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List of Publications by Year
in descending order

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58 papers	18,149 citations	71102 41 h-index	114465 63 g-index
64 all docs	64 docs citations	64 times ranked	27049 citing authors

#	Article	IF	Citations
1	A second generation human haplotype map of over 3.1 million SNPs. Nature, 2007, 449, 851-861.	27.8	4,137
2	A genome-wide association study identifies novel risk loci for type 2 diabetes. Nature, 2007, 445, 881-885.	27.8	2,651
3	Driver mutations in histone H3.3 and chromatin remodelling genes in paediatric glioblastoma. Nature, 2012, 482, 226-231.	27.8	2,129
4	K27M mutation in histone H3.3 defines clinically and biologically distinct subgroups of pediatric diffuse intrinsic pontine gliomas. Acta Neuropathologica, 2012, 124, 439-447.	7.7	799
5	Genome-wide association scan identifies a colorectal cancer susceptibility locus on chromosome 8q24. Nature Genetics, 2007, 39, 989-994.	21.4	676
6	Genome-wide association study for early-onset and morbid adult obesity identifies three new risk loci in European populations. Nature Genetics, 2009, 41, 157-159.	21.4	585
7	Genome-wide association scan identifies a colorectal cancer susceptibility locus on 11q23 and replicates risk loci at 8q24 and 18q21. Nature Genetics, 2008, 40, 631-637.	21.4	542
8	Genomic analysis of diffuse intrinsic pontine gliomas identifies three molecular subgroups and recurrent activating ACVR1 mutations. Nature Genetics, 2014, 46, 451-456.	21.4	525
9	Meta-analysis of genome-wide association data identifies four new susceptibility loci for colorectal cancer. Nature Genetics, 2008, 40, 1426-1435.	21.4	498
10	Susceptibility to leprosy is associated with PARK2 and PACRG. Nature, 2004, 427, 636-640.	27.8	426
11	Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia. Nature Genetics, 2009, 41, 1110-1115.	21.4	418
12	Concept, Design and Implementation of a Cardiovascular Gene-Centric 50 K SNP Array for Large-Scale Genomic Association Studies. PLoS ONE, 2008, 3, e3583.	2.5	339
13	A predominant role for the HLA class II region in the association of the MHC region with multiple sclerosis. Nature Genetics, 2005, 37, 1108-1112.	21.4	295
14	Mutations in SETD2 and genes affecting histone H3K36 methylation target hemispheric high-grade gliomas. Acta Neuropathologica, 2013, 125, 659-669.	7.7	250
15	Association of Vitamin D Receptor Genetic Variants with Susceptibility to Asthma and Atopy. American Journal of Respiratory and Critical Care Medicine, 2004, 170, 967-973.	5.6	217
16	H3K27M induces defective chromatin spread of PRC2-mediated repressive H3K27me2/me3 and is essential for glioma tumorigenesis. Nature Communications, 2019, 10, 1262.	12.8	215
17	Genetic Variants of FTO Influence Adiposity, Insulin Sensitivity, Leptin Levels, and Resting Metabolic Rate in the Quebec Family Study. Diabetes, 2008, 57, 1147-1150.	0.6	206
18	Global patterns of cis variation in human cells revealed by high-density allelic expression analysis. Nature Genetics, 2009, 41, 1216-1222.	21.4	206

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19	CAG Expansion in the Huntington Disease Gene Is Associated with a Specific and Targetable Predisposing Haplogroup. American Journal of Human Genetics, 2009, 84, 351-366.	6.2	204
20	Rare variants in the CYP27B1 gene are associated with multiple sclerosis. Annals of Neurology, 2011, 70, 881-886.	5.3	204
21	Integrated (epi)-Genomic Analyses Identify Subgroup-Specific Therapeutic Targets in CNS Rhabdoid Tumors. Cancer Cell, 2016, 30, 891-908.	16.8	191
22	NALP1 Influences Susceptibility to Human Congenital Toxoplasmosis, Proinflammatory Cytokine Response, and Fate ofToxoplasma gondii-Infected Monocytic Cells. Infection and Immunity, 2011, 79, 756-766.	2.2	169
23	Fusion of TTYH1 with the C19MC microRNA cluster drives expression of a brain-specific DNMT3B isoform in the embryonal brain tumor ETMR. Nature Genetics, 2014, 46, 39-44.	21.4	167
24	Molecular subgroups of atypical teratoid rhabdoid tumours in children: an integrated genomic and clinicopathological analysis. Lancet Oncology, The, 2015, 16, 569-582.	10.7	147
25	Disruption of AP1S1, Causing a Novel Neurocutaneous Syndrome, Perturbs Development of the Skin and Spinal Cord. PLoS Genetics, 2008, 4, e1000296.	3.5	131
26	MEDNIK syndrome: a novel defect of copper metabolism treatable by zinc acetate therapy. Brain, 2013, 136, 872-881.	7.6	130
27	Meta-analysis of Dense Genecentric Association Studies Reveals Common and Uncommon Variants Associated with Height. American Journal of Human Genetics, 2011, 88, 6-18.	6.2	122
28	An Evaluation of the Performance of Tag SNPs Derived from HapMap in a Caucasian Population. PLoS Genetics, 2006, 2, e27.	3.5	105
29	Toxoplasma Modulates Signature Pathways of Human Epilepsy, Neurodegeneration & Cancer. Scientific Reports, 2017, 7, 11496.	3.3	97
30	Analyses of associations with asthma in four asthma population samples from Canada and Australia. Human Genetics, 2009, 125, 445-459.	3.8	95
31	HLA class I alleles tag HLA-DRB1 * 1501 haplotypes for differential risk in multiple sclerosis susceptibility. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13069-13074.	7.1	86
32	Genetic Analysis of 103 Candidate Genes for Coronary Artery Disease and Associated Phenotypes in a Founder Population Reveals a New Association between Endothelin-1 and High-Density Lipoprotein Cholesterol. American Journal of Human Genetics, 2007, 80, 673-682.	6.2	79
33	Identification of susceptibility genes for complex diseases using pooling-based genome-wide association scans. Human Genetics, 2009, 125, 305-318.	3.8	74
34	Genome-wide profiling using single-nucleotide polymorphism arrays identifies novel chromosomal imbalances in pediatric glioblastomas. Neuro-Oncology, 2010, 12, 153-163.	1.2	72
35	Genetic Variants Associated With Myocardial Infarction Risk Factors in Over 8000 Individuals From Five Ethnic Groups. Circulation: Cardiovascular Genetics, 2009, 2, 16-25.	5.1	67
36	A PRDX1 mutant allele causes a MMACHC secondary epimutation in cblC patients. Nature Communications, 2018, 9, 67.	12.8	64

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37	Correction of Population Stratification in Large Multi-Ethnic Association Studies. PLoS ONE, 2008, 3, e1382.	2.5	60
38	Genome-wide assessment of imprinted expression in human cells. Genome Biology, 2011, 12, R25.	9.6	56
39	Association of Urokinase-type Plasminogen Activator with Asthma and Atopy. American Journal of Respiratory and Critical Care Medicine, 2007, 175, 1109-1116.	5.6	47
40	PRKCA and Multiple Sclerosis: Association in Two Independent Populations. PLoS Genetics, 2006, 2, e42.	3.5	45
41	A human ALDH1A2 gene variant is associated with increased newborn kidney size and serum retinoic acid. Kidney International, 2010, 78, 96-102.	5.2	41
42	A detailed transcriptional map of the chromosome 12p12 tumour suppressor locus. European Journal of Human Genetics, 2002, 10, 62-71.	2.8	38
43	Integrative genomic analysis of matched primary and metastatic pediatric osteosarcoma. Journal of Pathology, 2019, 249, 319-331.	4.5	36
44	An atypical form of erythrokeratodermia variabilis maps to chromosome 7q22. Human Genetics, 2005, 116, 167-171.	3.8	33
45	Evaluating the performance of commercial whole-genome marker sets for capturing common genetic variation. BMC Genomics, 2007, 8, 159.	2.8	29
46	ALOX12 in Human Toxoplasmosis. Infection and Immunity, 2014, 82, 2670-2679.	2.2	28
47	Genetic Control of Alternative Splicing in the TAP2 Gene: Possible Implication in the Genetics of Type 1 Diabetes. Diabetes, 2007, 56, 270-275.	0.6	27
48	Immunoseq: the identification of functionally relevant variants through targeted capture and sequencing of active regulatory regions in human immune cells. BMC Medical Genomics, 2016, 9, 59.	1.5	26
49	Impaired Innate Immunity in Mice Deficient in Interleukin-1 Receptor-Associated Kinase 4 Leads to Defective Type 1 T Cell Responses, B Cell Expansion, and Enhanced Susceptibility to Infection with Toxoplasma gondii. Infection and Immunity, 2012, 80, 4298-4308.	2.2	23
50	Genetic Information and the Prediction of Incident Type 2 Diabetes in a High-Risk Multiethnic Population. Diabetes Care, 2013, 36, 2836-2842.	8.6	22
51	Identification of a chromosome 8p locus for early-onset coronary heart disease in a French Canadian population. European Journal of Human Genetics, 2008, 16, 105-114.	2.8	17
52	Germline EPHB2 Receptor Variants in Familial Colorectal Cancer. PLoS ONE, 2008, 3, e2885.	2.5	16
53	Genetic variation in immune signaling genes differentially expressed in asthmatic lung tissues. Journal of Allergy and Clinical Immunology, 2008, 122, 529-536.e17.	2.9	14
54	Comparative analysis of the ETV6 gene in vertebrate genomes from pufferfish to human. Oncogene, 2001, 20, 3437-3442.	5.9	10

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55	Variation at the DPP4 locus influences apolipoprotein B levels in South Asians and exhibits heterogeneity in Europeans related to BMI. Diabetologia, 2014, 57, 738-745.	6.3	9
56	Fine Mapping of the Insulin-Induced Gene 2 Identifies a Variant Associated With LDL Cholesterol and Total Apolipoprotein B Levels. Circulation: Cardiovascular Genetics, 2010, 3, 454-461.	5.1	7
57	Analysis of the conservation of synteny between Fugu and human chromosome 12. BMC Genomics, 2003, 4, 30.	2.8	6
58	K45R variant of squalene synthase increases total cholesterol levels in two study samples from a French Canadian population. Human Mutation, 2008, 29, 689-694.	2.5	5