Eleftheria Zeggini

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/9210758/publications.pdf

Version: 2024-02-01

255 papers	50,346 citations	4955 84 h-index	1856 209 g-index
295 all docs	295 docs citations	295 times ranked	49290 citing authors

#	Article	IF	Citations
1	A Common Variant in the FTO Gene Is Associated with Body Mass Index and Predisposes to Childhood and Adult Obesity. Science, 2007, 316, 889-894.	6.0	3,884
2	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	9.4	2,421
3	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	6.0	2,040
4	New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk. Nature Genetics, 2010, 42, 105-116.	9.4	1,982
5	Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes. Nature Genetics, 2012, 44, 981-990.	9.4	1,748
6	Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nature Genetics, 2008, 40, 638-645.	9.4	1,683
7	Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589.	9.4	1,631
8	Six new loci associated with body mass index highlight a neuronal influence on body weight regulation. Nature Genetics, 2009, 41, 25-34.	9.4	1,572
9	Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. Nature Genetics, 2018, 50, 1505-1513.	9.4	1,331
10	Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337.	9.4	1,298
11	Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775.	9.4	1,179
12	Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676.	9.4	1,104
13	The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90.	13.7	1,014
14	Genome-wide trans-ancestry meta-analysis provides insight into the genetic architecture of type 2 diabetes susceptibility. Nature Genetics, 2014, 46, 234-244.	9.4	959
15	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
16	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	9.4	924
17	Genome-wide association study of CNVs in 16,000 cases of eight common diseases and 3,000 shared controls. Nature, 2010, 464, 713-720.	13.7	737
18	Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81.	9.4	662

#	Article	IF	Citations
19	An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902.	0.3	615
20	Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148.	9.4	591
21	Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391.	9.4	571
22	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	13.7	544
23	Functional annotation of noncoding sequence variants. Nature Methods, 2014, 11, 294-296.	9.0	493
24	The African Genome Variation Project shapes medical genetics in Africa. Nature, 2015, 517, 327-332.	13.7	473
25	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	9.4	470
26	An evaluation of statistical approaches to rare variant analysis in genetic association studies. Genetic Epidemiology, 2010, 34, 188-193.	0.6	452
27	Leukemia-Associated Somatic Mutations Drive Distinct Patterns of Age-Related Clonal Hemopoiesis. Cell Reports, 2015, 10, 1239-1245.	2.9	443
28	Novel Loci for Adiponectin Levels and Their Influence on Type 2 Diabetes and Metabolic Traits: A Multi-Ethnic Meta-Analysis of 45,891 Individuals. PLoS Genetics, 2012, 8, e1002607.	1.5	419
29	Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252.	13.7	406
30	Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814.	9.4	402
31	A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250.	9.4	373
32	Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823.	6.3	373
33	Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571.	9.4	356
34	The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679.	13.7	353
35	New genetic signals for lung function highlight pathways and chronic obstructive pulmonary disease associations across multiple ancestries. Nature Genetics, 2019, 51, 481-493.	9.4	350
36	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, 769-781.	5.2	346

#	Article	IF	Citations
37	The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860.	9.4	341
38	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	1.5	331
39	Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236.	9.4	331
40	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	9.4	328
41	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	9.4	286
42	Assessing the Combined Impact of 18 Common Genetic Variants of Modest Effect Sizes on Type 2 Diabetes Risk. Diabetes, 2008, 57, 3129-3135.	0.3	279
43	Common Variation in the FTO Gene Alters Diabetes-Related Metabolic Traits to the Extent Expected Given Its Effect on BMI. Diabetes, 2008, 57, 1419-1426.	0.3	277
44	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	9.4	261
45	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.	9.4	257
46	Multi-ancestry genetic study of type 2 diabetes highlights the power of diverse populations for discovery and translation. Nature Genetics, 2022, 54, 560-572.	9.4	250
47	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, 2402-2409.	6.7	242
48	Combining Information from Common Type 2 Diabetes Risk Polymorphisms Improves Disease Prediction. PLoS Medicine, 2006, 3, e374.	3.9	242
49	Association Analysis of 6,736 U.K. Subjects Provides Replication and ConfirmsTCF7L2as a Type 2 Diabetes Susceptibility Gene With a Substantial Effect on Individual Risk. Diabetes, 2006, 55, 2640-2644.	0.3	240
50	Rare Variant Association Analysis Methods for Complex Traits. Annual Review of Genetics, 2010, 44, 293-308.	3.2	238
51	Replication in Genome-Wide Association Studies. Statistical Science, 2009, 24, 561-573.	1.6	237
52	Meta-analysis in genome-wide association studies. Pharmacogenomics, 2009, 10, 191-201.	0.6	227
53	Common Variants of the Novel Type 2 Diabetes GenesCDKAL1andHHEX/IDEAre Associated With Decreased Pancreatic Î²-Cell Function. Diabetes, 2007, 56, 3101-3104.	0.3	226
54	Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558.	9.4	223

#	Article	IF	Citations
55	Genomics of disease risk in globally diverse populations. Nature Reviews Genetics, 2019, 20, 520-535.	7.7	217
56	Genome-wide association studies in type 2 diabetes. Current Diabetes Reports, 2009, 9, 164-171.	1.7	213
57	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.	2.6	209
58	A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202.	1.1	197
59	Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281.	9.4	193
60	Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17.	13.5	188
61	Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462.	13.7	173
62	Glucocorticoid Sensitivity Is Determined by a Specific Glucocorticoid Receptor Haplotype. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 892-897.	1.8	163
63	Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174.	9.4	156
64	Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36.	13.5	152
65	HLA-DRB1*11and 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, 15970-15975.	3.3	139
66	Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433.	0.3	135
67	Translational genomics and precision medicine: Moving from the lab to the clinic. Science, 2019, 365, 1409-1413.	6.0	133
68	Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884.	2.6	131
69	Meta-analysis of genome-wide association studies confirms a susceptibility locus for knee osteoarthritis on chromosome 7q22. Annals of the Rheumatic Diseases, 2011, 70, 349-355.	0.5	126
70	A functional promoter haplotype of macrophage migration inhibitory factor is linked and associated with juvenile idiopathic arthritis. Arthritis and Rheumatism, 2004, 50, 1604-1610.	6.7	124
71	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.	0.5	123
72	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	1.3	123

#	Article	IF	Citations
73	Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. Annals of the Rheumatic Diseases, 2011, 70, 864-867.	0.5	119
74	A Variant in MCF2L Is Associated with Osteoarthritis. American Journal of Human Genetics, 2011, 89, 446-450.	2.6	115
75	Statistical methods to detect pleiotropy in human complex traits. Open Biology, 2017, 7, 170125.	1.5	113
76	Multi-ancestry genome-wide geneâ€“smoking interaction study of 387,272 individuals identifies new loci associated with serum lipids. Nature Genetics, 2019, 51, 636-648.	9.4	112
77	TCF7L2: the biggest story in diabetes genetics since HLA?. Diabetologia, 2006, 50, 1-4.	2.9	110
78	Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510.	0.3	109
79	A novel common variant in DCST2 is associated with length in early life and height in adulthood. Human Molecular Genetics, 2015, 24, 1155-1168.	1.4	109
80	Assessment of Osteoarthritis Candidate Genes in a Metaâ€Analysis of Nine Genomeâ€Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949.	2.9	108
81	A meta-analysis of genome-wide association studies identifies novel variants associated with osteoarthritis of the hip. Annals of the Rheumatic Diseases, 2014, 73, 2130-2136.	0.5	108
82	Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. PLoS Biology, 2011, 9, e1000580.	2.6	102
83	An evaluation of HapMap sample size and tagging SNP performance in large-scale empirical and simulated data sets. Nature Genetics, 2005, 37, 1320-1322.	9.4	101
84	Genetic architecture of human thinness compared to severe obesity. PLoS Genetics, 2019, 15, e1007603.	1.5	98
85	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	9.4	96
86	Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718.	1.5	95
87	Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467.	0.3	93
88	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	9.4	91
89	A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51.	0.4	90
90	Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. Scientific Reports, 2017, 7, 8935.	1.6	90

#	Article	IF	Citations
91	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	9.4	89
92	Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008.	1.6	88
93	Is the thrifty genotype hypothesis supported by evidence based on confirmed type 2 diabetes- and obesity-susceptibility variants?. Diabetologia, 2009, 52, 1846-1851.	2.9	85
94	Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409.	4.1	83
95	Using population isolates in genetic association studies. Briefings in Functional Genomics, 2014, 13, 371-377.	1.3	82
96	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, 104-110.	1.4	81
97	Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. Nature Communications, 2017, 8, 15606.	5.8	79
98	A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872.	5.8	77
99	Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. PLoS Genetics, 2016, 12, e1006260.	1.5	76
100	Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681.	5.8	75
101	Trans-ethnic study design approaches for fine-mapping. European Journal of Human Genetics, 2016, 24, 1330-1336.	1.4	75
102	The transferability of lipid loci across African, Asian and European cohorts. Nature Communications, 2019, 10, 4330.	5.8	75
103	Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. Diabetes, 2015, 64, 2467-2476.	0.3	74
104	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74
105	GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054.	5.8	74
106	Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. Translational Psychiatry, 2018, 8, 252.	2.4	73
107	An association analysis of the HLA gene region in latent autoimmune diabetes in adults. Diabetologia, 2006, 50, 68-73.	2.9	72
108	Revisiting the Thrifty Gene Hypothesis via 65 Loci Associated with Susceptibility to Type 2 Diabetes. American Journal of Human Genetics, 2014, 94, 176-185.	2.6	72

#	Article	IF	Citations
109	Estimating Genomeâ€Wide Significance for Wholeâ€Genome Sequencing Studies. Genetic Epidemiology, 2014, 38, 281-290.	0.6	72
110	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, 2988-2993.	1.8	70
111	In search of low-frequency and rare variants affecting complex traits. Human Molecular Genetics, 2013, 22, R16-R21.	1.4	70
112	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.	5.2	69
113	Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561.	1.8	68
114	Linkage and association studies of single-nucleotide polymorphism-tagged tumor necrosis factor haplotypes in juvenile oligoarthritis. Arthritis and Rheumatism, 2002, 46, 3304-3311.	6.7	66
115	The effect ofFTOvariation on increased osteoarthritis risk is mediated through body mass index: a mendelian randomisation study. Annals of the Rheumatic Diseases, 2014, 73, 2082-2086.	0.5	66
116	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	9.4	66
117	Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927.	5.8	64
118	Underlying Genetic Models of Inheritance in Established Type 2 Diabetes Associations. American Journal of Epidemiology, 2009, 170, 537-545.	1.6	63
119	A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871.	5.8	62
120	Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345.	5.8	60
121	Next-generation association studies for complex traits. Nature Genetics, 2011, 43, 287-288.	9.4	59
122	The effect of next-generation sequencing technology on complex trait research. European Journal of Clinical Investigation, 2011, 41, 561-567.	1.7	58
123	Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nature Communications, 2021, 12, 2444.	5.8	58
124	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.	1.4	56
125	Synthetic associations in the context of genome-wide association scan signals. Human Molecular Genetics, 2010, 19, R137-R144.	1.4	53
126	A molecular quantitative trait locus map for osteoarthritis. Nature Communications, 2021, 12, 1309.	5.8	53

#	Article	IF	Citations
127	A powerful approach to subâ€phenotype analysis in populationâ€based genetic association studies. Genetic Epidemiology, 2010, 34, 335-343.	0.6	52
128	Genomeâ€wide association analysis of eating disorderâ€related symptoms, behaviors, and personality traits. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2012, 159B, 803-811.	1.1	52
129	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, 935-941.	0.5	52
130	ARIEL and AMELIA: Testing for an Accumulation of Rare Variants Using Next-Generation Sequencing Data. Human Heredity, 2012, 73, 84-94.	0.4	51
131	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, 1264-1265.	0.5	51
132	Advances in osteoarthritis genetics: TableÂ1. Journal of Medical Genetics, 2013, 50, 715-724.	1.5	51
133	Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394.	1.6	50
134	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
135	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
136	Large-scale studies of the association between variation at the TNF/LTA locus and susceptibility to type 2 diabetes. Diabetologia, 2005, 48, 2013-2017.	2.9	45
137	Genome-wide association study of developmental dysplasia of the hip identifies an association with GDF5. Communications Biology, 2018, 1, 56.	2.0	45
138	The Variable Number of Tandem Repeats Upstream of the Insulin Gene Is a Susceptibility Locus for Latent Autoimmune Diabetes in Adults. Diabetes, 2006, 55, 1890-1894.	0.3	43
139	Association of HLA-DRB1*13 with susceptibility to uveitis in juvenile idiopathic arthritis in two independent data sets. Rheumatology, 2006, 45, 972-974.	0.9	42
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, 3319-3322.	0.3	41
141	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, 2205-2213.	2.9	41
142	Large-scale association analysis of TNF/LTA gene region polymorphisms in type 2 diabetes. BMC Medical Genetics, 2010, 11, 69.	2.1	40
143	No evidence of an association between mitochondrial DNA variants and osteoarthritis in 7393 cases and 5122 controls. Annals of the Rheumatic Diseases, 2013, 72, 136-139.	0.5	39
144	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, 2318-2322.	2.9	38

#	Article	IF	Citations
145	Pathways to understanding the genomic aetiology of osteoarthritis. Human Molecular Genetics, 2017, 26, R193-R201.	1.4	38
146	Whole-genome sequencing analysis of the cardiometabolic proteome. Nature Communications, 2020, 11, 6336.	5.8	38
147	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.	7.2	38
148	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, 2541-2548.	0.3	37
149	Population-Specific Risk of Type 2 Diabetes Conferred by HNF4A P2 Promoter Variants: A Lesson for Replication Studies. Diabetes, 2008, 57, 3161-3165.	0.3	37
150	Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. American Journal of Human Genetics, 2016, 99, 1316-1324.	2.6	37
151	Genomeâ€Wide Association Analysis of Imputed Rare Variants: Application to Seven Common Complex Diseases. Genetic Epidemiology, 2012, 36, 785-796.	0.6	36
152	Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318.	0.9	36
153	Maternal and fetal genetic contribution to gestational weight gain. International Journal of Obesity, 2018, 42, 775-784.	1.6	36
154	Common Variation in the LMNA Gene (Encoding Lamin A/C) and Type 2 Diabetes: Association Analyses in 9,518 Subjects. Diabetes, 2007, 56, 879-883.	0.3	34
155	A new era for TypeÂ2 diabetes genetics. Diabetic Medicine, 2007, 24, 1181-1186.	1.2	34
156	Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. Annals of Human Genetics, 2011, 75, 10-19.	0.3	34
157	Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815.	1.4	33
158	Replication of Associations of Genetic Loci Outside the HLA Region With Susceptibility to Antiâ€“Cyclic Citrullinated Peptideâ€“Negative Rheumatoid Arthritis. Arthritis and Rheumatology, 2016, 68, 1603-1613.	2.9	33
159	Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674.	5.8	33
160	Accelerating functional gene discovery in osteoarthritis. Nature Communications, 2021, 12, 467.	5.8	33
161	Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180.	4.1	32
162	Activating Transcription Factor 6 (ATF6) Sequence Polymorphisms in Type 2 Diabetes and Pre-Diabetic Traits. Diabetes, 2007, 56, 856-862.	0.3	31

#	Article	IF	Citations
163	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
164	Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. Trends in Molecular Medicine, 2020, 26, 232-241.	3.5	31
165	Polymorphisms in the tumour necrosis factor gene are not associated with severity of inflammatory polyarthritis. Annals of the Rheumatic Diseases, 2004, 63, 280-284.	0.5	30
166	Linkage Disequilibrium Mapping of the Replicated Type 2 Diabetes Linkage Signal on Chromosome 1q. Diabetes, 2009, 58, 1704-1709.	0.3	30
167	Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357.	5.8	30
168	Rare variation at the TNFAIP3 locus and susceptibility to rheumatoid arthritis. Human Genetics, 2010, 128, 627-633.	1.8	29
169	Replication of Established Common Genetic Variants for Adult BMI and Childhood Obesity in Greek Adolescents: The TEENAGE Study. Annals of Human Genetics, 2013, 77, 268-274.	0.3	29
170	Whole Exome Re-Sequencing Implicates CCDC38 and Cilia Structure and Function in Resistance to Smoking Related Airflow Obstruction. PLoS Genetics, 2014, 10, e1004314.	1.5	29
171	Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363.	1.4	29
172	Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. Annals of the Rheumatic Diseases, 2017, 76, 1199-1206.	0.5	29
173	Mapping the serum proteome to neurological diseases using whole genome sequencing. Nature Communications, 2021, 12, 7042.	5.8	29
174	Functional genomics in osteoarthritis: Past, present, and future. Journal of Orthopaedic Research, 2016, 34, 1105-1110.	1.2	28
175	Familial Hypercholesterolemia and Type 2 Diabetes in the Old Order Amish. Diabetes, 2017, 66, 2054-2058.	0.3	28
176	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, 2168-2175.	2.9	27
177	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, 2631-2639.	0.3	27
178	The effect of genome-wide association scan quality control on imputation outcome for common variants. European Journal of Human Genetics, 2011, 19, 610-614.	1.4	27
179	A novel variant in GLIS3 is associated with osteoarthritis. Annals of the Rheumatic Diseases, 2018, 77, 620-623.	0.5	27
180	Using genetically isolated populations to understand the genomic basis of disease. Genome Medicine, 2014, 6, 83.	3.6	26

#	Article	IF	Citations
181	Genome-wide association of phenotypes based on clustering patterns of hand osteoarthritis identifyWNT9Aas novel osteoarthritis gene. Annals of the Rheumatic Diseases, 2021, 80, 367-375.	0.5	26
182	Evidence for linkage of HLA loci in juvenile idiopathic oligoarthritis: Independent effects of HLA-A and HLA-DRB1. Arthritis and Rheumatism, 2002, 46, 2716-2720.	6.7	25
183	Linking chondrocyte and synovial transcriptional profile to clinical phenotype in osteoarthritis. Annals of the Rheumatic Diseases, 2021, 80, 1070-1074.	0.5	25
184	Significant Linkage of BMI to Chromosome 10p in the U.K. Population and Evaluation of GAD2 as a Positional Candidate. Diabetes, 2006, 55, 1884-1889.	0.3	24
185	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.	3.1	24
186	Examining the relationships between the Pro12Ala variant in PPARG and Type 2 diabetes-related traits in UK samples. Diabetic Medicine, 2005, 22, 1696-1700.	1.2	23
187	Toll-like receptor 4 gene polymorphisms and susceptibility to juvenile idiopathic arthritis. Annals of the Rheumatic Diseases, 2005, 64, 767-769.	0.5	23
188	Genome-wide association scans for Type 2 diabetes: new insights into biology and therapy. Trends in Pharmacological Sciences, 2007, 28, 598-601.	4.0	23
189	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.	1.5	23
190	Rare and Low Frequency Variant Stratification in the UK Population: Description and Impact on Association Tests. PLoS ONE, 2012, 7, e46519.	1.1	23
191	Circulating Î²-carotene levels and type 2 diabetesâ€"cause or effect?. Diabetologia, 2009, 52, 2117-2121.	2.9	22
192	Imputation of Rare Variants in Next-Generation Association Studies. Human Heredity, 2012, 74, 196-204.	0.4	22
193	Extensive identification of genes involved in congenital and structural heart disorders and cardiomyopathy. , 2022, 1, 157-173.		22
194	Lack of Significant Effects of the Type 2 Diabetes Susceptibility LociJAZF1,CDC123/CAMK1D,NOTCH2,ADAMTS9,THADA, andTSPAN8/LGR5on Diabetes and Quantitative Metabolic Traits. Hormone and Metabolic Research, 2010, 42, 14-22.	0.7	21
195	Very low-depth sequencing in a founder population identifies a cardioprotectiveAPOC3signal missed by genome-wide imputation. Human Molecular Genetics, 2016, 25, 2360-2365.	1.4	21
196	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
197	Rare SLC13A1 variants associate with intervertebral disc disorder highlighting role of sulfate in disc pathology. Nature Communications, 2022, 13, 634.	5.8	21
198	Using multivariable Mendelian randomization to estimate the causal effect of bone mineral density on osteoarthritis risk, independently of body mass index. International Journal of Epidemiology, 2022, 51, 1254-1267.	0.9	20

#	Article	IF	Citations
199	Family-based analysis of vitamin D receptor gene polymorphisms and type 1 diabetes in the population of South Croatia. Journal of Human Genetics, 2008, 53, 210-214.	1.1	19
200	Finding common susceptibility variants for complex disease: past, present and future. Briefings in Functional Genomics & Proteomics, 2009, 8, 345-352.	3.8	19
201	Sex-specific differences in effect size estimates at established complex trait loci. International Journal of Epidemiology, 2012, 41, 1376-1382.	0.9	19
202	Widespread epigenomic, transcriptomic and proteomic differences between hip osteophytic and articular chondrocytes in osteoarthritis. Rheumatology, 2018, 57, 1481-1489.	0.9	19
203	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 2018, 3, 4.	0.9	19
204	Evidence for a novel rheumatoid arthritis susceptibility locus on chromosome 6p. Arthritis and Rheumatism, 2004, 50, 3823-3830.	6.7	18
205	Defining the power limits of genomeâ€wide association scan metaâ€analyses. Genetic Epidemiology, 2011, 35, 781-789.	0.6	18
206	Epistatic interactions between HLA-DRB1 and interleukin 4, but not interferon-gamma, increase susceptibility to giant cell arteritis. Journal of Rheumatology, 2004, 31, 2413-7.	1.0	18
207	Paraoxonase 2 (PON2) polymorphisms and development of renal dysfunction in type 2 diabetes: UKPDS 76. Diabetologia, 2006, 49, 2892-2899.	2.9	17
208	Genetics of type 2 diabetes. Current Diabetes Reports, 2006, 6, 147-154.	1.7	17
209	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, 679-684.	1.4	17
210	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.	1.1	17
211	The Genetic Epidemiology of Joint Shape and the Development of Osteoarthritis. Calcified Tissue International, 2021, 109, 257-276.	1.5	17
212	CCRaVAT and QuTie - enabling analysis of rare variants in large-scale case control and quantitative trait association studies. BMC Bioinformatics, 2010, 11, 527.	1.2	15
213	A molecular map of long non-coding RNA expression, isoform switching and alternative splicing in osteoarthritis. Human Molecular Genetics, 2022, 31, 2090-2105.	1.4	15
214	Family-based analysis of tumor necrosis factor and lymphotoxin-Î± tag polymorphisms with type 1 diabetes in the population of South Croatia. Human Immunology, 2009, 70, 195-199.	1.2	14
215	An evaluation of different meta-analysis approaches in the presence of allelic heterogeneity. European Journal of Human Genetics, 2012, 20, 709-712.	1.4	14
216	Insights into the molecular landscape of osteoarthritis in human tissues. Current Opinion in Rheumatology, 2022, 34, 79-90.	2.0	13

#	Article	IF	Citations
217	An epigenome-wide view of osteoarthritis in primary tissues. American Journal of Human Genetics, 2022, 109, 1255-1271.	2.6	13
218	An Evaluation of Different Target Enrichment Methods in Pooled Sequencing Designs for Complex Disease Association Studies. PLoS ONE, 2011, 6, e26279.	1.1	12
219	Tumour necrosis factor receptor II polymorphism and juvenile idiopathic arthritis. British Journal of Rheumatology, 2002, 41, 462-465.	2.5	11
220	Testing for rare variant associations in complex diseases. Genome Medicine, 2011, 3, 24.	3.6	11
221	Whole-exome sequencing in an isolated population from the Dalmatian island of Vis. European Journal of Human Genetics, 2016, 24, 1479-1487.	1.4	11
222	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	11
223	Risk Assessment for Hip and Knee Osteoarthritis Using Polygenic Risk Scores. Arthritis and Rheumatology, 2022, 74, 1488-1496.	2.9	11
224	Characterisation of the genomic architecture of human chromosome 17q and evaluation of different methods for haplotype block definition. BMC Genetics, 2005, 6, 21.	2.7	9
225	Ranking of genome-wide association scan signals by different measures. International Journal of Epidemiology, 2009, 38, 1364-1373.	0.9	9
226	A Dietary Pattern with High Sugar Content Is Associated with Cardiometabolic Risk Factors in the Pomak Population. Nutrients, 2019, 11, 3043.	1.7	9
227	The influence of rare variants in circulating metabolic biomarkers. PLoS Genetics, 2020, 16, e1008605.	1.5	9
228	MCP-1 gene haplotype association in biopsy proven giant cell arteritis. Journal of Rheumatology, 2005, 32, 507-10.	1.0	9
229	Insights into metabolic disease from studying genetics in isolated populations: stories from Greece to Greenland. Diabetologia, 2016, 59, 938-941.	2.9	8
230	The 2018 Otto Aufranc Award: How Does Genome-wide Variation Affect Osteolysis Risk After THA?. Clinical Orthopaedics and Related Research, 2019, 477, 297-309.	0.7	8
231	Examining the overlap between genome-wide rare variant association signals and linkage peaks in rheumatoid arthritis. Arthritis and Rheumatism, 2011, 63, 1522-1526.	6.7	7
232	The use of technology in the subcategorisation of osteoarthritis: a Delphi study approach. Osteoarthritis and Cartilage Open, 2020, 2, 100081.	0.9	7
233	Do genome-wide association scans have potential for translation?. Clinical Chemistry and Laboratory Medicine, 2012, 50, 255-60.	1.4	6
234	Biomedical Research Goes Viral: Dangers and Opportunities. Cell, 2020, 181, 1189-1193.	13.5	6

#	Article	IF	Citations
235	Linkage and association studies of discoidin domain receptor 1 (DDR1) single nucleotide polymorphisms (SNPs) in juvenile oligoarthritis. Rheumatology, 2004, 43, 1138-1141.	0.9	5
236	Rare Variant Association Testing for Next-Generation Sequencing Data via Hierarchical Clustering. Human Heredity, 2012, 74, 165-171.	0.4	5
237	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.	1.1	5
238	Identifying Susceptibility Variants for Type 2 Diabetes. Methods in Molecular Biology, 2007, 376, 235-250.	0.4	5
239	Lack of association between juvenile idiopathic arthritis and fas gene polymorphism. Journal of Rheumatology, 2002, 29, 166-8.	1.0	5
240	Genome-wide association study for osteoarthritis â€“ Authors' reply. Lancet, The, 2013, 381, 373.	6.3	4
241	A Bayesian Approach to the Overlap Analysis of Epidemiologically Linked Traits. Genetic Epidemiology, 2015, 39, 624-634.	0.6	4
242	Populationâ€wide copy number variation calling using variant call format files from 6,898 individuals. Genetic Epidemiology, 2020, 44, 79-89.	0.6	3
243	Genome-Wide Association Study to Identify Common Variants Associated with Brachial Circumference: A Meta-Analysis of 14 Cohorts. PLoS ONE, 2012, 7, e31369.	1.1	3
244	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. Molecular Metabolism, 2022, 61, 101509.	3.0	3
245	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.	1.6	2
246	Genetics of early-life head circumference and genetic correlations with neurological, psychiatric and cognitive outcomes. BMC Medical Genomics, 2022, 15, .	0.7	2
247	Fas mRNA EXPRESSION IN BLOOD IS REDUCED DURING EPISODES OF HUMAN CORNEAL GRAFT REJECTION1. Transplantation, 2001, 71, 702-705.	0.5	1
248	Reply to â€œHuman genetic studies on osteoarthritis from cliniciansâ€™ viewpointsâ€• Osteoarthritis and Cartilage, 2012, 20, 250-251.	0.6	1
249	Meta-Analysis of Rare Variants. , 2015, , 215-226.		1
250	Meta-analysis of exome array data identifies six novel genetic loci for lung function. Wellcome Open Research, 0, 3, 4.	0.9	1
251	AN EVALUATION OF POWER TO DETECT LOW-FREQUENCY VARIANT ASSOCIATIONS USING ALLELE-MATCHING TESTS THAT ACCOUNT FOR UNCERTAINTY. , 2010, , 100-105.		1
252	Type 2 diabetes genetics: starting to solve the puzzle. Practical Diabetes International: the International Journal for Diabetes Care Teams Worldwide, 2008, 25, 214-215.	0.2	0

#	Article	IF	Citations
253	Reply to Dlouha et al. European Journal of Human Genetics, 2010, 18, 1275-1275.	1.4	0
254	Type 2 diabetes. , 2009, , 326-336.		0
255	Identifying Susceptibility Variants for Type 2 Diabetes. , 0, , 235-250.		0