# Eleftheria Zeggini

List of Publications by Year
in descending order



| 255 | 50,346 | 4960 84 | 1857 209 |
|---|---|---|---|
| papers | citations | h-index | g-index |

| 295 | 295 | 295 | 49290 |
|---|---|---|---|
| all docs | docs citations | times ranked | 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. | 12.6 | 3,884 |
| 2 | A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283. | 21.4 | 2,421 |
| 3 | Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341. | 12.6 | 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. | 21.4 | 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. | 21.4 | 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. | 21.4 | 1,683 |
| 7 | Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis. Nature Genetics, 2010, 42, 579-589. | 21.4 | 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. | 21.4 | 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. | 21.4 | 1,331 |
| 10 | Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nature Genetics, 2007, 39, 1329-1337. | 21.4 | 1,298 |
| 11 | Common variants near MC4R are associated with fat mass, weight and risk of obesity. Nature Genetics, 2008, 40, 768-775. | 21.4 | 1,179 |
| 12 | Genome-wide association study identifies eight loci associated with blood pressure. Nature Genetics, 2009, 41, 666-676. | 21.4 | 1,104 |
| 13 | The UK10K project identifies rare variants in health and disease. Nature, 2015, 526, 82-90. | 27.8 | 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. | 21.4 | 959 |
| 15 | The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47. | 27.8 | 952 |
| 16 | Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425. | 21.4 | 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. | 27.8 | 737 |
| 18 | Variants in MTNR1B influence fasting glucose levels. Nature Genetics, 2009, 41, 77-81. | 21.4 | 662 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. Diabetes, 2017, 66, 2888-2902. | 0.6 | 615 |
| 20 | Genetic variation in GIPR influences the glucose and insulin responses to an oral glucose challenge. Nature Genetics, 2010, 42, 142-148. | 21.4 | 591 |
| 21 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. Nature Genetics, 2017, 49, 1385-1391. | 21.4 | 571 |
| 22 | Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190. | 27.8 | 544 |
| 23 | Functional annotation of noncoding sequence variants. Nature Methods, 2014, 11, 294-296. | 19.0 | 493 |
| 24 | The African Genome Variation Project shapes medical genetics in Africa. Nature, 2015, 517, 327-332. | 27.8 | 473 |
| 25 | Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766. | 21.4 | 470 |
| 26 | An evaluation of statistical approaches to rare variant analysis in genetic association studies. Genetic Epidemiology, 2010, 34, 188-193. | 1.3 | 452 |
| 27 | Leukemia-Associated Somatic Mutations Drive Distinct Patterns of Age-Related Clonal Hemopoiesis. Cell Reports, 2015, 10, 1239-1245. | 6.4 | 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. | 3.5 | 419 |
| 29 | Genome-wide associations for birth weight and correlations with adult disease. Nature, 2016, 538, 248-252. | 27.8 | 406 |
| 30 | Maternal and fetal genetic effects on birth weight and their relevance to cardio-metabolic risk factors. Nature Genetics, 2019, 51, 804-814. | 21.4 | 402 |
| 31 | A common variant of HMGA2 is associated with adult and childhood height in the general population. Nature Genetics, 2007, 39, 1245-1250. | 21.4 | 373 |
| 32 | Identification of new susceptibility loci for osteoarthritis (arcOGEN): a genome-wide association study. Lancet, The, 2012, 380, 815-823. | 13.7 | 373 |
| 33 | Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. Nature Genetics, 2018, 50, 559-571. | 21.4 | 356 |
| 34 | The power of genetic diversity in genome-wide association studies of lipids. Nature, 2021, 600, 675-679. | 27.8 | 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. | 21.4 | 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. | 10.7 | 346 |

| # | Article | IF | Citations |
|---|---|---|---|
| 37 | The trans-ancestral genomic architecture of glycemic traits. Nature Genetics, 2021, 53, 840-860. | 21.4 | 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. | 3.5 | 331 |
| 39 | Identification of new therapeutic targets for osteoarthritis through genome-wide analyses of UK Biobank data. Nature Genetics, 2019, 51, 230-236. | 21.4 | 331 |
| 40 | Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62. | 21.4 | 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. | 21.4 | 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. | 0.6 | 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. | 0.6 | 277 |
| 44 | Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161. | 21.4 | 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. | 21.4 | 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. | 21.4 | 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. | 8.4 | 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. | 0.6 | 240 |
| 50 | Rare Variant Association Analysis Methods for Complex Traits. Annual Review of Genetics, 2010, 44, 293-308. | 7.6 | 238 |
| 51 | Replication in Genome-Wide Association Studies. Statistical Science, 2009, 24, 561-573. | 2.8 | 237 |
| 52 | Meta-analysis in genome-wide association studies. Pharmacogenomics, 2009, 10, 191-201. | 1.3 | 227 |
| 53 | Common Variants of the Novel Type 2 Diabetes GenesCDKAL1andHHEX/IDEAre Associated With Decreased Pancreatic Î²-Cell Function. Diabetes, 2007, 56, 3101-3104. | 0.6 | 226 |
| 54 | Genome-wide analyses using UK Biobank data provide insights into the genetic architecture of osteoarthritis. Nature Genetics, 2018, 50, 549-558. | 21.4 | 223 |

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|---|---|---|---|
| 55 | Genomics of disease risk in globally diverse populations. Nature Reviews Genetics, 2019, 20, 520-535. | 16.3 | 217 |
| 56 | Genome-wide association studies in type 2 diabetes. Current Diabetes Reports, 2009, 9, 164-171. | 4.2 | 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. | 6.2 | 209 |
| 58 | A Genome-Wide Association Search for Type 2 Diabetes Genes in African Americans. PLoS ONE, 2012, 7, e29202. | 2.5 | 197 |
| 59 | Genome sequencing elucidates Sardinian genetic architecture and augments association analyses for lipid and blood inflammatory markers. Nature Genetics, 2015, 47, 1272-1281. | 21.4 | 193 |
| 60 | Deciphering osteoarthritis genetics across 826,690 individuals from 9 populations. Cell, 2021, 184, 4784-4818.e17. | 28.9 | 188 |
| 61 | Directional dominance on stature and cognition inÂdiverse human populations. Nature, 2015, 523, 459-462. | 27.8 | 173 |
| 62 | Glucocorticoid Sensitivity Is Determined by a Specific Glucocorticoid Receptor Haplotype. Journal of Clinical Endocrinology and Metabolism, 2004, 89, 892-897. | 3.6 | 163 |
| 63 | Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. Nature Genetics, 2018, 50, 172-174. | 21.4 | 156 |
| 64 | Uganda Genome Resource Enables Insights into Population History and Genomic Discovery in Africa. Cell, 2019, 179, 984-1002.e36. | 28.9 | 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. | 7.1 | 139 |
| 66 | Type 2 Diabetes Risk Alleles Are Associated With Reduced Size at Birth. Diabetes, 2009, 58, 1428-1433. | 0.6 | 135 |
| 67 | Translational genomics and precision medicine: Moving from the lab to the clinic. Science, 2019, 365, 1409-1413. | 12.6 | 133 |
| 68 | Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884. | 6.2 | 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. | 0.9 | 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. | 0.9 | 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, . | 2.7 | 123 |

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|---|---|---|---|
| 73 | Insights into the genetic architecture of osteoarthritis from stage 1 of the arcOGEN study. Annals of the Rheumatic Diseases, 2011, 70, 864-867. | 0.9 | 119 |
| 74 | A Variant in MCF2L Is Associated with Osteoarthritis. American Journal of Human Genetics, 2011, 89, 446-450. | 6.2 | 115 |
| 75 | Statistical methods to detect pleiotropy in human complex traits. Open Biology, 2017, 7, 170125. | 3.6 | 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. | 21.4 | 112 |
| 77 | TCF7L2: the biggest story in diabetes genetics since HLA?. Diabetologia, 2006, 50, 1-4. | 6.3 | 110 |
| 78 | Adiposity-Related Heterogeneity in Patterns of Type 2 Diabetes Susceptibility Observed in Genome-Wide Association Data. Diabetes, 2009, 58, 505-510. | 0.6 | 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. | 2.9 | 109 |
| 80 | Assessment of Osteoarthritis Candidate Genes in a Metaâ€Analysis of Nine Genomeâ€Wide Association Studies. Arthritis and Rheumatology, 2014, 66, 940-949. | 5.6 | 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. | 0.9 | 108 |
| 82 | Synthetic Associations Are Unlikely to Account for Many Common Disease Genome-Wide Association Signals. PLoS Biology, 2011, 9, e1000580. | 5.6 | 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. | 21.4 | 101 |
| 84 | Genetic architecture of human thinness compared to severe obesity. PLoS Genetics, 2019, 15, e1007603. | 3.5 | 98 |
| 85 | Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356. | 21.4 | 96 |
| 86 | Novel loci for childhood body mass index and shared heritability with adult cardiometabolic traits. PLoS Genetics, 2020, 16, e1008718. | 3.5 | 95 |
| 87 | Interrogating Type 2 Diabetes Genome-Wide Association Data Using a Biological Pathway-Based Approach. Diabetes, 2009, 58, 1463-1467. | 0.6 | 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. | 21.4 | 91 |
| 89 | A Combined Functional Annotation Score for Non-Synonymous Variants. Human Heredity, 2012, 73, 47-51. | 0.8 | 90 |
| 90 | Integrative epigenomics, transcriptomics and proteomics of patient chondrocytes reveal genes and pathways involved in osteoarthritis. Scientific Reports, 2017, 7, 8935. | 3.3 | 90 |

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|---|---|---|---|
| 91 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469. | 21.4 | 89 |
| 92 | Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. Scientific Reports, 2017, 7, 11008. | 3.3 | 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. | 6.3 | 85 |
| 94 | Meta-analysis of up to 622,409 individuals identifies 40 novel smoking behaviour associated genetic loci. Molecular Psychiatry, 2020, 25, 2392-2409. | 7.9 | 83 |
| 95 | Using population isolates in genetic association studies. Briefings in Functional Genomics, 2014, 13, 371-377. | 2.7 | 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. | 2.8 | 81 |
| 97 | Whole genome sequencing and imputation in isolated populations identify genetic associations with medically-relevant complex traits. Nature Communications, 2017, 8, 15606. | 12.8 | 79 |
| 98 | A rare functional cardioprotective APOC3 variant has risen in frequency in distinct population isolates. Nature Communications, 2013, 4, 2872. | 12.8 | 77 |
| 99 | Novel Genetic Variants for Cartilage Thickness and Hip Osteoarthritis. PLoS Genetics, 2016, 12, e1006260. | 3.5 | 76 |
| 100 | Whole-genome sequence-based analysis of thyroid function. Nature Communications, 2015, 6, 5681. | 12.8 | 75 |
| 101 | Trans-ethnic study design approaches for fine-mapping. European Journal of Human Genetics, 2016, 24, 1330-1336. | 2.8 | 75 |
| 102 | The transferability of lipid loci across African, Asian and European cohorts. Nature Communications, 2019, 10, 4330. | 12.8 | 75 |
| 103 | Dietary Intake, FTO Genetic Variants, and Adiposity: A Combined Analysis of Over 16,000 Children and Adolescents. Diabetes, 2015, 64, 2467-2476. | 0.6 | 74 |
| 104 | A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357. | 12.8 | 74 |
| 105 | GWAS of bone size yields twelve loci that also affect height, BMD, osteoarthritis or fractures. Nature Communications, 2019, 10, 2054. | 12.8 | 74 |
| 106 | Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. Translational Psychiatry, 2018, 8, 252. | 4.8 | 73 |
| 107 | An association analysis of the HLA gene region in latent autoimmune diabetes in adults. Diabetologia, 2006, 50, 68-73. | 6.3 | 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. | 6.2 | 72 |

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|---|---|---|---|
| 109 | Estimating Genomeâ€Wide Significance for Wholeâ€Genome Sequencing Studies. Genetic Epidemiology, 2014, 38, 281-290. | 1.3 | 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. | 3.6 | 70 |
| 111 | In search of low-frequency and rare variants affecting complex traits. Human Molecular Genetics, 2013, 22, R16-R21. | 2.9 | 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. | 10.7 | 69 |
| 113 | Very low-depth whole-genome sequencing in complex trait association studies. Bioinformatics, 2019, 35, 2555-2561. | 4.1 | 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. | 0.9 | 66 |
| 116 | Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312. | 21.4 | 66 |
| 117 | Enrichment of low-frequency functional variants revealed by whole-genome sequencing of multiple isolated European populations. Nature Communications, 2017, 8, 15927. | 12.8 | 64 |
| 118 | Underlying Genetic Models of Inheritance in Established Type 2 Diabetes Associations. American Journal of Epidemiology, 2009, 170, 537-545. | 3.4 | 63 |
| 119 | A rare variant in APOC3 is associated with plasma triglyceride and VLDL levels in Europeans. Nature Communications, 2014, 5, 4871. | 12.8 | 62 |
| 120 | Genetic characterization of Greek population isolates reveals strong genetic drift at missense and trait-associated variants. Nature Communications, 2014, 5, 5345. | 12.8 | 60 |
| 121 | Next-generation association studies for complex traits. Nature Genetics, 2011, 43, 287-288. | 21.4 | 59 |
| 122 | The effect of next-generation sequencing technology on complex trait research. European Journal of Clinical Investigation, 2011, 41, 561-567. | 3.4 | 58 |
| 123 | Osteocyte transcriptome mapping identifies a molecular landscape controlling skeletal homeostasis and susceptibility to skeletal disease. Nature Communications, 2021, 12, 2444. | 12.8 | 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. | 2.9 | 56 |
| 125 | Synthetic associations in the context of genome-wide association scan signals. Human Molecular Genetics, 2010, 19, R137-R144. | 2.9 | 53 |
| 126 | A molecular quantitative trait locus map for osteoarthritis. Nature Communications, 2021, 12, 1309. | 12.8 | 53 |

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|---|---|---|---|
| 127 | A powerful approach to subâ€phenotype analysis in populationâ€based genetic association studies. Genetic Epidemiology, 2010, 34, 335-343. | 1.3 | 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. | 1.7 | 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. | 0.9 | 52 |
| 130 | ARIEL and AMELIA: Testing for an Accumulation of Rare Variants Using Next-Generation Sequencing Data. Human Heredity, 2012, 73, 84-94. | 0.8 | 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. | 0.9 | 51 |
| 132 | Advances in osteoarthritis genetics: TableÂ1. Journal of Medical Genetics, 2013, 50, 715-724. | 3.2 | 51 |
| 133 | Rare Variant Analysis of Human and Rodent Obesity Genes in Individuals with Severe Childhood Obesity. Scientific Reports, 2017, 7, 4394. | 3.3 | 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. | 0.6 | 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. | 6.3 | 45 |
| 137 | Genome-wide association study of developmental dysplasia of the hip identifies an association with GDF5. Communications Biology, 2018, 1, 56. | 4.4 | 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. | 0.6 | 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. | 1.9 | 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. | 0.6 | 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. | 6.3 | 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. | 0.9 | 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. | 6.3 | 38 |

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|---|---|---|---|
| 145 | Pathways to understanding the genomic aetiology of osteoarthritis. Human Molecular Genetics, 2017, 26, R193-R201. | 2.9 | 38 |
| 146 | Whole-genome sequencing analysis of the cardiometabolic proteome. Nature Communications, 2020, 11, 6336. | 12.8 | 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. | 16.2 | 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. | 0.6 | 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. | 0.6 | 37 |
| 150 | Chad Genetic Diversity Reveals an African History Marked by Multiple Holocene Eurasian Migrations. American Journal of Human Genetics, 2016, 99, 1316-1324. | 6.2 | 37 |
| 151 | Genomeâ€Wide Association Analysis of Imputed Rare Variants: Application to Seven Common Complex Diseases. Genetic Epidemiology, 2012, 36, 785-796. | 1.3 | 36 |
| 152 | Evidence for large-scale gene-by-smoking interaction effects on pulmonary function. International Journal of Epidemiology, 2017, 46, dyw318. | 1.9 | 36 |
| 153 | Maternal and fetal genetic contribution to gestational weight gain. International Journal of Obesity, 2018, 42, 775-784. | 3.4 | 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. | 0.6 | 34 |
| 155 | A new era for TypeÂ2 diabetes genetics. Diabetic Medicine, 2007, 24, 1181-1186. | 2.3 | 34 |
| 156 | Genome-Wide Association Scan Allowing for Epistasis in Type 2 Diabetes. Annals of Human Genetics, 2011, 75, 10-19. | 0.8 | 34 |
| 157 | Genome-wide meta-analysis of common variant differences between men and women. Human Molecular Genetics, 2012, 21, 4805-4815. | 2.9 | 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. | 5.6 | 33 |
| 159 | Cohort-wide deep whole genome sequencing and the allelic architecture of complex traits. Nature Communications, 2018, 9, 4674. | 12.8 | 33 |
| 160 | Accelerating functional gene discovery in osteoarthritis. Nature Communications, 2021, 12, 467. | 12.8 | 33 |
| 161 | Investigation of common, low-frequency and rare genome-wide variation in anorexia nervosa. Molecular Psychiatry, 2018, 23, 1169-1180. | 7.9 | 32 |
| 162 | Activating Transcription Factor 6 (ATF6) Sequence Polymorphisms in Type 2 Diabetes and Pre-Diabetic Traits. Diabetes, 2007, 56, 856-862. | 0.6 | 31 |

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|---|---|---|---|
| 163 | Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179. | 5.3 | 31 |
| 164 | Strengthening Causal Inference for Complex Disease Using Molecular Quantitative Trait Loci. Trends in Molecular Medicine, 2020, 26, 232-241. | 6.7 | 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. | 0.9 | 30 |
| 166 | Linkage Disequilibrium Mapping of the Replicated Type 2 Diabetes Linkage Signal on Chromosome 1q. Diabetes, 2009, 58, 1704-1709. | 0.6 | 30 |
| 167 | Low-frequency variation in TP53 has large effects on head circumference and intracranial volume. Nature Communications, 2019, 10, 357. | 12.8 | 30 |
| 168 | Rare variation at the TNFAIP3 locus and susceptibility to rheumatoid arthritis. Human Genetics, 2010, 128, 627-633. | 3.8 | 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. | 0.8 | 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. | 3.5 | 29 |
| 171 | Discovery of novel heart rate-associated loci using the Exome Chip. Human Molecular Genetics, 2017, 26, 2346-2363. | 2.9 | 29 |
| 172 | Radiographic endophenotyping in hip osteoarthritis improves the precision of genetic association analysis. Annals of the Rheumatic Diseases, 2017, 76, 1199-1206. | 0.9 | 29 |
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