Patrick Sulem

List of Publications by Year
in descending order

162 papers	32,686 citations	7096 78 h-index	5394 164 g-index
180 all docs	180 docs citations	180 times ranked	48212 citing authors

#	Article	IF	Citations
1	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
2	A mutation in APP protects against Alzheimerâ€™s disease and age-related cognitive decline. Nature, 2012, 488, 96-99.	27.8	1,442
3	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	27.8	1,399
4	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	21.4	1,247
5	Spread of SARS-CoV-2 in the Icelandic Population. New England Journal of Medicine, 2020, 382, 2302-2315.	27.0	1,093
6	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	27.8	853
7	Humoral Immune Response to SARS-CoV-2 in Iceland. New England Journal of Medicine, 2020, 383, 1724-1734.	27.0	845
8	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	21.4	774
9	A common variant associated with prostate cancer in European and African populations. Nature Genetics, 2006, 38, 652-658.	21.4	738
10	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	21.4	709
11	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	21.4	670
12	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	21.4	663
13	Genetic determinants of hair, eye and skin pigmentation in Europeans. Nature Genetics, 2007, 39, 1443-1452.	21.4	659
14	Sequence variants at CHRNB3â€“CHRNA6 and CYP2A6 affect smoking behavior. Nature Genetics, 2010, 42, 448-453.	21.4	649
15	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
16	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. Blood, 2017, 130, 742-752.	1.4	582
17	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. Nature Genetics, 2009, 41, 221-227.	21.4	572
18	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548

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19	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. Nature Genetics, 2018, 50, 1234-1239.	21.4	547
20	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
21	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, 679-691.	6.2	489
22	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. Nature Genetics, 2010, 42, 1077-1085.	21.4	445
23	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
24	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.	21.4	426
25	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. Nature, 2017, 549, 519-522.	27.8	410
26	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
27	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	21.4	377
28	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
29	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. Nature Genetics, 2009, 41, 460-464.	21.4	353
30	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	21.4	340
31	Mutations in BRIP1 confer high risk of ovarian cancer. Nature Genetics, 2011, 43, 1104-1107.	21.4	338
32	Two newly identified genetic determinants of pigmentation in Europeans. Nature Genetics, 2008, 40, 835-837.	21.4	331
33	Seventy-five genetic loci influencing the human red blood cell. Nature, 2012, 492, 369-375.	27.8	320
34	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. Nature Communications, 2015, 6, 8464.	12.8	304
35	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. Nature Genetics, 2012, 44, 260-268.	21.4	303
36	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	21.4	294

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37	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	21.4	283
38	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	21.4	275
39	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	12.6	252
40	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	21.4	251
41	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
42	Cancer as a Complex Phenotype: Pattern of Cancer Distribution within and beyond the Nuclear Family. PLoS Medicine, 2004, 1, e65.	8.4	245
43	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. Nature, 2013, 497, 517-520.	27.8	236
44	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	21.4	214
45	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	21.4	214
46	Discovery of common variants associated with low TSH levels and thyroid cancer risk. Nature Genetics, 2012, 44, 319-322.	21.4	208
47	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	21.4	199
48	Genetic predisposition to mosaic Y chromosome loss in blood. Nature, 2019, 575, 652-657.	27.8	198
49	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. Nature Genetics, 2012, 44, 1326-1329.	21.4	178
50	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	21.4	178
51	Physical and neurobehavioral determinants of reproductive onset and success. Nature Genetics, 2016, 48, 617-623.	21.4	158
52	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.	21.4	156
53	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	21.4	155
54	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.	7.1	149

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55	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	21.4	147
56	Genetic Correction of PSA Values Using Sequence Variants Associated with PSA Levels. Science Translational Medicine, 2010, 2, 62ra92.	12.4	140
57	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	27.0	137
58	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	21.4	134
59	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. Human Molecular Genetics, 2011, 20, 4268-4281.	2.9	134
60	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.	21.4	131
61	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	2.8	127
62	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. PLoS Genetics, 2017, 13, e1006659.	3.5	126
63	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. Nature Genetics, 2013, 45, 1371-1374.	21.4	125
64	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	21.4	123
65	Common and rare variants associated with kidney stones and biochemical traits. Nature Communications, 2015, 6, 7975.	12.8	117
66	A genome-wide association study yields five novel thyroid cancer risk loci. Nature Communications, 2017, 8, 14517.	12.8	117
67	Genetic variants associated with mosaic Y chromosome loss highlight cell cycle genes and overlap with cancer susceptibility. Nature Genetics, 2017, 49, 674-679.	21.4	117
68	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	2.9	114
69	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. Molecular Psychiatry, 2012, 17, 1116-1129.	7.9	112
70	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530.	3.5	112
71	Multi-nucleotide de novo Mutations in Humans. PLoS Genetics, 2016, 12, e1006315.	3.5	111
72	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. Nature Communications, 2015, 6, 7213.	12.8	101

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73	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. Cancer Research, 2016, 76, 5103-5114.	0.9	100
74	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	12.8	99
75	Whole genome characterization of sequence diversity of 15,220 Icelanders. Scientific Data, 2017, 4, 170115.	5.3	98
76	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in MSH6 and PMS2. Nature Communications, 2017, 8, 14755.	12.8	96
77	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	12.8	95
78	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	21.4	90
79	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	2.2	89
80	Multiple transmissions of de novo mutations in families. Nature Genetics, 2018, 50, 1674-1680.	21.4	89
81	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. Leukemia, 2014, 28, 1371-1374.	7.2	85
82	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	21.4	85
83	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
84	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. Nature Genetics, 2019, 51, 267-276.	21.4	83
85	Differences between germline genomes of monozygotic twins. Nature Genetics, 2021, 53, 27-34.	21.4	83
86	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. PLoS Genetics, 2010, 6, e1001029.	3.5	82
87	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. Nature, 2020, 584, 619-623.	27.8	81
88	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. Nature Genetics, 2017, 49, 801-805.	21.4	75
89	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	12.8	74
90	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	12.8	74

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91	A Missense Variant in PLEC Increases RiskÂof Atrial Fibrillation. Journal of the American College of Cardiology, 2017, 70, 2157-2168.	2.8	73
92	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. Nature Communications, 2018, 9, 5101.	12.8	73
93	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	4.4	72
94	Diversity in non-repetitive human sequences not found in the reference genome. Nature Genetics, 2017, 49, 588-593.	21.4	70
95	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. Translational Psychiatry, 2017, 7, e1109-e1109.	4.8	67
96	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. Nature Communications, 2017, 8, 15789.	12.8	67
97	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	2.2	61
98	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. Nature Communications, 2016, 7, 10572.	12.8	60
99	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	5.3	59
100	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	12.8	59
101	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59
102	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. Nature Communications, 2020, 11, 393.	12.8	59
103	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. European Heart Journal, 2018, 39, 3243-3249.	2.2	57
104	A common variant at 8q24.21 is associated with renal cell cancer. Nature Communications, 2013, 4, 2776.	12.8	56
105	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. European Heart Journal, 2018, 39, 2172-2178.	2.2	53
106	Rare mutations associating with serum creatinine and chronic kidney disease. Human Molecular Genetics, 2014, 23, 6935-6943.	2.9	52
107	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	12.8	52
108	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. Nature Communications, 2016, 7, 12342.	12.8	50

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109	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. Nature Communications, 2017, 8, 14265.	12.8	48
110	COPA syndrome in an Icelandic family caused by a recurrent missense mutation in COPA. BMC Medical Genetics, 2017, 18, 129.	2.1	47
111	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	12.8	44
112	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	4.4	42
113	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, 1203-1214.	2.9	38
114	Rare coding variants and X-linked loci associated with age at menarche. Nature Communications, 2015, 6, 7756.	12.8	32
115	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. Communications Biology, 2020, 3, 189.	4.4	30
116	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	4.4	30
117	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.	6.3	29
118	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. BMC Medical Genetics, 2017, 18, 103.	2.1	28
119	Sequence variants with large effects on cardiac electrophysiology and disease. Nature Communications, 2019, 10, 4803.	12.8	28
120	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	2.9	28
121	Variants inNKX2-5andFLNCCause Dilated Cardiomyopathy and Sudden Cardiac Death. Circulation Genomic and Precision Medicine, 2018, 11, e002151.	3.6	27
122	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	2.2	27
123	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Largeâ€Scale Proteomics Scan in Iceland. Arthritis and Rheumatology, 2021, 73, 2025-2034.	5.6	27
124	A rare missense mutation in CHRNA4 associates with smoking behavior and its consequences. Molecular Psychiatry, 2016, 21, 594-600.	7.9	26
125	Multiomics analysis of rheumatoid arthritis yields sequence variants that have large effects on risk of the seropositive subset. Annals of the Rheumatic Diseases, 2022, 81, 1085-1095.	0.9	26
126	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005379.	3.5	24

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127	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. Nature Communications, 2019, 10, 1284.	12.8	24
128	Insertion of an SVA-E retrotransposon into theCASP8gene is associated with protection against prostate cancer. Human Molecular Genetics, 2016, 25, 1008-1018.	2.9	22
129	MAP1B mutations cause intellectual disability and extensive white matter deficit. Nature Communications, 2018, 9, 3456.	12.8	21
130	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	12.8	21
131	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. Nature Genetics, 2017, 49, 1398-1402.	21.4	20
132	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	4.4	20
133	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. Current Biology, 2020, 30, 4643-4653.e3.	3.9	19
134	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.	2.9	17
135	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	4.4	17
136	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. Npj Genomic Medicine, 2017, 2, 24.	3.8	16
137	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2616-2628.	2.4	16
138	Germline variants in tumor suppressor FBXW7 lead to impaired ubiquitination and a neurodevelopmental syndrome. American Journal of Human Genetics, 2022, 109, 601-617.	6.2	16
139	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.9	15
140	Sequence variant at 4q25 near PITX2 associates with appendicitis. Scientific Reports, 2017, 7, 3119.	3.3	14
141	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in LDLR. Circulation Genomic and Precision Medicine, 2021, 14, e003029.	3.6	12
142	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. Communications Biology, 2021, 4, 1148.	4.4	12
143	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	4.4	10
144	Cancer incidence among Icelandic deck officers in a population-based study. Scandinavian Journal of Work, Environment and Health, 2003, 29, 100-105.	3.4	10

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145	A truncating mutation in EPOR leads to hypo-responsiveness to erythropoietin with normal haemoglobin. Communications Biology, 2018, 1, 49.	4.4	9
146	Common and rare sequence variants influencing tumor biomarkers in blood. Cancer Epidemiology Biomarkers and Prevention, 2019, 29, cebp.1060.2018.	2.5	9
147	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. Nature Communications, 2021, 12, 730.	12.8	9
148	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	12.8	8
149	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	12.8	7
150	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene. Nature Communications, 2022, 13, 705.	12.8	7
151	GWAS of Hematuria. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 672-683.	4.5	7
152	A rare missense variant in NR1H4 associates with lower cholesterol levels. Communications Biology, 2018, 1, 14.	4.4	6
153	Identification of Lynch syndrome risk variants in the Romanian population. Journal of Cellular and Molecular Medicine, 2018, 22, 6068-6076.	3.6	5
154	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. European Journal of Human Genetics, 2021, 29, 1061-1070.	2.8	5
155	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.	2.8	4
156	Comment on â€œEvaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human geneticsâ€: Science Translational Medicine, 2021, 13, eabe8497.	12.4	4
157	Molecular benchmarks of a SARS-CoV-2 epidemic. Nature Communications, 2021, 12, 3633.	12.8	3
158	Comprehensive population-wide detection of Lynch syndrome in Iceland.. Journal of Clinical Oncology, 2016, 34, 1542-1542.	1.6	3
159	A sequence variant associating with educational attainment also affects childhood cognition. Scientific Reports, 2016, 6, 36189.	3.3	2
160	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. Intelligence, 2021, 88, 101565.	3.0	2
161	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	4.4	1
162	Response by BjÃ¶rnsson et al to Letter Regarding Article, â€œLarge-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Icelandâ€: Arteriosclerosis, Thrombosis, and Vascular Biology, 2022, 42, e46-e47.	2.4	0