

# Gudmar Thorleifsson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9395033/publications.pdf>

Version: 2024-02-01

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	Genome-wide association study on 13â€™167 individuals identifies regulators of blood CD34+cell levels. <i>Blood</i> , 2022, 139, 1659-1669.	1.4	4
2	Genetic Associations and Architecture of Asthma-COPD Overlap. <i>Chest</i> , 2022, 161, 1155-1166.	0.8	15
3	Polygenic prediction of educational attainment within and between families from genome-wide association analyses in 3 million individuals. <i>Nature Genetics</i> , 2022, 54, 437-449.	21.4	215
4	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. <i>Nature Genetics</i> , 2022, 54, 560-572.	21.4	250
5	Genome-wide association study identifies 48 common genetic variants associated with handedness. <i>Nature Human Behaviour</i> , 2021, 5, 59-70.	12.0	79
6	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. <i>European Heart Journal</i> , 2021, 42, 283-284.	2.2	4
7	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in <i>&lt;i&gt;LDLR&lt;/i&gt;</i> . <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003029.	3.6	12
8	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
9	Genetic insight into sick sinus syndrome. <i>European Heart Journal</i> , 2021, 42, 1959-1971.	2.2	27
10	Germline variants at SOHLH2 influence multiple myeloma risk. <i>Blood Cancer Journal</i> , 2021, 11, 76.	6.2	6
11	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021, 41, 2616-2628.	2.4	16
12	Large genome-wide association study identifies three novel risk variants for restless legs syndrome. <i>Communications Biology</i> , 2020, 3, 703.	4.4	40
13	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. <i>European Heart Journal</i> , 2020, 41, 2618-2628.	2.2	61
14	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. <i>Nature Communications</i> , 2020, 11, 2542.	12.8	59
15	Disentangling the genetics of lean mass. <i>American Journal of Clinical Nutrition</i> , 2019, 109, 276-287.	4.7	38
16	Characterizing mutagenic effects of recombination through a sequence-level genetic map. <i>Science</i> , 2019, 363, .	12.6	252
17	Genome-wide analysis yields new loci associating with aortic valve stenosis. <i>Nature Communications</i> , 2018, 9, 987.	12.8	91
18	Regulatory variants at KLF14 influence type 2 diabetes risk via a female-specific effect on adipocyte size and body composition. <i>Nature Genetics</i> , 2018, 50, 572-580.	21.4	143

#	ARTICLE	IF	CITATIONS
19	The nature of nurture: Effects of parental genotypes. <i>Science</i> , 2018, 359, 424-428.	12.6	720
20	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. <i>Nature Genetics</i> , 2018, 50, 42-53.	21.4	426
21	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <i>Nature Genetics</i> , 2018, 50, 1505-1513.	21.4	1,331
22	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3707.	12.8	86
23	Coding variants in RPL3L and MYZAP increase risk of atrial fibrillation. <i>Communications Biology</i> , 2018, 1, 68.	4.4	42
24	Relatedness disequilibrium regression estimates heritability without environmental bias. <i>Nature Genetics</i> , 2018, 50, 1304-1310.	21.4	147
25	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. <i>Nature Genetics</i> , 2018, 50, 524-537.	21.4	1,124
26	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.	7.1	149
27	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. <i>Nature Genetics</i> , 2017, 49, 993-1004.	21.4	114
28	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , 2017, 66, 2888-2902.	0.6	615
29	Genome-wide association analysis of insomnia complaints identifies risk genes and genetic overlap with psychiatric and metabolic traits. <i>Nature Genetics</i> , 2017, 49, 1584-1592.	21.4	248
30	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. <i>Nature Communications</i> , 2017, 8, 80.	12.8	147
31	Variant <i>ASGR1</i> Associated with a Reduced Risk of Coronary Artery Disease. <i>New England Journal of Medicine</i> , 2016, 374, 2131-2141.	27.0	137
32	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.	21.4	214
33	Genome-wide association study identifies 74 loci associated with educational attainment. <i>Nature</i> , 2016, 533, 539-542.	27.8	1,204
34	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. <i>American Journal of Human Genetics</i> , 2016, 99, 567-579.	6.2	26
35	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. <i>Nature Communications</i> , 2016, 7, 13357.	12.8	74
36	The rate of meiotic gene conversion varies by sex and age. <i>Nature Genetics</i> , 2016, 48, 1377-1384.	21.4	85

#	ARTICLE	IF	CITATIONS
37	Epigenetic and genetic components of height regulation. <i>Nature Communications</i> , 2016, 7, 13490.	12.8	52
38	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , 2016, 7, 12050.	12.8	146
39	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. <i>Nature Genetics</i> , 2016, 48, 1462-1472.	21.4	284
40	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. <i>PLoS Genetics</i> , 2015, 11, e1005378.	3.5	331
41	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. <i>PLoS Genetics</i> , 2015, 11, e1005379.	3.5	24
42	New genetic loci link adipose and insulin biology to body fat distribution. <i>Nature</i> , 2015, 518, 187-196.	27.8	1,328
43	Genetic studies of body mass index yield new insights for obesity biology. <i>Nature</i> , 2015, 518, 197-206.	27.8	3,823
44	Common Sequence Variants Associated With Coronary Artery Disease Correlate With the Extent of Coronary Atherosclerosis. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2015, 35, 1526-1531.	2.4	18
45	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. <i>Nature</i> , 2015, 526, 112-117.	27.8	483
46	Identifying genetic risk variants for coronary heart disease in familial hypercholesterolemia: an extreme genetics approach. <i>European Journal of Human Genetics</i> , 2015, 23, 381-387.	2.8	15
47	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. <i>Annals of the Rheumatic Diseases</i> , 2014, 73, 2130-2136.	0.9	108
48	Common and low-frequency variants associated with genome-wide recombination rate. <i>Nature Genetics</i> , 2014, 46, 11-16.	21.4	116
49	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
50	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
51	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. <i>Nature Genetics</i> , 2014, 46, 234-244.	21.4	959
52	Rare variants of large effect in BRCA2 and CHEK2 affect risk of lung cancer. <i>Nature Genetics</i> , 2014, 46, 736-741.	21.4	360
53	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. <i>Nature Genetics</i> , 2014, 46, 357-363.	21.4	428
54	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. <i>Nature Genetics</i> , 2013, 45, 902-906.	21.4	221

#	ARTICLE	IF	CITATIONS
55	Rate of de novo mutations and the importance of father's age to disease risk. Nature, 2012, 488, 471-475.	27.8	1,880
56	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. Nature Genetics, 2011, 43, 316-320.	21.4	275
57	Biological, clinical and population relevance of 95 loci for blood lipids. Nature, 2010, 466, 707-713.	27.8	3,249
58	Fine-scale recombination rate differences between sexes, populations and individuals. Nature, 2010, 467, 1099-1103.	27.8	559
59	Several common variants modulate heart rate, PR interval and QRS duration. Nature Genetics, 2010, 42, 117-122.	21.4	342
60	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	27.8	521
61	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
62	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. Nature Genetics, 2009, 41, 926-930.	21.4	248
63	A sequence variant in ZFX3 on 16q22 associates with atrial fibrillation and ischemic stroke. Nature Genetics, 2009, 41, 876-878.	21.4	434
64	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. Nature, 2008, 452, 638-642.	27.8	1,399
65	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	21.4	615
66	Detection of sharing by descent, long-range phasing and haplotype imputation. Nature Genetics, 2008, 40, 1068-1075.	21.4	409
67	Variants conferring risk of atrial fibrillation on chromosome 4q25. Nature, 2007, 448, 353-357.	27.8	853
68	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
69	Abstract 2318: The Type 2 Diabetes Gene <i>CDKAL1</i> Discovered by Genome-wide Association is Expressed in Beta Cells and Modulated by Glucose Concentration. Circulation, 2007, 116, .	1.6	1
70	Reply to "Many hypotheses but no replication for the association between PDE4D and stroke". Nature Genetics, 2006, 38, 1092-1093.	21.4	20
71	Recombination rate and reproductive success in humans. Nature Genetics, 2004, 36, 1203-1206.	21.4	176
72	The inheritance of rheumatoid arthritis in Iceland. Arthritis and Rheumatism, 2001, 44, 2247-2254.	6.7	61