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List of Publications by Year
in descending order

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48	12,718	76196	205818
papers	citations	40 h-index	48 g-index

51	51	51	22448
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
2	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.	0.5	26
3	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
4	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. European Journal of Human Genetics, 2021, 29, 1061-1070.	1.4	5
5	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
6	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
7	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	6.0	252
8	Genome-wide associations for benign prostatic hyperplasia reveal a genetic correlation with serum levels of PSA. Nature Communications, 2018, 9, 4568.	5.8	44
9	A homozygous loss-of-function mutation leading to CYBC1 deficiency causes chronic granulomatous disease. Nature Communications, 2018, 9, 4447.	5.8	95
10	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. Nature Genetics, 2018, 50, 1542-1552.	9.4	94
11	A genome-wide association study yields five novel thyroid cancer risk loci. Nature Communications, 2017, 8, 14517.	5.8	117
12	Clonal hematopoiesis, with and without candidate driver mutations, is common in the elderly. Blood, 2017, 130, 742-752.	0.6	582
13	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
14	A frameshift deletion in the sarcomere geneMYL4causes early-onset familial atrial fibrillation. European Heart Journal, 2017, 38, 27-34.	1.0	89
15	Compound heterozygous mutations in UBA5 causing early-onset epileptic encephalopathy in two sisters. BMC Medical Genetics, 2017, 18, 103.	2.1	28
16	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	5.8	52
17	Two Rare Mutations in the COL1A2 Gene Associate With Low Bone Mineral Density and Fractures in Iceland. Journal of Bone and Mineral Research, 2016, 31, 173-179.	3.1	35
18	Insertion of an SVA-E retrotransposon into theCASP8gene is associated with protection against prostate cancer. Human Molecular Genetics, 2016, 25, 1008-1018.	1.4	22

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19	Weighting sequence variants based on their annotation increases power of whole-genome association studies. Nature Genetics, 2016, 48, 314-317.	9.4	178
20	Sequence variants in the PTCH1 gene associate with spine bone mineral density and osteoporotic fractures. Nature Communications, 2016, 7, 10129.	5.8	58
21	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	2.4	59
22	Loss-of-function variants in ABCA7 confer risk of Alzheimer's disease. Nature Genetics, 2015, 47, 445-447.	9.4	283
23	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
24	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663
25	New basal cell carcinoma susceptibility loci. Nature Communications, 2015, 6, 6825.	5.8	59
26	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. Human Molecular Genetics, 2014, 23, 3045-3053.	1.4	48
27	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	9.4	294
28	Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. Human Molecular Genetics, 2014, 23, 5545-5557.	1.4	46
29	A common variant at 8q24.21 is associated with renal cell cancer. Nature Communications, 2013, 4, 2776.	5.8	56
30	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. Nature Genetics, 2012, 44, 1326-1329.	9.4	178
31	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	13.7	1,880
32	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	9.4	251
33	Identification of low-frequency variants associated with gout and serum uric acid levels. Nature Genetics, 2011, 43, 1127-1130.	9.4	134
34	Sequence variants at CYP1A1â€“CYP1A2 and AHR associate with coffee consumption. Human Molecular Genetics, 2011, 20, 2071-2077.	1.4	114
35	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	13.7	559
36	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	9.4	342

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37	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. Nature Genetics, 2010, 42, 415-419.	9.4	169
38	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. Nature Genetics, 2010, 42, 906-909.	9.4	357
39	Ancestry-Shift Refinement Mapping of the C6orf97-ESR1 Breast Cancer Susceptibility Locus. PLoS Genetics, 2010, 6, e1001029.	1.5	82
40	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	13.7	521
41	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	9.4	303
42	Common variants on chromosome 5p12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2008, 40, 703-706.	9.4	412
43	Two newly identified genetic determinants of pigmentation in Europeans. Nature Genetics, 2008, 40, 835-837.	9.4	331
44	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. Nature Genetics, 2008, 40, 1307-1312.	9.4	377
45	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. Nature Genetics, 2008, 40, 1313-1318.	9.4	111
46	Sequence Variants in the RNF212 Gene Associate with Genome-Wide Recombination Rate. Science, 2008, 319, 1398-1401.	6.0	183
47	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptorâ€“positive breast cancer. Nature Genetics, 2007, 39, 865-869.	9.4	774
48	A high-resolution recombination map of the human genome. Nature Genetics, 2002, 31, 241-247.	9.4	1,571