Unnur Thorsteinsdottir

List of Publications by Citations

288 papers	85,461 citations	140 h-index	292 g-index
309 ext. papers	100,243 ext. citations	24.7 avg, IF	6.18 L-index

#	Paper	IF	Citations
288	Biological, clinical and population relevance of 95 loci for blood lipids. *Nature*, **2010**, 466, 707-13	50.4	2742
287	Genetic studies of body mass index yield new insights for obesity biology. *Nature*, **2015**, 518, 197-206	50.4	2687
286	Association analyses of 249,796 individuals reveal 18 new loci associated with body mass index. *Nature Genetics*, **2010**, 42, 937-48	36.3	2267
285	Discovery and refinement of loci associated with lipid levels. *Nature Genetics*, **2013**, 45, 1274-1283	36.3	1904
284	Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes. *Nature Genetics*, **2006**, 38, 320-3	36.3	1725
283	Variant of TREM2 associated with the risk of Alzheimer's disease. *New England Journal of Medicine*, **2013**, 368, 107-16	59.2	1603
282	Plasma HDL cholesterol and risk of myocardial infarction: a mendelian randomisation study. *Lancet, The*, **2012**, 380, 572-80	40	1523
281	Hundreds of variants clustered in genomic loci and biological pathways affect human height. *Nature*, **2010**, 467, 832-8	50.4	1514
280	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. *Nature Genetics*, **2008**, 40, 638-45	36.3	1496
279	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. *Nature Genetics*, **2012**, 44, 981-90	36.3	1482
278	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
277	Large recurrent microdeletions associated with schizophrenia. *Nature*, **2008**, 455, 232-6	50.4	1427
276	Rate of de novo mutations and the importance of father's age to disease risk. *Nature*, **2012**, 488, 471-5	50.4	1417
275	Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease. *Nature Genetics*, **2011**, 43, 333-8	36.3	1394
274	Common variants conferring risk of schizophrenia. *Nature*, **2009**, 460, 744-7	50.4	1350
273	Defining the role of common variation in the genomic and biological architecture of adult human height. *Nature Genetics*, **2014**, 46, 1173-86	36.3	1339
272	A common variant on chromosome 9p21 affects the risk of myocardial infarction. *Science*, **2007**, 316, 1491-3	33.3	1322

271	A variant associated with nicotine dependence, lung cancer and peripheral arterial disease. *Nature*, **2008**, 452, 638-642	50.4	1239
270	A mutation in APP protects against Alzheimer's disease and age-related cognitive decline. *Nature*, **2012**, 488, 96-9	50.4	1194
269	Large-scale association analysis identifies new risk loci for coronary artery disease. *Nature Genetics*, **2013**, 45, 25-33	36.3	1172
268	Genome-wide association yields new sequence variants at seven loci that associate with measures of obesity. *Nature Genetics*, **2009**, 41, 18-24	36.3	1085
267	Genetics of gene expression and its effect on disease. *Nature*, **2008**, 452, 423-8	50.4	1058
266	New genetic loci link adipose and insulin biology to body fat distribution. *Nature*, **2015**, 518, 187-196	50.4	920
265	Genome-wide association of early-onset myocardial infarction with single nucleotide polymorphisms and copy number variants. *Nature Genetics*, **2009**, 41, 334-41	36.3	884
264	Genome-wide meta-analysis identifies 56 bone mineral density loci and reveals 14 loci associated with risk of fracture. *Nature Genetics*, **2012**, 44, 491-501	36.3	866
263	A variant in CDKAL1 influences insulin response and risk of type 2 diabetes. *Nature Genetics*, **2007**, 39, 770-5	36.3	851
262	Genome-wide association study identifies 74 loci associated with educational attainment. *Nature*, **2016**, 533, 539-42	50.4	850
261	Spread of SARS-CoV-2 in the Icelandic Population. *New England Journal of Medicine*, **2020**, 382, 2302-2315	59.2	842
260	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. *Nature Genetics*, **2014**, 46, 234-44	36.3	784
259	The gene encoding 5-lipoxygenase activating protein confers risk of myocardial infarction and stroke. *Nature Genetics*, **2004**, 36, 233-9	36.3	770
258	Genome-wide association study identifies a second prostate cancer susceptibility variant at 8q24. *Nature Genetics*, **2007**, 39, 631-7	36.3	739
257	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, 949-60	36.3	724
256	Common variants on chromosomes 2q35 and 16q12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2007**, 39, 865-9	36.3	715
255	Variants conferring risk of atrial fibrillation on chromosome 4q25. *Nature*, **2007**, 448, 353-7	50.4	702
254	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	36.3	675

253	A common variant associated with prostate cancer in European and African populations. *Nature Genetics*, **2006**, 38, 652-8	36.3	661
252	Sequence variants affecting eosinophil numbers associate with asthma and myocardial infarction. *Nature Genetics*, **2009**, 41, 342-7	36.3	627
251	Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes. *Nature Genetics*, **2007**, 39, 977-83	36.3	616
250	Genetic variants associated with subjective well-being, depressive symptoms, and neuroticism identified through genome-wide analyses. *Nature Genetics*, **2016**, 48, 624-33	36.3	602
249	Common variants associated with plasma triglycerides and risk for coronary artery disease. *Nature Genetics*, **2013**, 45, 1345-52	36.3	597
248	The same sequence variant on 9p21 associates with myocardial infarction, abdominal aortic aneurysm and intracranial aneurysm. *Nature Genetics*, **2008**, 40, 217-24	36.3	596
247	Humoral Immune Response to SARS-CoV-2 in Iceland. *New England Journal of Medicine*, **2020**, 383, 1724-1734	59.2	593
246	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584
245	Sequence variants at CHRNB3-CHRNA6 and CYP2A6 affect smoking behavior. *Nature Genetics*, **2010**, 42, 448-53	36.3	582
244	Twenty bone-mineral-density loci identified by large-scale meta-analysis of genome-wide association studies. *Nature Genetics*, **2009**, 41, 1199-206	36.3	566
243	Common sequence variants in the LOXL1 gene confer susceptibility to exfoliation glaucoma. *Science*, **2007**, 317, 1397-400	33.3	558
242	Genetic determinants of hair, eye and skin pigmentation in Europeans. *Nature Genetics*, **2007**, 39, 1443-52	36.3	545
241	Multiancestry genome-wide association study of 520,000 subjects identifies 32 loci associated with stroke and stroke subtypes. *Nature Genetics*, **2018**, 50, 524-537	36.3	536
240	Many sequence variants affecting diversity of adult human height. *Nature Genetics*, **2008**, 40, 609-15	36.3	522
239	Multiple genetic loci for bone mineral density and fractures. *New England Journal of Medicine*, **2008**, 358, 2355-65	59.2	511
238	Sequence variants at the TERT-CLPTM1L locus associate with many cancer types. *Nature Genetics*, **2009**, 41, 221-7	36.3	509
237	A genetic risk factor for periodic limb movements in sleep. *New England Journal of Medicine*, **2007**, 357, 639-47	59.2	491
236	Large-scale whole-genome sequencing of the Icelandic population. *Nature Genetics*, **2015**, 47, 435-44	36.3	486

235	Parental origin of sequence variants associated with complex diseases. *Nature*, **2009**, 462, 868-74	50.4	459
234	Genome-wide meta-analysis identifies 11 new loci for anthropometric traits and provides insights into genetic architecture. *Nature Genetics*, **2013**, 45, 501-12	36.3	437
233	Fine-scale recombination rate differences between sexes, populations and individuals. *Nature*, **2010**, 467, 1099-103	50.4	428
232	Refining the impact of TCF7L2 gene variants on type 2 diabetes and adaptive evolution. *Nature Genetics*, **2007**, 39, 218-25	36.3	420
231	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nature Genetics*, **2011**, 43, 1131-8	36.3	415
230	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
229	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
228	The nature of nurture: Effects of parental genotypes. *Science*, **2018**, 359, 424-428	33.3	409
227	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. *Nature*, **2014**, 514, 92-97	50.4	401
226	Genome-wide association scan meta-analysis identifies three Loci influencing adiposity and fat distribution. *PLoS Genetics*, **2009**, 5, e1000508	6	393
225	Common variants on chromosome 5p12 confer susceptibility to estrogen receptor-positive breast cancer. *Nature Genetics*, **2008**, 40, 703-6	36.3	378
224	Thirty new loci for age at menarche identified by a meta-analysis of genome-wide association studies. *Nature Genetics*, **2010**, 42, 1077-85	36.3	372
223	A sequence variant in ZFHX3 on 16q22 associates with atrial fibrillation and ischemic stroke. *Nature Genetics*, **2009**, 41, 876-8	36.3	365
222	Genetic risk factors for ischaemic stroke and its subtypes (the METASTROKE collaboration): a meta-analysis of genome-wide association studies. *Lancet Neurology, The*, **2012**, 11, 951-62	24.1	359
221	Loss-of-function mutations in SLC30A8 protect against type 2 diabetes. *Nature Genetics*, **2014**, 46, 357-63	36.3	351
220	Genome-wide association study identifies six new loci influencing pulse pressure and mean arterial pressure. *Nature Genetics*, **2011**, 43, 1005-11	36.3	338
219	Sequence variant on 8q24 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2008**, 40, 1307-12	36.3	332
218	Detection of sharing by descent, long-range phasing and haplotype imputation. *Nature Genetics*, **2008**, 40, 1068-75	36.3	329

217	Common sequence variants on 2p15 and Xp11.22 confer susceptibility to prostate cancer. *Nature Genetics*, **2008**, 40, 281-3	36.3	327
216	Mirror extreme BMI phenotypes associated with gene dosage at the chromosome 16p11.2 locus. *Nature*, **2011**, 478, 97-102	50.4	322
215	Genome-wide association study identifies a variant in HDAC9 associated with large vessel ischemic stroke. *Nature Genetics*, **2012**, 44, 328-33	36.3	314
214	Whole-genome sequencing identifies EN1 as a determinant of bone density and fracture. *Nature*, **2015**, 526, 112-7	50.4	308
213	Common variants on 9q22.33 and 14q13.3 predispose to thyroid cancer in European populations. *Nature Genetics*, **2009**, 41, 460-4	36.3	308
212	FTO genotype is associated with phenotypic variability of body mass index. *Nature*, **2012**, 490, 267-72	50.4	304
211	A variant of the gene encoding leukotriene A4 hydrolase confers ethnicity-specific risk of myocardial infarction. *Nature Genetics*, **2006**, 38, 68-74	36.3	304
210	Common variants near CAV1 and CAV2 are associated with primary open-angle glaucoma. *Nature Genetics*, **2010**, 42, 906-9	36.3	303
209	Several common variants modulate heart rate, PR interval and QRS duration. *Nature Genetics*, **2010**, 42, 117-22	36.3	293
208	Genetic fine mapping and genomic annotation defines causal mechanisms at type 2 diabetes susceptibility loci. *Nature Genetics*, **2015**, 47, 1415-25	36.3	292
207	New sequence variants associated with bone mineral density. *Nature Genetics*, **2009**, 41, 15-7	36.3	287
206	Mutations in BRIP1 confer high risk of ovarian cancer. *Nature Genetics*, **2011**, 43, 1104-7	36.3	285
205	Overexpression of the myeloid leukemia-associated Hoxa9 gene in bone marrow cells induces stem cell expansion. *Blood*, **2002**, 99, 121-9	2.2	283
204	Genome-wide association and replication studies identify four variants associated with prostate cancer susceptibility. *Nature Genetics*, **2009**, 41, 1122-6	36.3	281
203	Two newly identified genetic determinants of pigmentation in Europeans. *Nature Genetics*, **2008**, 40, 835-7	36.3	281
202	Sex-stratified genome-wide association studies including 270,000 individuals show sexual dimorphism in genetic loci for anthropometric traits. *PLoS Genetics*, **2013**, 9, e1003500	6	277
201	New common variants affecting susceptibility to basal cell carcinoma. *Nature Genetics*, **2009**, 41, 909-14	36.3	275
200	Genetic variation in the prostate stem cell antigen gene PSCA confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2009**, 41, 991-5	36.3	270

199	ASIP and TYR pigmentation variants associate with cutaneous melanoma and basal cell carcinoma. *Nature Genetics*, **2008**, 40, 886-91	36.3	265
198	Seventy-five genetic loci influencing the human red blood cell. *Nature*, **2012**, 492, 369-75	50.4	257
197	Biobank-driven genomic discovery yields new insight into atrial fibrillation biology. *Nature Genetics*, **2018**, 50, 1234-1239	36.3	254
196	The genetics of blood pressure regulation and its target organs from association studies in 342,415 individuals. *Nature Genetics*, **2016**, 48, 1171-1184	36.3	251
195	Multiancestry association study identifies new asthma risk loci that colocalize with immune-cell enhancer marks. *Nature Genetics*, **2018**, 50, 42-53	36.3	246
194	Shared genetic susceptibility to ischemic stroke and coronary artery disease: a genome-wide analysis of common variants. *Stroke*, **2014**, 45, 24-36	6.7	245
193	Meta-analyses identify 13 loci associated with age at menopause and highlight DNA repair and immune pathways. *Nature Genetics*, **2012**, 44, 260-8	36.3	243
192	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. *Nature Genetics*, **2014**, 46, 294-8	36.3	241
191	Genetic variation near IRS1 associates with reduced adiposity and an impaired metabolic profile. *Nature Genetics*, **2011**, 43, 753-60	36.3	237
190	Novel aspects of the pathogenesis of aneurysms of the abdominal aorta in humans. *Cardiovascular Research*, **2011**, 90, 18-27	9.9	235
189	Geographic differences in genetic susceptibility to IgA nephropathy: GWAS replication study and geospatial risk analysis. *PLoS Genetics*, **2012**, 8, e1002765	6	231
188	The impact of low-frequency and rare variants on lipid levels. *Nature Genetics*, **2015**, 47, 589-97	36.3	229
187	A rare variant in MYH6 is associated with high risk of sick sinus syndrome. *Nature Genetics*, **2011**, 43, 316-20	36.3	228
186	Large-scale genomic analyses link reproductive aging to hypothalamic signaling, breast cancer susceptibility and BRCA1-mediated DNA repair. *Nature Genetics*, **2015**, 47, 1294-1303	36.3	226
185	Defining roles for HOX and MEIS1 genes in induction of acute myeloid leukemia. *Molecular and Cellular Biology*, **2001**, 21, 224-34	4.8	226
184	Parental influence on human germline de novo mutations in 1,548 trios from Iceland. *Nature*, **2017**, 549, 519-522	50.4	223
183	Genome-wide association analyses identify multiple loci associated with central corneal thickness and keratoconus. *Nature Genetics*, **2013**, 45, 155-63	36.3	222
182	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. *Nature Genetics*, **2018**, 50, 559-571	36.3	221

181	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	6	220
180	Identification of heart rate-associated loci and their effects on cardiac conduction and rhythm disorders. *Nature Genetics*, **2013**, 45, 621-31	36.3	219
179	Genome-wide association and genetic functional studies identify autism susceptibility candidate 2 gene (AUTS2) in the regulation of alcohol consumption. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 7119-24	11.5	218
178	Collaborative meta-analysis: associations of 150 candidate genes with osteoporosis and osteoporotic fracture. *Annals of Internal Medicine*, **2009**, 151, 528-37	8	215
177	Sequence variants in the CLDN14 gene associate with kidney stones and bone mineral density. *Nature Genetics*, **2009**, 41, 926-30	36.3	213
176	Cancer as a complex phenotype: pattern of cancer distribution within and beyond the nuclear family. *PLoS Medicine*, **2004**, 1, e65	11.6	210
175	Risk variants for atrial fibrillation on chromosome 4q25 associate with ischemic stroke. *Annals of Neurology*, **2008**, 64, 402-9	9.4	208
174	Common variants near FRK/COL10A1 and VEGFA are associated with advanced age-related macular degeneration. *Human Molecular Genetics*, **2011**, 20, 3699-709	5.6	205
173	Causal mechanisms and balancing selection inferred from genetic associations with polycystic ovary syndrome. *Nature Communications*, **2015**, 6, 8464	17.4	203
172	A germline variant in the TP53 polyadenylation signal confers cancer susceptibility. *Nature Genetics*, **2011**, 43, 1098-103	36.3	203
171	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. *Nature Genetics*, **2014**, 46, 826-36	36.3	199
170	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. *Nature Genetics*, **2016**, 48, 1462-1472	36.3	198
169	Nonsense mutation in the LGR4 gene is associated with several human diseases and other traits. *Nature*, **2013**, 497, 517-20	50.4	192
168	Meta-analysis of genome-wide association studies identifies ten loci influencing allergic sensitization. *Nature Genetics*, **2013**, 45, 902-906	36.3	191
167	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. *Nature Genetics*, **2018**, 50, 26-41	36.3	186
166	Variant in the sequence of the LINGO1 gene confers risk of essential tremor. *Nature Genetics*, **2009**, 41, 277-9	36.3	183
165	Genome-wide analysis of multi-ancestry cohorts identifies new loci influencing intraocular pressure and susceptibility to glaucoma. *Nature Genetics*, **2014**, 46, 1126-1130	36.3	171
164	Genome-wide association study identifies sequence variants on 6q21 associated with age at menarche. *Nature Genetics*, **2009**, 41, 734-8	36.3	169

163	Discovery of common variants associated with low TSH levels and thyroid cancer risk. *Nature Genetics*, **2012**, 44, 319-22	36.3	167
162	Large-scale genome-wide meta-analysis of polycystic ovary syndrome suggests shared genetic architecture for different diagnosis criteria. *PLoS Genetics*, **2018**, 14, e1007813	6	166
161	Common variants at VRK2 and TCF4 conferring risk of schizophrenia. *Human Molecular Genetics*, **2011**, 20, 4076-81	5.6	162
160	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	6	162
159	Variants with large effects on blood lipids and the role of cholesterol and triglycerides in coronary disease. *Nature Genetics*, **2016**, 48, 634-9	36.3	162
158	Identification of a large set of rare complete human knockouts. *Nature Genetics*, **2015**, 47, 448-52	36.3	158
157	Overexpression of HOXB3 in hematopoietic cells causes defective lymphoid development and progressive myeloproliferation. *Immunity*, **1997**, 6, 13-22	32.3	157
156	Association of JAG1 with bone mineral density and osteoporotic fractures: a genome-wide association study and follow-up replication studies. *American Journal of Human Genetics*, **2010**, 86, 229-39	11	156
155	Genome-wide association study identifies a sequence variant within the DAB2IP gene conferring susceptibility to abdominal aortic aneurysm. *Nature Genetics*, **2010**, 42, 692-7	36.3	155
154	Genetically determined height and coronary artery disease. *New England Journal of Medicine*, **2015**, 372, 1608-18	59.2	152
153	A study based on whole-genome sequencing yields a rare variant at 8q24 associated with prostate cancer. *Nature Genetics*, **2012**, 44, 1326-9	36.3	151
152	Genetic evidence that raised sex hormone binding globulin (SHBG) levels reduce the risk of type 2 diabetes. *Human Molecular Genetics*, **2010**, 19, 535-44	5.6	150
151	Sequence variants in the RNF212 gene associate with genome-wide recombination rate. *Science*, **2008**, 319, 1398-401	33.3	147
150	Abdominal aortic aneurysm is associated with a variant in low-density lipoprotein receptor-related protein 1. *American Journal of Human Genetics*, **2011**, 89, 619-27	11	145
149	The role of adiposity in cardiometabolic traits: a Mendelian randomization analysis. *PLoS Medicine*, **2013**, 10, e1001474	11.6	144
148	Genome-wide association and Mendelian randomisation analysis provide insights into the pathogenesis of heart failure. *Nature Communications*, **2020**, 11, 163	17.4	140
147	A sequence variant at 4p16.3 confers susceptibility to urinary bladder cancer. *Nature Genetics*, **2010** , 42, 415-9	36.3	138
146	Association of variants at UMOD with chronic kidney disease and kidney stones-role of age and comorbid diseases. *PLoS Genetics*, **2010**, 6, e1001039	6	138

145	Common genetic variants associated with open-angle glaucoma. *Human Molecular Genetics*, **2011**, 20, 2464-71	5.6	134
144	Common variants at 6p21.1 are associated with large artery atherosclerotic stroke. *Nature Genetics*, **2012**, 44, 1147-51	36.3	126
143	Genetic correction of PSA values using sequence variants associated with PSA levels. *Science Translational Medicine*, **2010**, 2, 62ra92	17.5	125
142	Weighting sequence variants based on their annotation increases power of whole-genome association studies. *Nature Genetics*, **2016**, 48, 314-7	36.3	123
141	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. *Nature Genetics*, **2019**, 51, 1459-1474	36.3	122
140	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. *Nature Genetics*, **2018**, 50, 549-558	36.3	122
139	On the replication of genetic associations: timing can be everything!. *American Journal of Human Genetics*, **2008**, 82, 849-58	11	119
138	The association of a SNP upstream of INSIG2 with body mass index is reproduced in several but not all cohorts. *PLoS Genetics*, **2007**, 3, e61	6	119
137	Variants in the fetal genome near FLT1 are associated with risk of preeclampsia. *Nature Genetics*, **2017**, 49, 1255-1260	36.3	118
136	Apolipoprotein(a) genetic sequence variants associated with systemic atherosclerosis and coronary atherosclerotic burden but not with venous thromboembolism. *Journal of the American College of Cardiology*, **2012**, 60, 722-9	15.1	118
135	Variants in DENND1A are associated with polycystic ovary syndrome in women of European ancestry. *Journal of Clinical Endocrinology and Metabolism*, **2012**, 97, E1342-7	5.6	118
134	Physical and neurobehavioral determinants of reproductive onset and success. *Nature Genetics*, **2016**, 48, 617-623	36.3	118
133	Identification of low-frequency variants associated with gout and serum uric acid levels. *Nature Genetics*, **2011**, 43, 1127-30	36.3	117
132	A sequence variant on 17q21 is associated with age at onset and severity of asthma. *European Journal of Human Genetics*, **2010**, 18, 902-8	5.3	114
131	Ischemic stroke is associated with the ABO locus: the EuroCLOT study. *Annals of Neurology*, **2013**, 73, 16-31	9.4	105
130	European genome-wide association study identifies SLC14A1 as a new urinary bladder cancer susceptibility gene. *Human Molecular Genetics*, **2011**, 20, 4268-81	5.6	105
129	Severe osteoarthritis of the hand associates with common variants within the ALDH1A2 gene and with rare variants at 1p31. *Nature Genetics*, **2014**, 46, 498-502	36.3	104
128	A rare nonsynonymous sequence variant in C3 is associated with high risk of age-related macular degeneration. *Nature Genetics*, **2013**, 45, 1371-4	36.3	104

127	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. *Annals of the Rheumatic Diseases*, **2011**, 70, 349-55	2.4	102
126	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. *Nature Communications*, **2016**, 7, 12050	17.4	101
125	Loss-of-function variants in ATM confer risk of gastric cancer. *Nature Genetics*, **2015**, 47, 906-10	36.3	100
124	Meta-Analysis of Genome-Wide Association Studies for Abdominal Aortic Aneurysm Identifies Four New Disease-Specific Risk Loci. *Circulation Research*, **2017**, 120, 341-353	15.7	97
123	Characterizing mutagenic effects of recombination through a sequence-level genetic map. *Science*, **2019**, 363,	33.3	97
122	Leveraging cross-species transcription factor binding site patterns: from diabetes risk loci to disease mechanisms. *Cell*, **2014**, 156, 343-58	56.2	96
121	Common and rare variants associated with kidney stones and biochemical traits. *Nature Communications*, **2015**, 6, 7975	17.4	95
120	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. *Annals of the Rheumatic Diseases*, **2014**, 73, 2130-6	2.4	95
119	Sequence variants at CYP1A1-CYP1A2 and AHR associate with coffee consumption. *Human Molecular Genetics*, **2011**, 20, 2071-7	5.6	95
118	Variant ASGR1 Associated with a Reduced Risk of Coronary Artery Disease. *New England Journal of Medicine*, **2016**, 374, 2131-41	59.2	94
117	Common variants on 1p36 and 1q42 are associated with cutaneous basal cell carcinoma but not with melanoma or pigmentation traits. *Nature Genetics*, **2008**, 40, 1313-8	36.3	93
116	Male-pattern baldness susceptibility locus at 20p11. *Nature Genetics*, **2008**, 40, 1282-4	36.3	93
115	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. *Nature Genetics*, **2016**, 48, 318-22	36.3	92
114	Genetic variants linked to education predict longevity. *Proceedings of the National Academy of Sciences of the United States of America*, **2016**, 113, 13366-13371	11.5	90
113	Large meta-analysis of genome-wide association studies identifies five loci for lean body mass. *Nature Communications*, **2017**, 8, 80	17.4	88
112	Assessment of osteoarthritis candidate genes in a meta-analysis of nine genome-wide association studies. *Arthritis and Rheumatology*, **2014**, 66, 940-9	9.5	88
111	Familial risk of lung carcinoma in the Icelandic population. *JAMA - Journal of the American Medical Association*, **2004**, 292, 2977-83	27.4	87
110	Common and low-frequency variants associated with genome-wide recombination rate. *Nature Genetics*, **2014**, 46, 11-6	36.3	86

109	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	11.5	84
108	Relatedness disequilibrium regression estimates heritability without environmental bias. *Nature Genetics*, **2018**, 50, 1304-1310	36.3	84
107	Genetic predisposition to mosaic Y chromosome loss in blood. *Nature*, **2019**, 575, 652-657	50.4	83
106	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	36.3	82
105	A genome-wide association study of early menopause and the combined impact of identified variants. *Human Molecular Genetics*, **2013**, 22, 1465-72	5.6	82
104	A rare IL33 loss-of-function mutation reduces blood eosinophil counts and protects from asthma. *PLoS Genetics*, **2017**, 13, e1006659	6	79
103	Multi-nucleotide de novo Mutations in Humans. *PLoS Genetics*, **2016**, 12, e1006315	6	77
102	Lack of association between the Trp719Arg polymorphism in kinesin-like protein-6 and coronary artery disease in 19 case-control studies. *Journal of the American College of Cardiology*, **2010**, 56, 1552-63	15.1	75
101	Genome-wide meta-analysis for serum calcium identifies significantly associated SNPs near the calcium-sensing receptor (CASR) gene. *PLoS Genetics*, **2010**, 6, e1001035	6	74
100	A sequence variant associated with sortilin-1 (SORT1) on 1p13.3 is independently associated with abdominal aortic aneurysm. *Human Molecular Genetics*, **2013**, 22, 2941-7	5.6	73
99	Genetic association study of exfoliation syndrome identifies a protective rare variant at LOXL1 and five new susceptibility loci. *Nature Genetics*, **2017**, 49, 993-1004	36.3	72
98	Genetic architecture of vitamin B12 and folate levels uncovered applying deeply sequenced large datasets. *PLoS Genetics*, **2013**, 9, e1003530	6	72
97	Ancestry-shift refinement mapping of the C6orf97-ESR1 breast cancer susceptibility locus. *PLoS Genetics*, **2010**, 6, e1001029	6	72
96	Meta-analysis of genome-wide association studies identifies novel loci that influence cupping and the glaucomatous process. *Nature Communications*, **2014**, 5, 4883	17.4	71
95	European bone mineral density loci are also associated with BMD in East-Asian populations. *PLoS ONE*, **2010**, 5, e13217	3.7	67
94	Meta-analysis of Icelandic and UK data sets identifies missense variants in SMO, IL11, COL11A1 and 13 more new loci associated with osteoarthritis. *Nature Genetics*, **2018**, 50, 1681-1687	36.3	67
93	Whole genome characterization of sequence diversity of 15,220 Icelanders. *Scientific Data*, **2017**, 4, 170184	8.5	64
92	The oncoprotein E2A-Pbx1a collaborates with Hoxa9 to acutely transform primary bone marrow cells. *Molecular and Cellular Biology*, **1999**, 19, 6355-66	4.8	64

91	Lipoprotein(a) Concentration and Risks of Cardiovascular Disease and Diabetes. *Journal of the American College of Cardiology*, **2019**, 74, 2982-2994	15.1	61
90	Discovery and Fine-Mapping of Glycaemic and Obesity-Related Trait Loci Using High-Density Imputation. *PLoS Genetics*, **2015**, 11, e1005230	6	59
89	A variant in LDLR is associated with abdominal aortic aneurysm. *Circulation: Cardiovascular Genetics*, **2013**, 6, 498-504		58
88	Identification of sequence variants influencing immunoglobulin levels. *Nature Genetics*, **2017**, 49, 1182-1191	36.3	57
87	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. *Nature Communications*, **2018**, 9, 3707	17.4	57
86	Whole-genome sequencing identifies rare genotypes in COMP and CHADL associated with high risk of hip osteoarthritis. *Nature Genetics*, **2017**, 49, 801-805	36.3	56
85	Genome-wide analysis yields new loci associating with aortic valve stenosis. *Nature Communications* , **2018**, 9, 987	17.4	56
84	Insights into imprinting from parent-of-origin phased methylomes and transcriptomes. *Nature Genetics*, **2018**, 50, 1542-1552	36.3	56
83	Genetic predisposition to higher blood pressure increases coronary artery disease risk. *Hypertension*, **2013**, 61, 995-1001	8.5	55
82	Variants in ELL2 influencing immunoglobulin levels associate with multiple myeloma. *Nature Communications*, **2015**, 6, 7213	17.4	54
81	Meta-analysis of the INSIG2 association with obesity including 74,345 individuals: does heterogeneity of estimates relate to study design?. *PLoS Genetics*, **2009**, 5, e1000694	6	54
80	Hox homeobox genes as regulators of normal and leukemic hematopoiesis. *Hematology/Oncology Clinics of North America*, **1997**, 11, 1221-37	3.1	54
79	The BARD1 Cys557Ser variant and breast cancer risk in Iceland. *PLoS Medicine*, **2006**, 3, e217	11.6	54
78	Genetic variation at 16q24.2 is associated with small vessel stroke. *Annals of Neurology*, **2017**, 81, 383-394	9.4	51
77	Sequence variants from whole genome sequencing a large group of Icelanders. *Scientific Data*, **2015**, 2, 150011	8.2	51
76	Multiple transmissions of de novo mutations in families. *Nature Genetics*, **2018**, 50, 1674-1680	36.3	50
75	New basal cell carcinoma susceptibility loci. *Nature Communications*, **2015**, 6, 6825	17.4	49
74	A frameshift deletion in the sarcomere gene MYL4 causes early-onset familial atrial fibrillation. *European Heart Journal*, **2017**, 38, 27-34	9.5	47

73	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
72	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	36.3	44
71	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
70	A loss-of-function variant in ALOX15 protects against nasal polyps and chronic rhinosinusitis. *Nature Genetics*, **2019**, 51, 267-276	36.3	44
69	A Missense Variant in PLEC Increases Risk of Atrial Fibrillation. *Journal of the American College of Cardiology*, **2017**, 70, 2157-2168	15.1	43
68	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. *Nature Communications*, **2019**, 10, 4130	17.4	43
67	Diversity in non-repetitive human sequences not found in the reference genome. *Nature Genetics*, **2017**, 49, 588-593	36.3	42
66	Rare SCARB1 mutations associate with high-density lipoprotein cholesterol but not with coronary artery disease. *European Heart Journal*, **2018**, 39, 2172-2178	9.5	42
65	The rate of meiotic gene conversion varies by sex and age. *Nature Genetics*, **2016**, 48, 1377-1384	36.3	42
64	A protein-truncating R179X variant in RNF186 confers protection against ulcerative colitis. *Nature Communications*, **2016**, 7, 12342	17.4	41
63	Epigenetic and genetic components of height regulation. *Nature Communications*, **2016**, 7, 13490	17.4	39
62	Germline sequence variants in TGM3 and RGS22 confer risk of basal cell carcinoma. *Human Molecular Genetics*, **2014**, 23, 3045-53	5.6	39
61	Rare mutations associating with serum creatinine and chronic kidney disease. *Human Molecular Genetics*, **2014**, 23, 6935-43	5.6	39
60	Support for involvement of the AHI1 locus in schizophrenia. *European Journal of Human Genetics*, **2007**, 15, 988-91	5.3	38
59	Assessment of gene-by-sex interaction effect on bone mineral density. *Journal of Bone and Mineral Research*, **2012**, 27, 2051-64	6.3	37
58	PDE4D and ALOX5AP genetic variants and risk for Ischemic Cerebrovascular Disease in Sweden. *Journal of the Neurological Sciences*, **2007**, 263, 113-7	3.2	37
57	Evaluation of shared genetic aetiology between osteoarthritis and bone mineral density identifies SMAD3 as a novel osteoarthritis risk locus. *Human Molecular Genetics*, **2017**, 26, 3850-3858	5.6	34
56	A genome-wide copy number association study of osteoporotic fractures points to the 6p25.1 locus. *Journal of Medical Genetics*, **2014**, 51, 122-31	5.8	32

55	Eighty-eight variants highlight the role of T cell regulation and airway remodeling in asthma pathogenesis. *Nature Communications*, **2020**, 11, 393	17.4	29
54	A rare missense mutation in MYH6 associates with non-syndromic coarctation of the aorta. *European Heart Journal*, **2018**, 39, 3243-3249	9.5	29
53	Genome-wide association study yields variants at 20p12.2 that associate with urinary bladder cancer. *Human Molecular Genetics*, **2014**, 23, 5545-57	5.6	29
52	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, 173-9	6.3	27
51	Rare genomic structural variants in complex disease: lessons from the replication of associations with obesity. *PLoS ONE*, **2013**, 8, e58048	3.7	27
50	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. *Nature Genetics*, **2020**, 52, 1314-1332	36.3	26
49	Genetic variability in the absorption of dietary sterols affects the risk of coronary artery disease. *European Heart Journal*, **2020**, 41, 2618-2628	9.5	26
48	Disentangling the genetics of lean mass. *American Journal of Clinical Nutrition*, **2019**, 109, 276-287	7	24
47	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	38.6	24
46	Differences between germline genomes of monozygotic twins. *Nature Genetics*, **2021**, 53, 27-34	36.3	24
45	Genetic variants primarily associated with type 2 diabetes are related to coronary artery disease risk. *Atherosclerosis*, **2015**, 241, 419-26	3.1	23
44	FLT3 stop mutation increases FLT3 ligand level and risk of autoimmune thyroid disease. *Nature*, **2020**, 584, 619-623	50.4	23
43	Rare coding variants and X-linked loci associated with age at menarche. *Nature Communications*, **2015**, 6, 7756	17.4	23
42	Coding variants in and increase risk of atrial fibrillation. *Communications Biology*, **2018**, 1, 68	6.7	21
41	Genome-wide significant association between a sequence variant at 15q15.2 and lung cancer risk. *Cancer Research*, **2011**, 71, 1356-61	10.1	21
40	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, 2279-85	0.9	20
39	A drastic reduction in the life span of cystatin C L68Q carriers due to life-style changes during the last two centuries. *PLoS Genetics*, **2008**, 4, e1000099	6	20
38	Interstitial deletions including chromosome 3 common eliminated region 1 (C3CER1) prevail in human solid tumors from 10 different tissues. *Genes Chromosomes and Cancer*, **2004**, 41, 232-42	5	20

37	Insertion of an SVA-E retrotransposon into the CASP8 gene is associated with protection against prostate cancer. *Human Molecular Genetics*, **2016**, 25, 1008-18	5.6	18
36	A Splice Region Variant in LDLR Lowers Non-high Density Lipoprotein Cholesterol and Protects against Coronary Artery Disease. *PLoS Genetics*, **2015**, 11, e1005379	6	17
35	Large-scale integration of the plasma proteome with genetics and disease. *Nature Genetics*, **2021**, 53, 1712-1721	36.3	17
34	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. *Journal of Clinical Endocrinology and Metabolism*, **2020**, 105,	5.6	17
33	Adiposity-Dependent Regulatory Effects on Multi-tissue Transcriptomes. *American Journal of Human Genetics*, **2016**, 99, 567-579	11	17
32	Multi-ancestry GWAS of the electrocardiographic PR interval identifies 202 loci underlying cardiac conduction. *Nature Communications*, **2020**, 11, 2542	17.4	16
31	Association of Genetically Predicted Lipid Levels With the Extent of Coronary Atherosclerosis in Icelandic Adults. *JAMA Cardiology*, **2020**, 5, 13-20	16.2	15
30	Common sequence variants associated with coronary artery disease correlate with the extent of coronary atherosclerosis. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2015**, 35, 1526-31	9.4	14
29	Effect of sequence variants on variance in glucose levels predicts type 2 diabetes risk and accounts for heritability. *Nature Genetics*, **2017**, 49, 1398-1402	36.3	13
28	Sequence variants associating with urinary biomarkers. *Human Molecular Genetics*, **2019**, 28, 1199-1211	5.6	13
27	Roadmap for a precision-medicine initiative in the Nordic region. *Nature Genetics*, **2019**, 51, 924-930	36.3	12
26	Sequence variants with large effects on cardiac electrophysiology and disease. *Nature Communications*, **2019**, 10, 4803	17.4	12
25	A rare splice donor mutation in the haptoglobin gene associates with blood lipid levels and coronary artery disease. *Human Molecular Genetics*, **2017**, 26, 2364-2376	5.6	11
24	Loss of heterozygosity at the FHIT gene in different solid human tumours and its association with survival in colorectal cancer patients. *Anticancer Research*, **2002**, 22, 3205-12	2.3	11
23	Sequence Variants in TAAR5 and Other Loci Affect Human Odor Perception and Naming. *Current Biology*, **2020**, 30, 4643-4653.e3	6.3	10
22	Genetic insight into sick sinus syndrome. *European Heart Journal*, **2021**, 42, 1959-1971	9.5	7
21	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
20	The CRTAC1 Protein in Plasma Is Associated With Osteoarthritis and Predicts Progression to Joint Replacement: A Large-Scale Proteomics Scan in Iceland. *Arthritis and Rheumatology*, **2021**, 73, 2025-2034	9.5	6

19	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. *Human Genomics*, **2019**, 13, 37	6.8	5
18	Distinction between the effects of parental and fetal genomes on fetal growth. *Nature Genetics*, **2021**, 53, 1135-1142	36.3	5
17	Lifelong Reduction in LDL (Low-Density Lipoprotein) Cholesterol due to a Gain-of-Function Mutation in. *Circulation Genomic and Precision Medicine*, **2021**, 14, e003029	5.2	5
16	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	6.3	5
15	Identification of 371 genetic variants for age at first sex and birth linked to externalising behaviour. *Nature Human Behaviour*, **2021**,	12.8	5
14	Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2021**, 41, 2616-2628	9.4	4
13	Estimating heritability without environmental bias		3
12	Common and Rare Sequence Variants Influencing Tumor Biomarkers in Blood. *Cancer Epidemiology Biomarkers and Prevention*, **2020**, 29, 225-235	4	3
11	Loss-of-Function Variants in the Tumor-Suppressor Gene Confer Increased Cancer Risk. *Cancer Research*, **2021**, 81, 1954-1964	10.1	2
10	Reconstruction of a large-scale outbreak of SARS-CoV-2 infection in Iceland informs vaccination strategies.. *Clinical Microbiology and Infection*, **2022**,	9.5	2
9	Comment on "Evaluating the cardiovascular safety of sclerostin inhibition using evidence from meta-analysis of clinical trials and human genetics". *Science Translational Medicine*, **2021**, 13, eabe8497	17.5	1
8	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,	16.7	1
7	Genetic Predisposition to Coronary Artery Disease in Type 2 Diabetes Mellitus. *Circulation Genomic and Precision Medicine*, **2020**, 13, e002769	5.2	1
6	Allele frequency of variants reported to cause adenine phosphoribosyltransferase deficiency. *European Journal of Human Genetics*, **2021**, 29, 1061-1070	5.3	1
5	Germline variants at SOHLH2 influence multiple myeloma risk. *Blood Cancer Journal*, **2021**, 11, 76	7	1
4	Sequence variants in malignant hyperthermia genes in Iceland: classification and actionable findings in a population database. *European Journal of Human Genetics*, **2021**, 29, 1819-1824	5.3	0
3	Genetic variants associated with platelet count are predictive of human disease and physiological markers. *Communications Biology*, **2021**, 4, 1132	6.7	0
2	Cohort profile: Copenhagen Hospital Biobank - Cardiovascular Disease Cohort (CHB-CVDC): Construction of a large-scale genetic cohort to facilitate a better understanding of heart diseases. *BMJ Open*, **2021**, 11, e049709	3	0

1	Response by BjÐnsson et al to Letter Regarding Article, "Large-Scale Screening for Monogenic and Clinically Defined Familial Hypercholesterolemia in Iceland".. *Arteriosclerosis, Thrombosis, and Vascular Biology*, **2022**, 42, e46-e47	9.4