# Alisa K Manning

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/7299283/publications.pdf

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| 62 | 7,715 | 147801 | 149698 |
|---|---|---|---|
| papers | citations | 31 h-index | 56 g-index |

| 75 | 75 | 75 | 16075 |
|---|---|---|---|
| all docs | docs citations | times ranked | citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299. | 27.8 | 1,069 |
| 2 | The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47. | 27.8 | 952 |
| 3 | A genome-wide approach accounting for body mass index identifies genetic variants influencing fasting glycemic traits and insulin resistance. Nature Genetics, 2012, 44, 659-669. | 21.4 | 762 |
| 4 | Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190. | 27.8 | 544 |
| 5 | Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766. | 21.4 | 470 |
| 6 | 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 |
| 7 | Distribution and Medical Impact of Loss-of-Function Variants in the Finnish Founder Population. PLoS Genetics, 2014, 10, e1004494. | 3.5 | 351 |
| 8 | 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 |
| 9 | Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161. | 21.4 | 261 |
| 10 | Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76. | 27.8 | 248 |
| 11 | The (in)famous GWAS P-value threshold revisited and updated for low-frequency variants. European Journal of Human Genetics, 2016, 24, 1202-1205. | 2.8 | 225 |
| 12 | Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245. | 6.2 | 193 |
| 13 | Meta-analysis of gene-environment interaction: joint estimation of SNP and SNP Ã— environment regression coefficients. Genetic Epidemiology, 2011, 35, 11-18. | 1.3 | 158 |
| 14 | Whole-Genome Sequencing Coupled to Imputation Discovers Genetic Signals for Anthropometric Traits. American Journal of Human Genetics, 2017, 100, 865-884. | 6.2 | 131 |
| 15 | A Large-Scale Multi-ancestry Genome-wide Study Accounting for Smoking Behavior Identifies Multiple Significant Loci for Blood Pressure. American Journal of Human Genetics, 2018, 102, 375-400. | 6.2 | 123 |
| 16 | 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 |
| 17 | Identification and Functional Characterization of G6PC2 Coding Variants Influencing Glycemic Traits Define an Effector Transcript at the G6PC2-ABCB11 Locus. PLoS Genetics, 2015, 11, e1004876. | 3.5 | 95 |
| 18 | Novel genetic associations for blood pressure identified via gene-alcohol interaction in up to 570K individuals across multiple ancestries. PLoS ONE, 2018, 13, e0198166. | 2.5 | 94 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. Nature Genetics, 2017, 49, 1560-1563. | 21.4 | 93 |
| 20 | 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 |
| 21 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469. | 21.4 | 89 |
| 22 | Multiancestry Genome-Wide Association Study of Lipid Levels Incorporating Gene-Alcohol Interactions. American Journal of Epidemiology, 2019, 188, 1033-1054. | 3.4 | 85 |
| 23 | Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992. | 12.8 | 68 |
| 24 | Genome-Wide Association Study of the Modified Stumvoll Insulin Sensitivity Index Identifies BCL2 and FAM19A2 as Novel Insulin Sensitivity Loci. Diabetes, 2016, 65, 3200-3211. | 0.6 | 67 |
| 25 | Multi-ancestry study of blood lipid levels identifies four loci interacting with physical activity. Nature Communications, 2019, 10, 376. | 12.8 | 64 |
| 26 | Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121. | 12.8 | 62 |
| 27 | New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, . | 5.1 | 48 |
| 28 | 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 |
| 29 | Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718. | 6.2 | 44 |
| 30 | A Partial Loss-of-Function Variant in AKT2 Is Associated With Reduced Insulin-Mediated Glucose Uptake in Multiple Insulin-Sensitive Tissues: A Genotype-Based Callback Positron Emission Tomography Study. Diabetes, 2018, 67, 334-342. | 0.6 | 37 |
| 31 | The First Genome-Wide Association Study for Type 2 Diabetes in Youth: The Progress in Diabetes Genetics in Youth (ProDiGY) Consortium. Diabetes, 2021, 70, 996-1005. | 0.6 | 37 |
| 32 | TCF7L2 Genetic Variation Augments Incretin Resistance and Influences Response to a Sulfonylurea and Metformin: The Study to Understand the Genetics of the Acute Response to Metformin and Glipizide in Humans (SUGAR-MGH). Diabetes Care, 2018, 41, 554-561. | 8.6 | 35 |
| 33 | Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179. | 5.3 | 31 |
| 34 | A multi-ancestry genome-wide study incorporating geneâ€“smoking interactions identifies multiple new loci for pulse pressure and mean arterial pressure. Human Molecular Genetics, 2019, 28, 2615-2633. | 2.9 | 31 |
| 35 | Type 2 Diabetes Partitioned Polygenic Scores Associate With Disease Outcomes in 454,193 Individuals Across 13 Cohorts. Diabetes Care, 2022, 45, 674-683. | 8.6 | 29 |
| 36 | Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384. | 7.1 | 28 |

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|---|---|---|---|
| 37 | The Study to Understand the Genetics of the Acute Response to Metformin and Glipizide in Humans (SUGAR-MGH): Design of a pharmacogenetic Resource for Type 2 Diabetes. PLoS ONE, 2015, 10, e0121553. | 2.5 | 20 |
| 38 | An Empirical Comparison of Joint and Stratified Frameworks for Studying G Ã— E Interactions: Systolic Blood Pressure and Smoking in the CHARGE Geneâ€Lifestyle Interactions Working Group. Genetic Epidemiology, 2016, 40, 404-415. | 1.3 | 18 |
| 39 | Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77. | 1.6 | 17 |
| 40 | Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125. | 7.9 | 17 |
| 41 | GEM: scalable and flexible geneâ€“environment interaction analysis in millions of samples. Bioinformatics, 2021, 37, 3514-3520. | 4.1 | 17 |
| 42 | Variation in Maturity-Onset Diabetes of the Young Genes Influence Response to Interventions for Diabetes Prevention. Journal of Clinical Endocrinology and Metabolism, 2017, 102, 2678-2689. | 3.6 | 16 |
| 43 | Efficient geneâ€“environment interaction tests for large biobankâ€scale sequencing studies. Genetic Epidemiology, 2020, 44, 908-923. | 1.3 | 15 |
| 44 | A Long Non-coding RNA, LOC157273, Is an Effector Transcript at the Chromosome 8p23.1-PPP1R3B Metabolic Traits and Type 2 Diabetes Risk Locus. Frontiers in Genetics, 2020, 11, 615. | 2.3 | 14 |
| 45 | Multi-ancestry genome-wide geneâ€“sleep interactions identify novel loci for blood pressure. Molecular Psychiatry, 2021, 26, 6293-6304. | 7.9 | 13 |
| 46 | Opportunities and challenges for the use of common controls in sequencing studies. Nature Reviews Genetics, 2022, 23, 665-679. | 16.3 | 13 |
| 47 | Genome-wide geneâ€“diet interaction analysis in the UK Biobank identifies novel effects on hemoglobin A1c. Human Molecular Genetics, 2021, 30, 1773-1783. | 2.9 | 11 |
| 48 | Gene-lifestyle interactions in the genomics of human complex traits. European Journal of Human Genetics, 2022, 30, 730-739. | 2.8 | 11 |
| 49 | Testing the role of predicted gene knockouts in human anthropometric trait variation. Human Molecular Genetics, 2016, 25, 2082-2092. | 2.9 | 10 |
| 50 | Clinical and metabolomic predictors of regression to normoglycemia in a population at intermediate cardiometabolic risk. Cardiovascular Diabetology, 2021, 20, 56. | 6.8 | 10 |
| 51 | Genomic Risk Prediction for Breast Cancer in Older Women. Cancers, 2021, 13, 3533. | 3.7 | 6 |
| 52 | Aspirin and the Risk of Colorectal Cancer According to Genetic Susceptibility among Older Individuals. Cancer Prevention Research, 2022, 15, 447-454. | 1.5 | 5 |
| 53 | Deriving stratified effects from joint models investigating gene-environment interactions. BMC Bioinformatics, 2020, 21, 251. | 2.6 | 2 |
| 54 | Multi-ancestry genome-wide association study accounting for gene-psychosocial factor interactions identifies novel loci for blood pressure traits. Human Genetics and Genomics Advances, 2021, 2, 100013. | 1.7 | 2 |

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|---|---|---|---|
| 55 | Predicting diabetes risk in diverse populations: what next?. Lancet Diabetes and Endocrinology,the, 2021, 9, 808-810. | 11.4 | 2 |
| 56 | Gene-Environment Interaction Analysis Incorporating Sex, Cardiometabolic Diseases, and Multiple Deprivation Index Reveals Novel Genetic Associations With COVID-19 Severity. Frontiers in Genetics, 2021, 12, 782172. | 2.3 | 1 |
| 57 | Large-Scale, Genome-Wide Gene-Diet Interaction Testing for HbA1c Using Derived Dietary Patterns in the UK Biobank. Current Developments in Nutrition, 2020, 4, nzaa058_038. | 0.3 | 0 |
| 58 | The SLC16A11 Risk Haplotype for Type 2 Diabetes (T2D) Is Associated to Differentiated Responses in Weight Loss, and Glucose Metabolism After Treatments to Prevent T2D. Current Developments in Nutrition, 2020, 4, nzaa058_033. | 0.3 | 0 |
| 59 | Metabolites Associated With Regression to Normoglycemia After a Lifestyle Intervention in Individuals With Prediabetes. Current Developments in Nutrition, 2021, 5, 1007. | 0.3 | 0 |
| 60 | Identification of Gene-Diet Interactions Impacting Glycemic Biomarkers in the Multi-Ethnic TOPMed Cohorts. Current Developments in Nutrition, 2021, 5, 952. | 0.3 | 0 |
| 61 | Abstract P3-13-01: Association of polygenic risk score with 2 year risk of poor prognosis breast cancer. Cancer Research, 2022, 82, P3-13-01-P3-13-01. | 0.9 | 0 |
| 62 | Little Contribution of Genome-Wide Gene-Diet Interactions to Cardiometabolic Risk Factors in the UK Biobank. Current Developments in Nutrition, 2022, 6, 1127. | 0.3 | 0 |