Valgerdur Steinthorsdottir

List of Publications by Year
in descending order

94 papers	43,694 citations	15466 65 h-index	33814 99 g-index
109 all docs	109 docs citations	109 times ranked	43244 citing authors

#	Article	IF	Citations
1	Genetic overlap analysis of endometriosis and asthma identifies shared loci implicating sex hormones and thyroid signalling pathways. Human Reproduction, 2022, 37, 366-383.	0.4	19
2	Multi-ancestry genome-wide association study of gestational diabetes mellitus highlights genetic links with type 2 diabetes. Human Molecular Genetics, 2022, 31, 3377-3391.	1.4	47
3	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
4	Loss-of-Function Variants in the Tumor-Suppressor Gene PTPN14 Confer Increased Cancer Risk. Cancer Research, 2021, 81, 1954-1964.	0.4	15
5	Distinction between the effects of parental and fetal genomes on fetal growth. Nature Genetics, 2021, 53, 1135-1142.	9.4	41
6	Genetic analyses of gynecological disease identify genetic relationships between uterine fibroids and endometrial cancer, and a novel endometrial cancer genetic risk region at the WNT4 1p36.12 locus. Human Genetics, 2021, 140, 1353-1365.	1.8	18
7	Genetic propensities for verbal and spatial ability have opposite effects on body mass index and risk of schizophrenia. Intelligence, 2021, 88, 101565.	1.6	2
8	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. Arteriosclerosis, Thrombosis, and Vascular Biology, 2021, 41, 2616-2628.	1.1	16
9	Large-scale integration of the plasma proteome with genetics and disease. Nature Genetics, 2021, 53, 1712-1721.	9.4	340
10	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. European Heart Journal, 2020, 41, 2618-2628.	1.0	61
11	Genetic predisposition to hypertension is associated with preeclampsia in European and Central Asian women. Nature Communications, 2020, 11, 5976.	5.8	102
12	Genome-wide association identifies seven loci for pelvic organ prolapse in Iceland and the UK Biobank. Communications Biology, 2020, 3, 129.	2.0	20
13	A PRPH splice-donor variant associates with reduced sural nerve amplitude and risk of peripheral neuropathy. Nature Communications, 2019, 10, 1777.	5.8	7
14	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
15	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. Journal of the American College of Cardiology, 2019, 74, 2982-2994.	1.2	127
16	Sequence variants associating with urinary biomarkers. Human Molecular Genetics, 2019, 28, 1199-1211.	1.4	28
17	Genome-wide analysis yields new loci associating with aortic valve stenosis. Nature Communications, 2018, 9, 987.	5.8	91
18	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356

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19	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.	9.4	1,331
20	Variants associating with uterine leiomyoma highlight genetic background shared by various cancers and hormone-related traits. Nature Communications, 2018, 9, 3636.	5.8	74
21	Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. Nature Communications, 2018, 9, 2252.	5.8	99
22	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
23	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
24	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. Nature Genetics, 2017, 49, 1255-1260.	9.4	205
25	Meta-analysis identifies five novel loci associated with endometriosis highlighting key genes involved in hormone metabolism. Nature Communications, 2017, 8, 15539.	5.8	230
26	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
27	Analysis of potential protein-modifying variants in 9000 endometriosis patients and 150000 controls of European ancestry. Scientific Reports, 2017, 7, 11380.	1.6	16
28	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. Nature Genetics, 2017, 49, 1398-1402.	9.4	20
29	VariantASGR1Associated with a Reduced Risk of Coronary Artery Disease. New England Journal of Medicine, 2016, 374, 2131-2141.	13.9	137
30	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. Nature Genetics, 2016, 48, 634-639.	9.4	214
31	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
32	Common variants upstream of KDR encoding VEGFR2 and in TTC39B associate with endometriosis. Nature Communications, 2016, 7, 12350.	5.8	31
33	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.	1.5	331
34	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. PLoS Genetics, 2015, 11, e1005230.	1.5	77
35	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. PLoS Genetics, 2015, 11, e1005379.	1.5	24
36	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	13.7	1,328

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37	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	13.7	3,823
38	Association Analysis of 29,956 Individuals Confirms That a Low-Frequency Variant at CCND2 Halves the Risk of Type 2 Diabetes by Enhancing Insulin Secretion. Diabetes, 2015, 64, 2279-2285.	0.3	24
39	The impact of low-frequency and rare variants on lipid levels. Nature Genetics, 2015, 47, 589-597.	9.4	310
40	The epidemiology of pituitary adenomas in Iceland, 1955â€“2012: a nationwide population-based study. European Journal of Endocrinology, 2015, 173, 655-664.	1.9	255
41	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. Nature Genetics, 2015, 47, 1415-1425.	9.4	365
42	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
43	Leveraging Cross-Species Transcription Factor Binding Site Patterns: From Diabetes Risk Loci to Disease Mechanisms. Cell, 2014, 156, 343-358.	13.5	113
44	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	9.4	1,818
45	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
46	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. Nature Genetics, 2014, 46, 357-363.	9.4	428
47	InterPregGen:genetic studies of pre-eclampsia in three continents. Norsk Epidemiologi, 2014, 24, 141-146.	0.2	12
48	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. Nature Genetics, 2013, 45, 501-512.	9.4	578
49	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. PLoS Genetics, 2013, 9, e1003500.	1.5	371
50	Genetic Architecture of Vitamin B12 and Folate Levels Uncovered Applying Deeply Sequenced Large Datasets. PLoS Genetics, 2013, 9, e1003530.	1.5	112
51	The Role of Adiposity in Cardiometabolic Traits: A Mendelian Randomization Analysis. PLoS Medicine, 2013, 10, e1001474.	3.9	178
52	Stratifying Type 2 Diabetes Cases by BMI Identifies Genetic Risk Variants in LAMA1 and Enrichment for Risk Variants in Lean Compared to Obese Cases. PLoS Genetics, 2012, 8, e1002741.	1.5	190
53	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
54	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748

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55	FTO genotype is associated with phenotypic variability of body mass index. Nature, 2012, 490, 267-272.	13.7	383
56	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
57	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. Nature Genetics, 2011, 43, 1098-1103.	9.4	251
58	Evaluating differences in linkage disequilibrium between populations. Annals of Human Genetics, 2010, 74, 233-247.	0.3	3
59	Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature, 2010, 467, 832-838.	13.7	1,789
60	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
61	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
62	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. Nature Genetics, 2010, 42, 692-697.	9.4	181
63	Meta-analysis identifies 13 new loci associated with waist-hip ratio and reveals sexual dimorphism in the genetic basis of fat distribution. Nature Genetics, 2010, 42, 949-960.	9.4	836
64	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. Nature Genetics, 2010, 42, 937-948.	9.4	2,634
65	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. Human Molecular Genetics, 2010, 19, 535-544.	1.4	176
66	Common Variants at 10 Genomic Loci Influence Hemoglobin A1C Levels via Glycemic and Nonglycemic Pathways. Diabetes, 2010, 59, 3229-3239.	0.3	387
67	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
68	Genome-Wide Association Scan Meta-Analysis Identifies Three Loci Influencing Adiposity and Fat Distribution. PLoS Genetics, 2009, 5, e1000508.	1.5	453
69	The T-381C SNP in BNP gene may be modestly associated with type 2 diabetes: an updated meta-analysis in 49 279 subjects. Human Molecular Genetics, 2009, 18, 2495-2501.	1.4	30
70	Parental origin of sequence variants associated with complex diseases. Nature, 2009, 462, 868-874.	13.7	521
71	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. Nature Genetics, 2009, 41, 18-24.	9.4	1,247
72	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662

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73	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. Nature Genetics, 2009, 41, 342-347.	9.4	709
74	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. Nature Genetics, 2009, 41, 734-738.	9.4	199
75	New common variants affecting susceptibility to basal cell carcinoma. Nature Genetics, 2009, 41, 909-914.	9.4	303
76	Genetics of gene expression and its effect on disease. Nature, 2008, 452, 423-428.	13.7	1,209
77	Many sequence variants affecting diversity of adult human height. Nature Genetics, 2008, 40, 609-615.	9.4	615
78	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. Nature Genetics, 2008, 40, 217-224.	9.4	668
79	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
80	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. Nature Genetics, 2007, 39, 770-775.	9.4	966
81	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. Nature Genetics, 2007, 39, 977-983.	9.4	670
82	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
83	Recurrence of hypertensive disorder in second pregnancy. American Journal of Obstetrics and Gynecology, 2006, 194, 916-920.	0.7	66
84	A common inversion under selection in Europeans. Nature Genetics, 2005, 37, 129-137.	9.4	747
85	Neuregulin 1 and schizophrenia. Annals of Medicine, 2004, 36, 62-71.	1.5	119
86	Paternity Change and the Recurrence Risk in Familial Hypertensive Disorder in Pregnancy. Hypertension in Pregnancy, 2004, 23, 219-225.	0.5	19
87	Multiple novel transcription initiation sites for NRG1. Gene, 2004, 342, 97-105.	1.0	139
88	Association of Neuregulin 1 with Schizophrenia Confirmed in a Scottish Population. American Journal of Human Genetics, 2003, 72, 83-87.	2.6	518
89	Neuregulin 1 and Susceptibility to Schizophrenia. American Journal of Human Genetics, 2002, 71, 877-892.	2.6	1,550
90	Clostridium perfringens beta-toxin forms multimeric transmembrane pores in human endothelial cells. Microbial Pathogenesis, 2000, 28, 45-50.	1.3	72

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91	Properties of the Adenovirus Type 40 E1B Promoter That Contribute to Its Low Transcriptional Activity. Virology, 1999, 265, 10-19.	1.1	11
92	Site-directed mutagenesis ofClostridium perfringensbeta-toxin: expression of wild-type and mutant toxins inBacillus subtilis. FEMS Microbiology Letters, 1998, 158, 17-23.	0.7	41
93	Enteric adenovirus type 40: E1B transcription map and identification of novel E1Aâ€“E1B cotranscripts in lytically infected cells. Virology, 1991, 181, 139-149.	1.1	13
94	Complementation of enteric adenovirus type 40 for lytic growth in tissue culture by E1B 55K function of adenovirus types 5 and 12. Virology, 1989, 171, 619-622.	1.1	34