

# Patrick Sulem

## List of Publications by Year in descending order

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Version: 2024-02-01

162  
papers

32,686  
citations

7069

78  
h-index

5364

164  
g-index

180  
all docs

180  
docs citations

180  
times ranked

48212  
citing authors

#	ARTICLE	IF	CITATIONS
1	Response by Björnsdóttir 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.	1.1	0
2	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
3	Population-level deficit of homozygosity unveils CPSF3 as an intellectual disability syndrome gene. Nature Communications, 2022, 13, 705.	5.8	7
4	A genome-wide meta-analysis identifies 50 genetic loci associated with carpal tunnel syndrome. Nature Communications, 2022, 13, 1598.	5.8	8
5	Germline variants in tumor suppressor FBXW7 lead to impaired ubiquitination and a neurodevelopmental syndrome. American Journal of Human Genetics, 2022, 109, 601-617.	2.6	16
6	Multimomics 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.	0.5	26
7	GWAS of Hematuria. Clinical Journal of the American Society of Nephrology: CJASN, 2022, 17, 672-683.	2.2	7
8	Genetic architecture of band neutrophil fraction in Iceland. Communications Biology, 2022, 5, .	2.0	1
9	Differential and shared genetic effects on kidney function between diabetic and non-diabetic individuals. Communications Biology, 2022, 5, .	2.0	17
10	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in <i>LDLR</i> . Circulation Genomic and Precision Medicine, 2021, 14, e003029.	1.6	12
11	Loss-of-Function Variants in the Tumor-Suppressor Gene <i>PTPN14</i> Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
12	PopDel identifies medium-size deletions simultaneously in tens of thousands of genomes. Nature Communications, 2021, 12, 730.	5.8	9
13	A genome-wide meta-analysis yields 46 new loci associating with biomarkers of iron homeostasis. Communications Biology, 2021, 4, 156.	2.0	72
14	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	1.0	27
15	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. European Journal of Human Genetics, 2021, 29, 1061-1070.	1.4	5
16	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.	9.4	156
17	The genetic architecture of age-related hearing impairment revealed by genome-wide association analysis. Communications Biology, 2021, 4, 706.	2.0	30
18	Predicting the probability of death using proteomics. Communications Biology, 2021, 4, 758.	2.0	10

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19	Molecular benchmarks of a SARS-CoV-2 epidemic. <i>Nature Communications</i> , 2021, 12, 3633.	5.8	3
20	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.	1.4	4
21	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.	2.9	27
22	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. <i>Intelligence</i> , 2021, 88, 101565.	1.6	2
23	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2616-2628.	1.1	16
24	Differences between germline genomes of monozygotic twins. <i>Nature Genetics</i> , 2021, 53, 27-34.	9.4	83
25	A genome-wide meta-analysis uncovers six sequence variants conferring risk of vertigo. <i>Communications Biology</i> , 2021, 4, 1148.	2.0	12
26	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.	5.8	4
27	Large-scale integration of the plasma proteome with genetics and disease. <i>Nature Genetics</i> , 2021, 53, 1712-1721.	9.4	340
28	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. <i>Current Biology</i> , 2020, 30, 4643-4653.e3.	1.8	19
29	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020, 41, 2618-2628.	1.0	61
30	Humoral Immune Response to SARS-CoV-2 in Iceland. <i>New England Journal of Medicine</i> , 2020, 383, 1724-1734.	13.9	845
31	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	5.8	59
32	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. <i>Nature</i> , 2020, 584, 619-623.	13.7	81
33	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. <i>Communications Biology</i> , 2020, 3, 129.	2.0	20
34	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. <i>Nature Communications</i> , 2020, 11, 393.	5.8	59
35	Predicted loss and gain of function mutations in ACO1 are associated with erythropoiesis. <i>Communications Biology</i> , 2020, 3, 189.	2.0	30
36	Spread of SARS-CoV-2 in the Icelandic Population. <i>New England Journal of Medicine</i> , 2020, 382, 2302-2315.	13.9	1,093

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37	Sequence variants with large effects on cardiac electrophysiology and disease. <i>Nature Communications</i> , 2019, 10, 4803.	5.8	28
38	Associations of autozygosity with a broad range of human phenotypes. <i>Nature Communications</i> , 2019, 10, 4957.	5.8	84
39	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	9.4	251
40	Characterizing mutagenic effects of recombination through a sequence-level genetic map. <i>Science</i> , 2019, 363, .	6.0	252
41	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. <i>Nature Communications</i> , 2019, 10, 1777.	5.8	7
42	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. <i>Nature Communications</i> , 2019, 10, 2054.	5.8	74
43	Sequence variation at ANAPC1 accounts for 24% of the variability in corneal endothelial cell density. <i>Nature Communications</i> , 2019, 10, 1284.	5.8	24
44	Genetic predisposition to mosaic Y chromosome loss in blood. <i>Nature</i> , 2019, 575, 652-657.	13.7	198
45	Common and rare sequence variants influencing tumor biomarkers in blood. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 29, cebp.1060.2018.	1.1	9
46	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. <i>Journal of the American College of Cardiology</i> , 2019, 74, 2982-2994.	1.2	127
47	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. <i>Nature Genetics</i> , 2019, 51, 267-276.	9.4	83
48	Sequence variants associating with urinary biomarkers. <i>Human Molecular Genetics</i> , 2019, 28, 1199-1211.	1.4	28
49	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. <i>European Heart Journal</i> , 2018, 39, 2172-2178.	1.0	53
50	A rare missense variant in NR1H4 associates with lower cholesterol levels. <i>Communications Biology</i> , 2018, 1, 14.	2.0	6
51	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. <i>Nature Communications</i> , 2018, 9, 4568.	5.8	44
52	Multiple transmissions of de novo mutations in families. <i>Nature Genetics</i> , 2018, 50, 1674-1680.	9.4	89
53	Genome-wide association meta-analysis yields 20 loci associated with gallstone disease. <i>Nature Communications</i> , 2018, 9, 5101.	5.8	73
54	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. <i>Nature Communications</i> , 2018, 9, 4447.	5.8	95

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55	Variants in <i>NKX2-5</i> and <i>FLNC</i> Cause Dilated Cardiomyopathy and Sudden Cardiac Death. <i>Circulation Genomic and Precision Medicine</i> , 2018, 11, e002151.	1.6	27
56	Meta-analysis of Icelandic and UK data sets identifies missense variants in <i>SMO</i> , <i>IL11</i> , <i>COL11A1</i> and 13 more new loci associated with osteoarthritis. <i>Nature Genetics</i> , 2018, 50, 1681-1687.	9.4	131
57	Identification of Lynch syndrome risk variants in the Romanian population. <i>Journal of Cellular and Molecular Medicine</i> , 2018, 22, 6068-6076.	1.6	5
58	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. <i>Nature Communications</i> , 2018, 9, 3636.	5.8	74
59	<i>MAP1B</i> mutations cause intellectual disability and extensive white matter deficit. <i>Nature Communications</i> , 2018, 9, 3456.	5.8	21
60	Association of <i>BRCA2</i> 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.	3.0	29
61	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. <i>Nature Genetics</i> , 2018, 50, 1234-1239.	9.4	547
62	Coding variants in <i>RPL3L</i> and <i>MYZAP</i> increase risk of atrial fibrillation. <i>Communications Biology</i> , 2018, 1, 68.	2.0	42
63	A rare missense mutation in <i>MYH6</i> associates with non-syndromic coarctation of the aorta. <i>European Heart Journal</i> , 2018, 39, 3243-3249.	1.0	57
64	Relatedness disequilibrium regression estimates heritability without environmental bias. <i>Nature Genetics</i> , 2018, 50, 1304-1310.	9.4	147
65	A truncating mutation in <i>EPOR</i> leads to hypo-responsiveness to erythropoietin with normal haemoglobin. <i>Communications Biology</i> , 2018, 1, 49.	2.0	9
66	Genetic inactivation of <i>ANGPTL4</i> improves glucose homeostasis and is associated with reduced risk of diabetes. <i>Nature Communications</i> , 2018, 9, 2252.	5.8	99
67	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.	3.3	149
68	A genome-wide association study yields five novel thyroid cancer risk loci. <i>Nature Communications</i> , 2017, 8, 14517.	5.8	117
69	Sequence variant at 8q24.21 associates with sciatica caused by lumbar disc herniation. <i>Nature Communications</i> , 2017, 8, 14265.	5.8	48
70	Diversity in non-repetitive human sequences not found in the reference genome. <i>Nature Genetics</i> , 2017, 49, 588-593.	9.4	70
71	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.	9.4	426
72	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. <i>Blood</i> , 2017, 130, 742-752.	0.6	582

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73	Comprehensive population-wide analysis of Lynch syndrome in Iceland reveals founder mutations in MSH6 and PMS2. <i>Nature Communications</i> , 2017, 8, 14755.	5.8	96
74	15q11.2 CNV affects cognitive, structural and functional correlates of dyslexia and dyscalculia. <i>Translational Psychiatry</i> , 2017, 7, e1109-e1109.	2.4	67
75	Identification of sequence variants influencing immunoglobulin levels. <i>Nature Genetics</i> , 2017, 49, 1182-1191.	9.4	90
76	Sequence variants in ARHGAP15, COLQ and FAM155A associate with diverticular disease and diverticulitis. <i>Nature Communications</i> , 2017, 8, 15789.	5.8	67
77	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.	9.4	117
78	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.	1.4	17
79	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.	9.4	75
80	Whole genome characterization of sequence diversity of 15,220 Icelanders. <i>Scientific Data</i> , 2017, 4, 170115.	2.4	98
81	A Missense Variant in PLEC Increases Risk of Atrial Fibrillation. <i>Journal of the American College of Cardiology</i> , 2017, 70, 2157-2168.	1.2	73
82	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. <i>Nature</i> , 2017, 549, 519-522.	13.7	410
83	Fourteen sequence variants that associate with multiple sclerosis discovered by meta-analysis informed by genetic correlations. <i>Npj Genomic Medicine</i> , 2017, 2, 24.	1.7	16
84	Sequence variant at 4q25 near PITX2 associates with appendicitis. <i>Scientific Reports</i> , 2017, 7, 3119.	1.6	14
85	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.	9.4	20
86	A frameshift deletion in the sarcomere gene <i>MYL4</i> causes early-onset familial atrial fibrillation. <i>European Heart Journal</i> , 2017, 38, 27-34.	1.0	89
87	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. <i>BMC Medical Genetics</i> , 2017, 18, 103.	2.1	28
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	47
89	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. <i>PLoS Genetics</i> , 2017, 13, e1006659.	1.5	126
90	A sequence variant associating with educational attainment also affects childhood cognition. <i>Scientific Reports</i> , 2016, 6, 36189.	1.6	2

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91	Variant <i>ASGR1</i> Associated with a Reduced Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016, 374, 2131-2141.	13.9	137
92	Physical and neurobehavioral determinants of reproductive onset and success. <i>Nature Genetics</i> , 2016, 48, 617-623.	9.4	158
93	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. <i>Nature Genetics</i> , 2016, 48, 634-639.	9.4	214
94	Cross-Cancer Genome-Wide Analysis of Lung, Ovary, Breast, Prostate, and Colorectal Cancer Reveals Novel Pleiotropic Associations. <i>Cancer Research</i> , 2016, 76, 5103-5114.	0.4	100
95	A protein-truncating R179X variant in <i>RNF186</i> confers protection against ulcerative colitis. <i>Nature Communications</i> , 2016, 7, 12342.	5.8	50
96	The rate of meiotic gene conversion varies by sex and age. <i>Nature Genetics</i> , 2016, 48, 1377-1384.	9.4	85
97	Epigenetic and genetic components of height regulation. <i>Nature Communications</i> , 2016, 7, 13490.	5.8	52
98	A rare missense mutation in <i>CHRNA4</i> associates with smoking behavior and its consequences. <i>Molecular Psychiatry</i> , 2016, 21, 594-600.	4.1	26
99	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, 1008-1018.	1.4	22
100	Common and rare variants associating with serum levels of creatine kinase and lactate dehydrogenase. <i>Nature Communications</i> , 2016, 7, 10572.	5.8	60
101	Weighting sequence variants based on their annotation increases power of whole-genome association studies. <i>Nature Genetics</i> , 2016, 48, 314-317.	9.4	178
102	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. <i>Nature Genetics</i> , 2016, 48, 318-322.	9.4	123
103	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, 1203-1214.	1.4	38
104	Comprehensive population-wide detection of Lynch syndrome in Iceland. <i>Journal of Clinical Oncology</i> , 2016, 34, 1542-1542.	0.8	3
105	Multi-nucleotide de novo Mutations in Humans. <i>PLoS Genetics</i> , 2016, 12, e1006315.	1.5	111
106	Sequence variants from whole genome sequencing a large group of Icelanders. <i>Scientific Data</i> , 2015, 2, 150011.	2.4	59
107	A Splice Region Variant in <i>LDLR</i> Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005379.	1.5	24
108	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015, 6, 7756.	5.8	32

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109	Loss-of-function variants in ATM confer risk of gastric cancer. <i>Nature Genetics</i> , 2015, 47, 906-910.	9.4	155
110	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. <i>Nature Genetics</i> , 2015, 47, 445-447.	9.4	283
111	Identification of a large set of rare complete human knockouts. <i>Nature Genetics</i> , 2015, 47, 448-452.	9.4	214
112	Large-scale whole-genome sequencing of the Icelandic population. <i>Nature Genetics</i> , 2015, 47, 435-444.	9.4	663
113	Common and rare variants associated with kidney stones and biochemical traits. <i>Nature Communications</i> , 2015, 6, 7975.	5.8	117
114	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. <i>Nature Communications</i> , 2015, 6, 8464.	5.8	304
115	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. <i>Nature Communications</i> , 2015, 6, 7213.	5.8	101
116	New basal cell carcinoma susceptibility loci. <i>Nature Communications</i> , 2015, 6, 6825.	5.8	59
117	The germline sequence variant rs2736100_C in TERT associates with myeloproliferative neoplasms. <i>Leukemia</i> , 2014, 28, 1371-1374.	3.3	85
118	Rare mutations associating with serum creatinine and chronic kidney disease. <i>Human Molecular Genetics</i> , 2014, 23, 6935-6943.	1.4	52
119	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 294-298.	9.4	294
120	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	13.7	548
121	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	9.4	360
122	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	9.4	428
123	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. <i>Nature</i> , 2013, 497, 517-520.	13.7	236
124	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. <i>PLoS Genetics</i> , 2013, 9, e1003530.	1.5	112
125	A common variant at 8q24.21 is associated with renal cell cancer. <i>Nature Communications</i> , 2013, 4, 2776.	5.8	56
126	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. <i>Nature Genetics</i> , 2013, 45, 1371-1374.	9.4	125



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127	Genome-wide association analysis of coffee drinking suggests association with CYP1A1/CYP1A2 and NRCAM. <i>Molecular Psychiatry</i> , 2012, 17, 1116-1129.	4.1	112
128	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. <i>Nature Genetics</i> , 2012, 44, 1326-1329.	9.4	178
129	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	13.7	320
130	Rate of de novo mutations and the importance of father's age to disease risk. <i>Nature</i> , 2012, 488, 471-475.	13.7	1,880
131	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. <i>Nature Genetics</i> , 2012, 44, 260-268.	9.4	303
132	Discovery of common variants associated with low TSH levels and thyroid cancer risk. <i>Nature Genetics</i> , 2012, 44, 319-322.	9.4	208
133	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. <i>Nature</i> , 2012, 488, 96-99.	13.7	1,442
134	Mutations in BRIP1 confer high risk of ovarian cancer. <i>Nature Genetics</i> , 2011, 43, 1104-1107.	9.4	338
135	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. <i>Nature Genetics</i> , 2011, 43, 1098-1103.	9.4	251
136	Identification of low-frequency variants associated with gout and serum uric acid levels. <i>Nature Genetics</i> , 2011, 43, 1127-1130.	9.4	134
137	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. <i>Nature Genetics</i> , 2011, 43, 316-320.	9.4	275
138	Sequence variants at CYP1A1 and CYP1A2 and AHR associate with coffee consumption. <i>Human Molecular Genetics</i> , 2011, 20, 2071-2077.	1.4	114
139	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. <i>Human Molecular Genetics</i> , 2011, 20, 4268-4281.	1.4	134
140	Sequence variants at CHRN3 and CHRNA6 and CYP2A6 affect smoking behavior. <i>Nature Genetics</i> , 2010, 42, 448-453.	9.4	649
141	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. <i>Nature Genetics</i> , 2010, 42, 1077-1085.	9.4	445
142	Genetic Correction of PSA Values Using Sequence Variants Associated with PSA Levels. <i>Science Translational Medicine</i> , 2010, 2, 62ra92.	5.8	140
143	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. <i>PLoS Genetics</i> , 2010, 6, e1001029.	1.5	82
144	Parental origin of sequence variants associated with complex diseases. <i>Nature</i> , 2009, 462, 868-874.	13.7	521

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145	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. <i>Nature Genetics</i> , 2009, 41, 18-24.	9.4	1,247
146	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. <i>Nature Genetics</i> , 2009, 41, 221-227.	9.4	572
147	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. <i>Nature Genetics</i> , 2009, 41, 342-347.	9.4	709
148	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. <i>Nature Genetics</i> , 2009, 41, 460-464.	9.4	353
149	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. <i>Nature Genetics</i> , 2009, 41, 734-738.	9.4	199
150	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, 679-691.	2.6	489
151	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. <i>Nature</i> , 2008, 452, 638-642.	13.7	1,399
152	Many sequence variants affecting diversity of adult human height. <i>Nature Genetics</i> , 2008, 40, 609-615.	9.4	615
153	Two newly identified genetic determinants of pigmentation in Europeans. <i>Nature Genetics</i> , 2008, 40, 835-837.	9.4	331
154	Detection of sharing by descent, long-range phasing and haplotype imputation. <i>Nature Genetics</i> , 2008, 40, 1068-1075.	9.4	409
155	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. <i>Nature Genetics</i> , 2008, 40, 1307-1312.	9.4	377
156	Genetic determinants of hair, eye and skin pigmentation in Europeans. <i>Nature Genetics</i> , 2007, 39, 1443-1452.	9.4	659
157	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, 977-983.	9.4	670
158	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor <sup>+</sup> positive breast cancer. <i>Nature Genetics</i> , 2007, 39, 865-869.	9.4	774
159	Variants conferring risk of atrial fibrillation on chromosome 4q25. <i>Nature</i> , 2007, 448, 353-357.	13.7	853
160	A common variant associated with prostate cancer in European and African populations. <i>Nature Genetics</i> , 2006, 38, 652-658.	9.4	738
161	Cancer as a Complex Phenotype: Pattern of Cancer Distribution within and beyond the Nuclear Family. <i>PLoS Medicine</i> , 2004, 1, e65.	3.9	245
162	Cancer incidence among Icelandic deck officers in a population-based study. <i>Scandinavian Journal of Work, Environment and Health</i> , 2003, 29, 100-105.	1.7	10