Eleftheria Zeggini

List of Publications by Citations

262 papers	37,613 citations	77 h-index	193 g-index
295 ext. papers	45,158 ext. citations	13.6 avg, IF	6.23 L-index

#	Paper	IF	Citations
262	A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. *Science*, **2007**, 316, 889-94	33.3	3294
261	Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes. *Science*, **2007**, 316, 1336-41	33.3	1823
260	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. *Nature Genetics*, **2010**, 42, 105-16	36.3	1673
259	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
258	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
257	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
256	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
255	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. *Nature Genetics*, **2009**, 41, 25-34	36.3	1368
254	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. *Nature Genetics*, **2007**, 39, 1329-37	36.3	1130
253	Common variants near MC4R are associated with fat mass, weight and risk of obesity. *Nature Genetics*, **2008**, 40, 768-75	36.3	1048
252	Genome-wide association study identifies eight loci associated with blood pressure. *Nature Genetics*, **2009**, 41, 666-76	36.3	970
251	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
250	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
249	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
248	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
247	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. *Nature*, **2010**, 464, 713-20	50.4	639
246	Variants in MTNR1B influence fasting glucose levels. *Nature Genetics*, **2009**, 41, 77-81	36.3	584

245	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
244	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	39	414
243	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
242	An evaluation of statistical approaches to rare variant analysis in genetic association studies. *Genetic Epidemiology*, **2010**, 34, 188-93	2.6	402
241	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. *Nature Genetics*, **2018**, 50, 1412-1425	36.3	386
240	Functional annotation of noncoding sequence variants. *Nature Methods*, **2014**, 11, 294-6	21.6	368
239	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
238	Leukemia-associated somatic mutations drive distinct patterns of age-related clonal hemopoiesis. *Cell Reports*, **2015**, 10, 1239-45	10.6	343
237	The African Genome Variation Project shapes medical genetics in Africa. *Nature*, **2015**, 517, 327-32	50.4	340
236	A common variant of HMGA2 is associated with adult and childhood height in the general population. *Nature Genetics*, **2007**, 39, 1245-50	36.3	330
235	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	6	326
234	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	39	310
233	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. *Lancet, The*, **2012**, 380, 815-23	40	275
232	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
231	Common variation in the FTO gene alters diabetes-related metabolic traits to the extent expected given its effect on BMI. *Diabetes*, **2008**, 57, 1419-26	0.9	260
230	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245
229	Assessing the combined impact of 18 common genetic variants of modest effect sizes on type 2 diabetes risk. *Diabetes*, **2008**, 57, 3129-35	0.9	245
228	Association analysis of 6,736 U.K. subjects provides replication and confirms TCF7L2 as a type 2 diabetes susceptibility gene with a substantial effect on individual risk. *Diabetes*, **2006**, 55, 2640-4	0.9	222

227	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
226	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
225	Combining information from common type 2 diabetes risk polymorphisms improves disease prediction. *PLoS Medicine*, **2006**, 3, e374	11.6	214
224	Mutation screening of the macrophage migration inhibitory factor gene: positive association of a functional polymorphism of macrophage migration inhibitory factor with juvenile idiopathic arthritis. *Arthritis and Rheumatism*, **2002**, 46, 2402-9		207
223	Common variants of the novel type 2 diabetes genes CDKAL1 and HHEX/IDE are associated with decreased pancreatic beta-cell function. *Diabetes*, **2007**, 56, 3101-4	0.9	203
222	Rare variant association analysis methods for complex traits. *Annual Review of Genetics*, **2010**, 44, 293-308	14.5	200
221	Meta-analysis in genome-wide association studies. *Pharmacogenomics*, **2009**, 10, 191-201	2.6	199
220	Whole-genome scan, in a complex disease, using 11,245 single-nucleotide polymorphisms: comparison with microsatellites. *American Journal of Human Genetics*, **2004**, 75, 54-64	11	198
219	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
218	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. *Nature Genetics*, **2019**, 51, 804-814	36.3	181
217	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
216	Replication in genome-wide association studies. *Statistical Science*, **2009**, 24, 561-573	2.4	177
215	Genome-wide association studies in type 2 diabetes. *Current Diabetes Reports*, **2009**, 9, 164-71	5.6	174
214	Genome-wide association analyses for lung function and chronic obstructive pulmonary disease identify new loci and potential druggable targets. *Nature Genetics*, **2017**, 49, 416-425	36.3	170
213	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. *Nature Genetics*, **2019**, 51, 481-493	36.3	156
212	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
211	Glucocorticoid sensitivity is determined by a specific glucocorticoid receptor haplotype. *Journal of Clinical Endocrinology and Metabolism*, **2004**, 89, 892-7	5.6	150
210	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. *Nature Genetics*, **2019**, 51, 230-236	36.3	143

209	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
208	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. *Nature Genetics*, **2015**, 47, 1272-1281	36.3	129
207	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. *Nature Genetics*, **2018**, 50, 549-558	36.3	122
206	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	30.4	119
205	Type 2 diabetes risk alleles are associated with reduced size at birth. *Diabetes*, **2009**, 58, 1428-33	0.9	117
204	A functional promoter haplotype of macrophage migration inhibitory factor is linked and associated with juvenile idiopathic arthritis. *Arthritis and Rheumatism*, **2004**, 50, 1604-10		115
203	Genomics of disease risk in globally diverse populations. *Nature Reviews Genetics*, **2019**, 20, 520-535	30.1	105
202	HLA-DRB1*11 and variants of the MHC class II locus are strong risk factors for systemic juvenile idiopathic arthritis. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 15970-5	11.5	103
201	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
200	A variant in MCF2L is associated with osteoarthritis. *American Journal of Human Genetics*, **2011**, 89, 446-50	11	102
199	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. *Diabetes*, **2009**, 58, 505-10	0.9	98
198	TCF7L2: the biggest story in diabetes genetics since HLA?. *Diabetologia*, **2007**, 50, 1-4	10.3	98
197	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. *Nature Genetics*, **2018**, 50, 172-174	36.3	97
196	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
195	Genetic architecture distinguishes systemic juvenile idiopathic arthritis from other forms of juvenile idiopathic arthritis: clinical and therapeutic implications. *Annals of the Rheumatic Diseases*, **2017**, 76, 906-913	2.4	89
194	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
193	Synthetic associations are unlikely to account for many common disease genome-wide association signals. *PLoS Biology*, **2011**, 9, e1000580	9.7	88
192	An evaluation of HapMap sample size and tagging SNP performance in large-scale empirical and simulated data sets. *Nature Genetics*, **2005**, 37, 1320-2	36.3	88

191	Interrogating type 2 diabetes genome-wide association data using a biological pathway-based approach. *Diabetes*, **2009**, 58, 1463-7	0.9	87
190	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. *Hypertension*, **2017**,	8.5	85
189	Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. *Annals of the Rheumatic Diseases*, **2011**, 70, 864-7	2.4	85
188	A combined functional annotation score for non-synonymous variants. *Human Heredity*, **2012**, 73, 47-51	1.1	79
187	Reply to Dlouha et al. *European Journal of Human Genetics*, **2010**, 18, 1275-1275	5.3	78
186	A novel common variant in DCST2 is associated with length in early life and height in adulthood. *Human Molecular Genetics*, **2015**, 24, 1155-68	5.6	77
185	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
184	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
183	Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*, **2015**, 47, 1352-1356	36.3	71
182	Association of FTO variants with BMI and fat mass in the self-contained population of Sorbs in Germany. *European Journal of Human Genetics*, **2010**, 18, 104-10	5.3	71
181	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. *Nature Communications*, **2013**, 4, 2872	17.4	70
180	Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants?. *Diabetologia*, **2009**, 52, 1846-51	10.3	69
179	Translational genomics and precision medicine: Moving from the lab to the clinic. *Science*, **2019**, 365, 1409-1413	33.3	68
178	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. *Diabetes*, **2015**, 64, 2467-76	0.9	66
177	In search of low-frequency and rare variants affecting complex traits. *Human Molecular Genetics*, **2013**, 22, R16-21	5.6	65
176	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. *Scientific Reports*, **2017**, 7, 8935	4.9	62
175	An association analysis of the HLA gene region in latent autoimmune diabetes in adults. *Diabetologia*, **2007**, 50, 68-73	10.3	62
174	Analysis of multiple data sets reveals no association between the insulin gene variable number tandem repeat element and polycystic ovary syndrome or related traits. *Journal of Clinical Endocrinology and Metabolism*, **2005**, 90, 2988-93	5.6	62

173	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. *PLoS Genetics*, **2016**, 12, e1006260	6	61
172	Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. *Nature Communications*, **2017**, 8, 15606	17.4	60
171	Underlying genetic models of inheritance in established type 2 diabetes associations. *American Journal of Epidemiology*, **2009**, 170, 537-45	3.8	60
170	Multi-ancestry genome-wide gene-smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. *Nature Genetics*, **2019**, 51, 636-648	36.3	59
169	Revisiting the thrifty gene hypothesis via 65 loci associated with susceptibility to type 2 diabetes. *American Journal of Human Genetics*, **2014**, 94, 176-85	11	59
168	Estimating genome-wide significance for whole-genome sequencing studies. *Genetic Epidemiology*, **2014**, 38, 281-90	2.6	58
167	Statistical methods to detect pleiotropy in human complex traits. *Open Biology*, **2017**, 7,	7	58
166	Linkage and association studies of single-nucleotide polymorphism-tagged tumor necrosis factor haplotypes in juvenile oligoarthritis. *Arthritis and Rheumatism*, **2002**, 46, 3304-11		57
165	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
164	Using population isolates in genetic association studies. *Briefings in Functional Genomics*, **2014**, 13, 371-7	4.9	55
163	Genetic architecture of human thinness compared to severe obesity. *PLoS Genetics*, **2019**, 15, e1007603	6	51
162	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
161	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. *Scientific Reports*, **2017**, 7, 11008	4.9	49
160	Trans-ethnic study design approaches for fine-mapping. *European Journal of Human Genetics*, **2016**, 24, 1330-6	5.3	48
159	The DOT1L rs12982744 polymorphism is associated with osteoarthritis of the hip with genome-wide statistical significance in males. *Annals of the Rheumatic Diseases*, **2013**, 72, 1264-5	2.4	48
158	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
157	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
156	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. *Nature Communications*, **2014**, 5, 5345	17.4	46

155	Synthetic associations in the context of genome-wide association scan signals. *Human Molecular Genetics*, **2010**, 19, R137-44	5.6	45
154	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. *Molecular Psychiatry*, **2020**, 25, 2392-2409	15.1	45
153	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
152	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
151	Genome-wide association analysis of eating disorder-related symptoms, behaviors, and personality traits. *American Journal of Medical Genetics Part B: Neuropsychiatric Genetics*, **2012**, 159B, 803-11	3.5	43
150	Advances in osteoarthritis genetics. *Journal of Medical Genetics*, **2013**, 50, 715-24	5.8	40
149	The variable number of tandem repeats upstream of the insulin gene is a susceptibility locus for latent autoimmune diabetes in adults. *Diabetes*, **2006**, 55, 1890-4	0.9	40
148	Large-scale studies of the association between variation at the TNF/LTA locus and susceptibility to type 2 diabetes. *Diabetologia*, **2005**, 48, 2013-7	10.3	40
147	ARIEL and AMELIA: testing for an accumulation of rare variants using next-generation sequencing data. *Human Heredity*, **2012**, 73, 84-94	1.1	39
146	A powerful approach to sub-phenotype analysis in population-based genetic association studies. *Genetic Epidemiology*, **2010**, 34, 335-43	2.6	39
145	Gene variants influencing measures of inflammation or predisposing to autoimmune and inflammatory diseases are not associated with the risk of type 2 diabetes. *Diabetologia*, **2008**, 51, 2205-13	10.3	38
144	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nature Communications*, **2017**, 8, 15927	17.4	37
143	Disparate genetic influences on polycystic ovary syndrome (PCOS) and type 2 diabetes revealed by a lack of association between common variants within the TCF7L2 gene and PCOS. *Diabetologia*, **2007**, 50, 2318-22	10.3	37
142	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. *Nature Communications*, **2019**, 10, 2054	17.4	36
141	The effect of next-generation sequencing technology on complex trait research. *European Journal of Clinical Investigation*, **2011**, 41, 561-7	4.6	36
140	Association studies of insulin receptor substrate 1 gene (IRS1) variants in type 2 diabetes samples enriched for family history and early age of onset. *Diabetes*, **2004**, 53, 3319-22	0.9	36
139	Evaluation of the genetic overlap between osteoarthritis with body mass index and height using genome-wide association scan data. *Annals of the Rheumatic Diseases*, **2013**, 72, 935-41	2.4	35
138	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

137	Large-scale association analysis of TNF/LTA gene region polymorphisms in type 2 diabetes. *BMC Medical Genetics*, **2010**, 11, 69	2.1	34
136	Association of HLA-DRB1*13 with susceptibility to uveitis in juvenile idiopathic arthritis in two independent data sets. *Rheumatology*, **2006**, 45, 972-4	3.9	34
135	Very low-depth whole-genome sequencing in complex trait association studies. *Bioinformatics*, **2019**, 35, 2555-2561	7.2	34
134	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. *Translational Psychiatry*, **2018**, 8, 252	8.6	34
133	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
132	Population-specific risk of type 2 diabetes conferred by HNF4A P2 promoter variants: a lesson for replication studies. *Diabetes*, **2008**, 57, 3161-5	0.9	33
131	Variation within the gene encoding the upstream stimulatory factor 1 does not influence susceptibility to type 2 diabetes in samples from populations with replicated evidence of linkage to chromosome 1q. *Diabetes*, **2006**, 55, 2541-8	0.9	33
130	The effect of FTO variation on increased osteoarthritis risk is mediated through body mass index: a Mendelian randomisation study. *Annals of the Rheumatic Diseases*, **2014**, 73, 2082-6	2.4	32
129	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, **2017**, 7, 4394	4.9	31
128	A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. *Diabetes*, **2017**, 66, 2019-2032	0.9	29
127	Genome-wide association scan allowing for epistasis in type 2 diabetes. *Annals of Human Genetics*, **2011**, 75, 10-9	2.2	29
126	Chronic obstructive pulmonary disease and related phenotypes: polygenic risk scores in population-based and case-control cohorts. *Lancet Respiratory Medicine,the*, **2020**, 8, 696-708	35.1	29
125	A new era for Type 2 diabetes genetics. *Diabetic Medicine*, **2007**, 24, 1181-6	3.5	28
124	Activating transcription factor 6 (ATF6) sequence polymorphisms in type 2 diabetes and pre-diabetic traits. *Diabetes*, **2007**, 56, 856-62	0.9	28
123	Replication of established common genetic variants for adult BMI and childhood obesity in Greek adolescents: the TEENAGE study. *Annals of Human Genetics*, **2013**, 77, 268-74	2.2	27
122	Rare variation at the TNFAIP3 locus and susceptibility to rheumatoid arthritis. *Human Genetics*, **2010**, 128, 627-33	6.3	27
121	Common variation in the LMNA gene (encoding lamin A/C) and type 2 diabetes: association analyses in 9,518 subjects. *Diabetes*, **2007**, 56, 879-83	0.9	27
120	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. *American Journal of Human Genetics*, **2016**, 99, 1316-1324	11	26

119	Genome-wide association study of developmental dysplasia of the hip identifies an association with. *Communications Biology*, **2018**, 1, 56	6.7	26
118	Genome-wide association analysis of imputed rare variants: application to seven common complex diseases. *Genetic Epidemiology*, **2012**, 36, 785-96	2.6	26
117	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
116	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
115	No evidence of an association between mitochondrial DNA variants and osteoarthritis in 7393 cases and 5122 controls. *Annals of the Rheumatic Diseases*, **2013**, 72, 136-9	2.4	25
114	The effect of genome-wide association scan quality control on imputation outcome for common variants. *European Journal of Human Genetics*, **2011**, 19, 610-4	5.3	25
113	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
112	Functional genomics in osteoarthritis: Past, present, and future. *Journal of Orthopaedic Research*, **2016**, 34, 1105-10	3.8	25
111	The transferability of lipid loci across African, Asian and European cohorts. *Nature Communications*, **2019**, 10, 4330	17.4	24
110	Whole exome re-sequencing implicates CCDC38 and cilia structure and function in resistance to smoking related airflow obstruction. *PLoS Genetics*, **2014**, 10, e1004314	6	24
109	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
108	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
107	Replication of Associations of Genetic Loci Outside the HLA Region With Susceptibility to Anti-Cyclic Citrullinated Peptide-Negative Rheumatoid Arthritis. *Arthritis and Rheumatology*, **2016**, 68, 1603-13	9.5	24
106	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. *Molecular Psychiatry*, **2018**, 23, 1169-1180	15.1	24
105	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	38.6	24
104	Linkage disequilibrium mapping of the replicated type 2 diabetes linkage signal on chromosome 1q. *Diabetes*, **2009**, 58, 1704-9	0.9	23
103	Polymorphisms in the glucokinase-associated, dual-specificity phosphatase 12 (DUSP12) gene under chromosome 1q21 linkage peak are associated with type 2 diabetes. *Diabetes*, **2006**, 55, 2631-9	0.9	23
102	A novel variant in is associated with osteoarthritis. *Annals of the Rheumatic Diseases*, **2018**, 77, 620-623	2.4	22

101	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
100	Significant linkage of BMI to chromosome 10p in the U.K. population and evaluation of GAD2 as a positional candidate. *Diabetes*, **2006**, 55, 1884-9	0.9	22
99	Analysis of the contribution to type 2 diabetes susceptibility of sequence variation in the gene encoding stearoyl-CoA desaturase, a key regulator of lipid and carbohydrate metabolism. *Diabetologia*, **2004**, 47, 2168-75	10.3	22
98	Rare and low frequency variant stratification in the UK population: description and impact on association tests. *PLoS ONE*, **2012**, 7, e46519	3.7	22
97	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. *Annals of the Rheumatic Diseases*, **2017**, 76, 1199-1206	2.4	21
96	Circulating beta-carotene levels and type 2 diabetes-cause or effect?. *Diabetologia*, **2009**, 52, 2117-21	10.3	21
95	Polymorphisms in the tumour necrosis factor gene are not associated with severity of inflammatory polyarthritis. *Annals of the Rheumatic Diseases*, **2004**, 63, 280-4	2.4	21
94	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. *Human Molecular Genetics*, **2016**, 25, 2070-2081	5.6	20
93	Genome-wide association scans for Type 2 diabetes: new insights into biology and therapy. *Trends in Pharmacological Sciences*, **2007**, 28, 598-601	13.2	20
92	Evidence for linkage of HLA loci in juvenile idiopathic oligoarthritis: independent effects of HLA-A and HLA-DRB1. *Arthritis and Rheumatism*, **2002**, 46, 2716-20		20
91	Maternal and fetal genetic contribution to gestational weight gain. *International Journal of Obesity*, **2018**, 42, 775-784	5.5	19
90	Pathways to understanding the genomic aetiology of osteoarthritis. *Human Molecular Genetics*, **2017**, 26, R193-R201	5.6	19
89	Examining the relationships between the Pro12Ala variant in PPARG and Type 2 diabetes-related traits in UK samples. *Diabetic Medicine*, **2005**, 22, 1696-700	3.5	19
88	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. *Nature Communications*, **2018**, 9, 4674	17.4	19
87	Lack of significant effects of the type 2 diabetes susceptibility loci JAZF1, CDC123/CAMK1D, NOTCH2, ADAMTS9, THADA, and TSPAN8/LGR5 on diabetes and quantitative metabolic traits. *Hormone and Metabolic Research*, **2010**, 42, 14-22	3.1	18
86	Sex-specific differences in effect size estimates at established complex trait loci. *International Journal of Epidemiology*, **2012**, 41, 1376-82	7.8	18
85	Toll-like receptor 4 gene polymorphisms and susceptibility to juvenile idiopathic arthritis. *Annals of the Rheumatic Diseases*, **2005**, 64, 767-9	2.4	18
84	Fine-mapping of an expanded set of type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps		18

83	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
82	Finding common susceptibility variants for complex disease: past, present and future. *Briefings in Functional Genomics & Proteomics*, **2009**, 8, 345-52		17
81	Relationship between E23K (an established type II diabetes-susceptibility variant within KCNJ11), polycystic ovary syndrome and androgen levels. *European Journal of Human Genetics*, **2007**, 15, 679-84	5.3	17
80	Evidence for a novel rheumatoid arthritis susceptibility locus on chromosome 6p. *Arthritis and Rheumatism*, **2004**, 50, 3823-30		17
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