Eleftheria Zeggini

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Insights into the genetic architecture of haematological traits from deep phenotyping and whole-genome sequencing for two Mediterranean isolated populations.. *Scientific Reports*, **2022**, 12, 1131	4.9	0
261	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology.. *Nature Communications*, **2022**, 13, 634	17.4	3
260	Insights into the molecular landscape of osteoarthritis in human tissues. *Current Opinion in Rheumatology*, **2022**, 34, 79-90	5.3	1
259	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy **2022**, 1, 157-173		2
258	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation.. *Nature Genetics*, **2022**,	36.3	7
257	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations.. *Molecular Metabolism*, **2022**, 101509	8.8	0
256	The Genetic Epidemiology of Joint Shape and the Development of Osteoarthritis. *Calcified Tissue International*, **2021**, 109, 257-276	3.9	6
255	The power of genetic diversity in genome-wide association studies of lipids. *Nature*, **2021**,	50.4	24
254	Mapping the serum proteome to neurological diseases using whole genome sequencing. *Nature Communications*, **2021**, 12, 7042	17.4	3
253	Linking chondrocyte and synovial transcriptional profile to clinical phenotype in osteoarthritis. *Annals of the Rheumatic Diseases*, **2021**,	2.4	5
252	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. *Nature Communications*, **2021**, 12, 2444	17.4	12
251	The trans-ancestral genomic architecture of glycemic traits. *Nature Genetics*, **2021**, 53, 840-860	36.3	44
250	A molecular quantitative trait locus map for osteoarthritis. *Nature Communications*, **2021**, 12, 1309	17.4	8
249	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. *Cell*, **2021**, 184, 4784-4818.e17	56.2	14
248	Accelerating functional gene discovery in osteoarthritis. *Nature Communications*, **2021**, 12, 467	17.4	12
247	Whole-genome sequencing analysis of the cardiometabolic proteome. *Nature Communications*, **2020**, 11, 6336	17.4	7
246	Biomedical Research Goes Viral: Dangers and Opportunities. *Cell*, **2020**, 181, 1189-1193	56.2	4

245	Exome Sequencing Identifies Genes and Gene Sets Contributing to Severe Childhood Obesity, Linking PHIP Variants to Repressed POMC Transcription. *Cell Metabolism*, **2020**, 31, 1107-1119.e12	24.6	16
244	The influence of rare variants in circulating metabolic biomarkers. *PLoS Genetics*, **2020**, 16, e1008605	6	3
243	Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. *Trends in Molecular Medicine*, **2020**, 26, 232-241	11.5	10
242	Population-wide copy number variation calling using variant call format files from 6,898 individuals. *Genetic Epidemiology*, **2020**, 44, 79-89	2.6	1
241	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. *PLoS Genetics*, **2020**, 16, e1008718	6	25
240	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
239	The use of technology in the subcategorisation of osteoarthritis: a Delphi study approach. *Osteoarthritis and Cartilage Open*, **2020**, 2, 100081	1.5	3
238	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
237	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
236	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identify as novel osteoarthritis gene. *Annals of the Rheumatic Diseases*, **2020**,	2.4	7
235	The transferability of lipid loci across African, Asian and European cohorts. *Nature Communications*, **2019**, 10, 4330	17.4	24
234	Translational genomics and precision medicine: Moving from the lab to the clinic. *Science*, **2019**, 365, 1409-1413	33.3	68
233	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. *Nature Communications*, **2019**, 10, 357	17.4	12
232	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. *Nature Genetics*, **2019**, 51, 230-236	36.3	143
231	Genetic architecture of human thinness compared to severe obesity. *PLoS Genetics*, **2019**, 15, e1007603	6	51
230	Genomics of disease risk in globally diverse populations. *Nature Reviews Genetics*, **2019**, 20, 520-535	30.1	105
229	Mendelian Randomization Analysis Reveals a Causal Influence of Circulating Sclerostin Levels on Bone Mineral Density and Fractures. *Journal of Bone and Mineral Research*, **2019**, 34, 1824-1836	6.3	11
228	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. *Nature Communications*, **2019**, 10, 2054	17.4	36

227	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
226	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
225	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
224	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. *Cell*, **2019**, 179, 984-1002.e36	56.2	76
223	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. *Nature Genetics*, **2019**, 51, 452-469	36.3	44
222	A Dietary Pattern with High Sugar Content Is Associated with Cardiometabolic Risk Factors in the Pomak Population. *Nutrients*, **2019**, 11,	6.7	3
221	The 2018 Otto Aufranc Award: How Does Genome-wide Variation Affect Osteolysis Risk After THA?. *Clinical Orthopaedics and Related Research*, **2019**, 477, 297-309	2.2	6
220	Very low-depth whole-genome sequencing in complex trait association studies. *Bioinformatics*, **2019**, 35, 2555-2561	7.2	34
219	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. *Nature Genetics*, **2019**, 51, 51-62	36.3	152
218	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
217	A novel variant in is associated with osteoarthritis. *Annals of the Rheumatic Diseases*, **2018**, 77, 620-623	2.4	22
216	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. *Nature Genetics*, **2018**, 50, 172-174	36.3	97
215	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. *Nature Genetics*, **2018**, 50, 549-558	36.3	122
214	Maternal and fetal genetic contribution to gestational weight gain. *International Journal of Obesity*, **2018**, 42, 775-784	5.5	19
213	Combination therapy as a potential risk factor for the development of type 2 diabetes in patients with schizophrenia: the GOMAP study. *BMC Psychiatry*, **2018**, 18, 249	4.2	2
212	Genome-wide association study of developmental dysplasia of the hip identifies an association with. *Communications Biology*, **2018**, 1, 56	6.7	26
211	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. *Rheumatology*, **2018**, 57, 1481-1489	3.9	14
210	Meta-analysis of exome array data identifies six novel genetic loci for lung function. *Wellcome Open Research*, **2018**, 3, 4	4.8	16

209	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
208	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. *Molecular Psychiatry*, **2018**, 23, 1169-1180	15.1	24
207	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. *Nature Communications*, **2018**, 9, 4674	17.4	19
206	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. *Translational Psychiatry*, **2018**, 8, 252	8.6	34
205	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
204	ProxECAT: Proxy External Controls Association Test. A new case-control gene region association test using allele frequencies from public controls. *PLoS Genetics*, **2018**, 14, e1007591	6	13
203	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
202	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. *International Journal of Epidemiology*, **2017**, 46, 894-904	7.8	25
201	Rare and low-frequency coding variants alter human adult height. *Nature*, **2017**, 542, 186-190	50.4	412
200	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
199	Familial Hypercholesterolemia and Type 2 Diabetes in the Old Order Amish. *Diabetes*, **2017**, 66, 2054-2058	8.9	15
198	Discovery of novel heart rate-associated loci using the Exome Chip. *Human Molecular Genetics*, **2017**, 26, 2346-2363	5.6	17
197	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. *Annals of the Rheumatic Diseases*, **2017**, 76, 1199-1206	2.4	21
196	Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. *Nature Communications*, **2017**, 8, 15606	17.4	60
195	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. *American Journal of Human Genetics*, **2017**, 100, 865-884	11	74
194	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. *Diabetes*, **2017**, 66, 2888-2902	8.9	414
193	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
192	The mountainous Cretan dietary patterns and their relationship with cardiovascular risk factors: the Hellenic Isolated Cohorts MANOLIS study. *Public Health Nutrition*, **2017**, 20, 1063-1074	3.3	10

191	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
190	Exome-wide association study of plasma lipids in >300,000 individuals. *Nature Genetics*, **2017**, 49, 1758-1766	36.3	310
189	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475 000 Individuals. *Circulation: Cardiovascular Genetics*, **2017**, 10,		33
188	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. *Scientific Reports*, **2017**, 7, 11008	4.9	49
187	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. *Scientific Reports*, **2017**, 7, 8935	4.9	62
186	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
185	Association analyses based on false discovery rate implicate new loci for coronary artery disease. *Nature Genetics*, **2017**, 49, 1385-1391	36.3	361
184	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. *Nature Communications*, **2017**, 8, 15927	17.4	37
183	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. *Scientific Reports*, **2017**, 7, 4394	4.9	31
182	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. *Scientific Data*, **2017**, 4, 170179	8.2	22
181	Pathways to understanding the genomic aetiology of osteoarthritis. *Human Molecular Genetics*, **2017**, 26, R193-R201	5.6	19
180	Statistical methods to detect pleiotropy in human complex traits. *Open Biology*, **2017**, 7,	7	58
179	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
178	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
177	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. *Nature Communications*, **2016**, 7, 13357	17.4	46
176	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. *American Journal of Human Genetics*, **2016**, 99, 1316-1324	11	26
175	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. *Nature Genetics*, **2016**, 48, 1151-1161	36.3	181
174	Trans-ethnic study design approaches for fine-mapping. *European Journal of Human Genetics*, **2016**, 24, 1330-6	5.3	48

173	Whole-exome sequencing in an isolated population from the Dalmatian island of Vis. *European Journal of Human Genetics*, **2016**, 24, 1479-87	5.3	5
172	Very low-depth sequencing in a founder population identifies a cardioprotective APOC3 signal missed by genome-wide imputation. *Human Molecular Genetics*, **2016**, 25, 2360-2365	5.6	14
171	Insights into metabolic disease from studying genetics in isolated populations: stories from Greece to Greenland. *Diabetologia*, **2016**, 59, 938-41	10.3	8
170	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
169	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. *PLoS Genetics*, **2016**, 12, e1006260	6	61
168	The genetic architecture of type 2 diabetes. *Nature*, **2016**, 536, 41-47	50.4	704
167	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. *Nature Genetics*, **2016**, 48, 1303-1312	36.3	51
166	Genome-wide associations for birth weight and correlations with adult disease. *Nature*, **2016**, 538, 248-252	50.4	266
165	Functional genomics in osteoarthritis: Past, present, and future. *Journal of Orthopaedic Research*, **2016**, 34, 1105-10	3.8	25
164	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
163	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
162	Directional dominance on stature and cognition in diverse human populations. *Nature*, **2015**, 523, 459-462	50.4	119
161	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
160	Meta-Analysis of Rare Variants **2015**, 215-226		1
159	The UK10K project identifies rare variants in health and disease. *Nature*, **2015**, 526, 82-90	50.4	776
158	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
157	Height-reducing variants and selection for short stature in Sardinia. *Nature Genetics*, **2015**, 47, 1352-1356	36.3	71
156	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

155	The African Genome Variation Project shapes medical genetics in Africa. *Nature*, **2015**, 517, 327-32	50.4	340
154	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. *Genetic Epidemiology*, **2015**, 39, 624-34	2.6	3
153	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
152	Whole-genome sequence-based analysis of thyroid function. *Nature Communications*, **2015**, 6, 5681	17.4	56
151	Leukemia-associated somatic mutations drive distinct patterns of age-related clonal hemopoiesis. *Cell Reports*, **2015**, 10, 1239-45	10.6	343
150	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
149	Functional annotation of noncoding sequence variants. *Nature Methods*, **2014**, 11, 294-6	21.6	368
148	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
147	Estimating genome-wide significance for whole-genome sequencing studies. *Genetic Epidemiology*, **2014**, 38, 281-90	2.6	58
146	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. *Nature Communications*, **2014**, 5, 4871	17.4	46
145	Using population isolates in genetic association studies. *Briefings in Functional Genomics*, **2014**, 13, 371-7	4.9	55
144	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
143	Using genetically isolated populations to understand the genomic basis of disease. *Genome Medicine*, **2014**, 6, 83	14.4	15
142	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
141	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. *Nature Communications*, **2014**, 5, 5345	17.4	46
140	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
139	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
138	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

137	Genome-wide association study for osteoarthritis □AuthorsOreply. *Lancet, The*, **2013**, 381, 373	40	2
136	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. *Nature Communications*, **2013**, 4, 2872	17.4	70
135	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
134	Advances in osteoarthritis genetics. *Journal of Medical Genetics*, **2013**, 50, 715-24	5.8	40
133	In search of low-frequency and rare variants affecting complex traits. *Human Molecular Genetics*, **2013**, 22, R16-21	5.6	65
132	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
131	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
130	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
129	Reply to "Human genetic studies on osteoarthritis from cliniciansOviewpoints". *Osteoarthritis and Cartilage*, **2012**, 20, 250-1; author reply 252	6.2	1
128	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. *Lancet, The*, **2012**, 380, 815-23	40	275
127	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
126	Genome-wide meta-analysis of common variant differences between men and women. *Human Molecular Genetics*, **2012**, 21, 4805-15	5.6	24
125	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
124	Genome-wide association analysis of imputed rare variants: application to seven common complex diseases. *Genetic Epidemiology*, **2012**, 36, 785-96	2.6	26
123	Imputation of rare variants in next-generation association studies. *Human Heredity*, **2012**, 74, 196-204	1.1	10
122	A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **2012**, 7, e29202	3.7	138
121	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
120	Sex-specific differences in effect size estimates at established complex trait loci. *International Journal of Epidemiology*, **2012**, 41, 1376-82	7.8	18

119	An evaluation of different meta-analysis approaches in the presence of allelic heterogeneity. *European Journal of Human Genetics*, **2012**, 20, 709-12	5.3	14
118	A combined functional annotation score for non-synonymous variants. *Human Heredity*, **2012**, 73, 47-51	1.1	79
117	ARIEL and AMELIA: testing for an accumulation of rare variants using next-generation sequencing data. *Human Heredity*, **2012**, 73, 84-94	1.1	39
116	Rare variant association testing for next-generation sequencing data via hierarchical clustering. *Human Heredity*, **2012**, 74, 165-71	1.1	3
115	Genome-wide association study to identify common variants associated with brachial circumference: a meta-analysis of 14 cohorts. *PLoS ONE*, **2012**, 7, e31369	3.7	2
114	Rare and low frequency variant stratification in the UK population: description and impact on association tests. *PLoS ONE*, **2012**, 7, e46519	3.7	22
113	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
112	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
111	The effect of next-generation sequencing technology on complex trait research. *European Journal of Clinical Investigation*, **2011**, 41, 561-7	4.6	36
110	Genome-wide association scan allowing for epistasis in type 2 diabetes. *Annals of Human Genetics*, **2011**, 75, 10-9	2.2	29
109	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
108	A variant in MCF2L is associated with osteoarthritis. *American Journal of Human Genetics*, **2011**, 89, 446-50	11	102
107	Defining the power limits of genome-wide association scan meta-analyses. *Genetic Epidemiology*, **2011**, 35, 781-9	2.6	14
106	Examining the overlap between genome-wide rare variant association signals and linkage peaks in rheumatoid arthritis. *Arthritis and Rheumatism*, **2011**, 63, 1522-6		7
105	Synthetic associations are unlikely to account for many common disease genome-wide association signals. *PLoS Biology*, **2011**, 9, e1000580	9.7	88
104	Do genome-wide association scans have potential for translation?. *Clinical Chemistry and Laboratory Medicine*, **2011**, 50, 255-60	5.9	4
103	An evaluation of different target enrichment methods in pooled sequencing designs for complex disease association studies. *PLoS ONE*, **2011**, 6, e26279	3.7	11
102	An evaluation of power to detect low-frequency variant associations using allele-matching tests that account for uncertainty. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing* , **2011**, 100-5	1.3	1

101	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
100	Reply to Dlouha et al. *European Journal of Human Genetics*, **2010**, 18, 1275-1275	5.3	78
99	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
98	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. *Nature Genetics*, **2010**, 42, 142-8	36.3	527
97	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. *Nature Genetics*, **2010**, 42, 579-89	36.3	1449
96	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
95	Synthetic associations in the context of genome-wide association scan signals. *Human Molecular Genetics*, **2010**, 19, R137-44	5.6	45
94	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
93	Rare variant association analysis methods for complex traits. *Annual Review of Genetics*, **2010**, 44, 293-308	14.5	200
92	Rare variation at the TNFAIP3 locus and susceptibility to rheumatoid arthritis. *Human Genetics*, **2010**, 128, 627-33	6.3	27
91	CCRaVAT and QuTie-enabling analysis of rare variants in large-scale case control and quantitative trait association studies. *BMC Bioinformatics*, **2010**, 11, 527	3.6	14
90	An evaluation of statistical approaches to rare variant analysis in genetic association studies. *Genetic Epidemiology*, **2010**, 34, 188-93	2.6	402
89	A powerful approach to sub-phenotype analysis in population-based genetic association studies. *Genetic Epidemiology*, **2010**, 34, 335-43	2.6	39
88	Large-scale association analysis of TNF/LTA gene region polymorphisms in type 2 diabetes. *BMC Medical Genetics*, **2010**, 11, 69	2.1	34
87	Testing for rare variant associations in complex diseases. *Genome Medicine*, **2009**, 1, 24	14.4	9
86	Finding common susceptibility variants for complex disease: past, present and future. *Briefings in Functional Genomics & Proteomics*, **2009**, 8, 345-52		17
85	Interrogating type 2 diabetes genome-wide association data using a biological pathway-based approach. *Diabetes*, **2009**, 58, 1463-7	0.9	87
84	Underlying genetic models of inheritance in established type 2 diabetes associations. *American Journal of Epidemiology*, **2009**, 170, 537-45	3.8	60

83	Adiposity-related heterogeneity in patterns of type 2 diabetes susceptibility observed in genome-wide association data. *Diabetes*, **2009**, 58, 505-10	0.9	98
82	Linkage disequilibrium mapping of the replicated type 2 diabetes linkage signal on chromosome 1q. *Diabetes*, **2009**, 58, 1704-9	0.9	23
81	Ranking of genome-wide association scan signals by different measures. *International Journal of Epidemiology*, **2009**, 38, 1364-73	7.8	9
80	Type 2 diabetes risk alleles are associated with reduced size at birth. *Diabetes*, **2009**, 58, 1428-33	0.9	117
79	Genome-wide association studies in type 2 diabetes. *Current Diabetes Reports*, **2009**, 9, 164-71	5.6	174
78	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
77	Circulating beta-carotene levels and type 2 diabetes-cause or effect?. *Diabetologia*, **2009**, 52, 2117-21	10.3	21
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12	A reference panel of 64,976 haplotypes for genotype imputation		15

11	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes	4
10	Very low depth whole genome sequencing in complex trait association studies	9
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8	Osteocyte Transcriptome Mapping Identifies a Molecular Landscape Controlling Skeletal Homeostasis and Susceptibility to Skeletal Disease	3
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6	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
5	New genetic signals for lung function highlight pathways and pleiotropy, and chronic obstructive pulmonary disease associations across multiple ancestries	5
4	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank	2
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2	Decoding the genomic basis of osteoarthritis	4
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