Gudmar Thorleifsson

List of Publications by Year
in descending order

72 papers	31,675 citations	34105 52 h-index	74163 75 g-index
82 all docs	82 docs citations	82 times ranked	39647 citing authors

#	Article	IF	Citations
1	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
2	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
3	Rate of de novo mutations and the importance of fatherâ€™s age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
4	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
5	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	27.8	1,399
6	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	21.4	1,331
7	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
8	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
9	Genome-wide association study identifies 74 loci associated with educational attainment. Nature, 2016, 533, 539-542.	27.8	1,204
10	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. Nature Genetics, 2018, 50, 524-537.	21.4	1,124
11	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	21.4	959
12	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	27.8	853
13	The nature of nurture: Effects of parental genotypes. Science, 2018, 359, 424-428.	12.6	720
14	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
15	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.6	615
16	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	27.8	559
17	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. Nature, 2014, 514, 92-97.	27.8	548
18	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521

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19	Wholeâ€genome sequencing identifies EN1 as a determinant of bone density and fracture. Nature, 2015, 526, 112-117.	27.8	483
20	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	21.4	434
21	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	21.4	428
22	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. Nature Genetics, 2018, 50, 42-53.	21.4	426
23	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
24	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. Nature Genetics, 2014, 46, 736-741.	21.4	360
25	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	21.4	342
26	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
27	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
28	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	21.4	275
29	Characterizing mutagenic effects of recombination through a sequence-level genetic map. Science, 2019, 363, .	12.6	252
30	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	21.4	250
31	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	21.4	248
32	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. Nature Genetics, 2017, 49, 1584-1592.	21.4	248
33	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. Nature Genetics, 2013, 45, 902-906.	21.4	221
34	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. Nature Genetics, 2022, 54, 437-449.	21.4	215
35	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
36	Recombination rate and reproductive success in humans. Nature Genetics, 2004, 36, 1203-1206.	21.4	176

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37	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
38	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. Nature Communications, 2017, 8, 80.	12.8	147
39	Relatedness disequilibrium regression estimates heritability without environmental bias. Nature Genetics, 2018, 50, 1304-1310.	21.4	147
40	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
41	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. Nature Genetics, 2018, 50, 572-580.	21.4	143
42	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	27.0	137
43	Common and low-frequency variants associated with genome-wide recombination rate. Nature Genetics, 2014, 46, 11-16.	21.4	116
44	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. Nature Genetics, 2017, 49, 993-1004.	21.4	114
45	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.9	108
46	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	12.8	91
47	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. Nature Communications, 2021, 12, 24.	12.8	87
48	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
49	The rate of meiotic gene conversion varies by sex and age. Nature Genetics, 2016, 48, 1377-1384.	21.4	85
50	Genome-wide association study identifies 48 common genetic variants associated with handedness. Nature Human Behaviour, 2021, 5, 59-70.	12.0	79
51	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
52	The inheritance of rheumatoid arthritis in Iceland. Arthritis and Rheumatism, 2001, 44, 2247-2254.	6.7	61
53	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
54	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. Nature Communications, 2020, 11, 2542.	12.8	59

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55	Epigenetic and genetic components of height regulation. Nature Communications, 2016, 7, 13490.	12.8	52
56	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. Communications Biology, 2018, 1, 68.	4.4	42
57	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. Communications Biology, 2020, 3, 703.	4.4	40
58	Disentangling the genetics of lean mass. American Journal of Clinical Nutrition, 2019, 109, 276-287.	4.7	38
59	Genetic insight into sick sinus syndrome. European Heart Journal, 2021, 42, 1959-1971.	2.2	27
60	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. American Journal of Human Genetics, 2016, 99, 567-579.	6.2	26
61	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
62	Reply to â€œMany hypotheses but no replication for the association between PDE4D and strokeâ€: Nature Genetics, 2006, 38, 1092-1093.	21.4	20
63	Common Sequence Variants Associated With Coronary Artery Disease Correlate With the Extent of Coronary Atherosclerosis. Arteriosclerosis, Thrombosis, and Vascular Biology, 2015, 35, 1526-1531.	2.4	18
64	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2616-2628.	2.4	16
65	Identifying genetic risk variants for coronary heart disease in familial hypercholesterolemia: an extreme genetics approach. European Journal of Human Genetics, 2015, 23, 381-387.	2.8	15
66	Genetic Associations and Architecture of Asthma-COPD Overlap. Chest, 2022, 161, 1155-1166.	0.8	15
67	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
68	Germline variants at SOHLH2 influence multiple myeloma risk. Blood Cancer Journal, 2021, 11, 76.	6.2	6
69	Increased absorption of phytosterols is the simplest and most plausible explanation for coronary artery disease risk not accounted for by non-HDL cholesterol in high cholesterol absorbers. European Heart Journal, 2021, 42, 283-284.	2.2	4
70	Genome-wide association study on 13â€‰167 individuals identifies regulators of blood CD34+cell levels. Blood, 2022, 139, 1659-1669.	1.4	4
71	Abstract 2318: The Type 2 Diabetes Gene CDKAL1 Discovered by Genome-wide Association is Expressed in Beta Cells and Modulated by Glucose Concentration. Circulation, 2007, 116, .	1.6	1
72	Abstract 2921: Genome-wide Association Reveals Sequence Variants on 4q25 that Affect the Risk of Atrial Fibrillation and Stroke. Circulation, 2007, 116, .	1.6	0