESR1 breast cancer susceptibility locus. *PLoS Genetics*, **2010**, 6, e1001029	6	72
99	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. *Nature Communications*, **2018**, 9, 2252	17.4	71
98	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. *Nature Genetics*, **2017**, 49, 674-679	36.3	70
97	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

96	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. *Cancer Research*, **2016**, 76, 5103-14	10.1	66
95	Whole genome characterization of sequence diversity of 15,220 Icelanders. *Scientific Data*, **2017**, 4, 170184	8.2	64
94	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. *Journal of the American College of Cardiology*, **2019**, 74, 2982-2994	15.1	61
93	Identification of sequence variants influencing immunoglobulin levels. *Nature Genetics*, **2017**, 49, 1182-1191	36.3	57
92	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in MSH6 and PMS2. *Nature Communications*, **2017**, 8, 14755	17.4	56
91	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
90	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. *Nature Communications*, **2015**, 6, 7213	17.4	54
89	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. *Nature Communications*, **2018**, 9, 4447	17.4	54
88	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. *Translational Psychiatry*, **2017**, 7, e1109	8.6	52
87	Sequence variants from whole genome sequencing a large group of Icelanders. *Scientific Data*, **2015**, 2, 150011	8.2	51
86	Multiple transmissions of de novo mutations in families. *Nature Genetics*, **2018**, 50, 1674-1680	36.3	50
85	New basal cell carcinoma susceptibility loci. *Nature Communications*, **2015**, 6, 6825	17.4	49
84	A common variant at 8q24.21 is associated with renal cell cancer. *Nature Communications*, **2013**, 4, 2776	17.4	48
83	A frameshift deletion in the sarcomere gene MYL4 causes early-onset familial atrial fibrillation. *European Heart Journal*, **2017**, 38, 27-34	9.5	47
82	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
81	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. *Nature Genetics*, **2019**, 51, 267-276	36.3	44
80	A Missense Variant in PLEC Increases Risk of Atrial Fibrillation. *Journal of the American College of Cardiology*, **2017**, 70, 2157-2168	15.1	43
79	Diversity in non-repetitive human sequences not found in the reference genome. *Nature Genetics*, **2017**, 49, 588-593	36.3	42

78	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
77	The rate of meiotic gene conversion varies by sex and age. *Nature Genetics*, **2016**, 48, 1377-1384	36.3	42
76	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. *Nature Communications*, **2016**, 7, 10572	17.4	42
75	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. *Nature Communications*, **2016**, 7, 12342	17.4	41
74	Associations of autozygosity with a broad range of human phenotypes. *Nature Communications*, **2019**, 10, 4957	17.4	40
73	Epigenetic and genetic components of height regulation. *Nature Communications*, **2016**, 7, 13490	17.4	39
72	Rare mutations associating with serum creatinine and chronic kidney disease. *Human Molecular Genetics*, **2014**, 23, 6935-43	5.6	39
71	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. *Nature Communications*, **2017**, 8, 15789	17.4	37
70	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. *Nature Communications*, **2019**, 10, 2054	17.4	36
69	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. *BMC Medical Genetics*, **2017**, 18, 129	2.1	36
68	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. *Nature Communications*, **2018**, 9, 3636	17.4	31
67	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. *Nature Communications*, **2020**, 11, 393	17.4	29
66	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. *European Heart Journal*, **2018**, 39, 3243-3249	9.5	29
65	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. *Nature Communications*, **2018**, 9, 5101	17.4	29
64	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
63	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. *Nature Communications*, **2018**, 9, 4568	17.4	24
62	Differences between germline genomes of monozygotic twins. *Nature Genetics*, **2021**, 53, 27-34	36.3	24
61	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. *Nature*, **2020**, 584, 619-623	50.4	23

60	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
59	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. *Nature Communications*, **2017**, 8, 14265	17.4	22
58	Long read sequencing of 3,622 Icelanders provides insight into the role of structural variants in human diseases and other traits		22
57	Coding variants in and increase risk of atrial fibrillation. *Communications Biology*, **2018**, 1, 68	6.7	21
56	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. *Human Molecular Genetics*, **2016**, 25, 1203-14	5.6	20
55	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. *Molecular Psychiatry*, **2016**, 21, 594-600	15.1	19
54	Variants in NKX2-5 and FLNC Cause Dilated Cardiomyopathy and Sudden Cardiac Death. *Circulation Genomic and Precision Medicine*, **2018**, 11, e002151	5.2	19
53	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
52	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
51	Large-scale integration of the plasma proteome with genetics and disease. *Nature Genetics*, **2021**, 53, 1712-1721	36.3	17
50	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
49	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
48	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. *BMC Medical Genetics*, **2017**, 18, 103	2.1	15
47	MAP1B mutations cause intellectual disability and extensive white matter deficit. *Nature Communications*, **2018**, 9, 3456	17.4	15
46	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. *Nature Communications*, **2019**, 10, 1284	17.4	13
45	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
44	Sequence variants associating with urinary biomarkers. *Human Molecular Genetics*, **2019**, 28, 1199-1211	5.6	13
43	Sequence variants with large effects on cardiac electrophysiology and disease. *Nature Communications*, **2019**, 10, 4803	17.4	12

42	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. *Human Molecular Genetics*, **2017**, 26, 2364-2376	5.6	11
41	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. *Communications Biology*, **2021**, 4, 156	6.7	11
40	Sequence variant at 4q25 near PITX2 associates with appendicitis. *Scientific Reports*, **2017**, 7, 3119	4.9	10
39	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. *Current Biology*, **2020**, 30, 4643-4653.e3	6.3	10
38	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. *Communications Biology*, **2020**, 3, 189	6.7	8
37	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. *Communications Biology*, **2018**, 1, 49	6.7	8
36	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. *Npj Genomic Medicine*, **2017**, 2, 24	6.2	8
35	Cancer incidence among Icelandic deck officers in a population-based study. *Scandinavian Journal of Work, Environment and Health*, **2003**, 29, 100-5	4.3	8
34	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. *Communications Biology*, **2020**, 3, 129	6.7	7
33	Genetic insight into sick sinus syndrome. *European Heart Journal*, **2021**, 42, 1959-1971	9.5	7
32	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Large-Scale Proteomics Scan in Iceland. *Arthritis and Rheumatology*, **2021**, 73, 2025-2034	9.5	6
31	A rare missense variant in associates with lower cholesterol levels. *Communications Biology*, **2018**, 1, 14	6.7	5
30	The sequences of 150,119 genomes in the UK biobank		5
29	Genetic predisposition to mosaic Y chromosome loss in blood is associated with genomic instability in other tissues and susceptibility to non-haematological cancers		5
28	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003029	5.2	5
27	Genome-wide association study of 1 million people identifies 111 loci for atrial fibrillation		4
26	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. *Communications Biology*, **2021**, 4, 706	6.7	4
25	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. *Nature Communications*, **2021**, 12, 730	17.4	4

24	Identification of Lynch syndrome risk variants in the Romanian population. *Journal of Cellular and Molecular Medicine*, **2018**, 22, 6068-6076	5.6	4
23	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 2616-2628	9.4	4
22	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. *Nature Communications*, **2019**, 10, 1777	17.4	3
21	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. *Nature Communications*, **2022**, 13, 634	17.4	3
20	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. *Communications Biology*, **2021**, 4, 1148	6.7	3
19	A rare missense mutation inMYH6confers high risk of coarctation of the aorta		3
18	Estimating heritability without environmental bias		3
17	Common and Rare Sequence Variants Influencing Tumor Biomarkers in Blood. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 225-235	4	3
16	Comprehensive population-wide detection of Lynch syndrome in Iceland.. *Journal of Clinical Oncology*, **2016**, 34, 1542-1542	2.2	2
15	Recurrence of de novo mutations in families		2
14	Predicting the probability of death using proteomics. *Communications Biology*, **2021**, 4, 758	6.7	2
13	Loss-of-Function Variants in the Tumor-Suppressor Gene Confer Increased Cancer Risk. *Cancer Research*, **2021**, 81, 1954-1964	10.1	2
12	Comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". *Science Translational Medicine*, **2021**, 13, eabe8497	17.5	1
11	Mutations in RPL3L and MYZAP increase risk of atrial fibrillation		1
10	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. *European Journal of Human Genetics*, **2021**, 29, 1061-1070	5.3	1
9	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome.. *Nature Communications*, **2022**, 13, 1598	17.4	1
8	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. *Communications Biology*, **2022**, 5,	6.7	1
7	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene.. *Nature Communications*, **2022**, 13, 705	17.4	0

6	Molecular benchmarks of a SARS-CoV-2 epidemic. *Nature Communications*, **2021**, 12, 3633	17.4	0
5	Sequence variants in malignant hyperthermia genes in Iceland: classification and actionable findings in a population database. *European Journal of Human Genetics*, **2021**, 29, 1819-1824	5.3	0
4	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. *Intelligence*, **2021**, 88, 101565	3	0
3	Germline variants in tumor suppressor FBXW7 lead to impaired ubiquitination and a neurodevelopmental syndrome.. *American Journal of Human Genetics*, **2022**, 109, 601-617	11	0
2	Response by Bjï¿½nsson et al to Letter Regarding Article, "Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland".. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2022**, 42, e46-e47	9.4	
1	A sequence variant associating with educational attainment also affects childhood cognition. *Scientific Reports*, **2016**, 6, 36189	4.9	