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The genetic architecture of type 2 diabetes

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|-----|--|------|-----------|
| 876 | A review of maturity onset diabetes of the young (MODY) and challenges in the management of glucokinase-MODY. <b>2016</b> , 205, 480-485                 |      | 24        |
| 875 | Diabetes: Still a geneticist's nightmare. <i>Nature</i> , <b>2016</b> , 536, 37-8  | 50.4 | 18        |
| 874 | Type 2 diabetes: genetic data sharing to advance complex disease research. <b>2016</b> , 17, 535-49  |      | 92        |
| 873 | Whole genome sequence analysis of serum amino acid levels. <b>2016</b> , 17, 237   |      | 12        |
| 872 | Using Genotype-Based Recall to Estimate the Effects of AMY1 Copy Number Variation in Substrate Metabolism. <i>Diabetes</i> , <b>2016</b> , 65, 3240-3242 | 0.9  | 2         |
| 871 | Genetics: Implications for Prevention and Management of Coronary Artery Disease. <b>2016</b> , 68, 2797-281  | 8    | 65        |
| 870 | Expanding the Immunology Toolbox: Embracing Public-Data Reuse and Crowdsourcing. <b>2016</b> , 45, 1191-   | 1204 | 13        |
| 869 | Modeling Type 2 Diabetes GWAS Candidate Gene Function in hESCs. <b>2016</b> , 19, 281-2  |      | 4         |
| 868 | What Can hiPSC-Cardiomyocytes Teach Us about Modeling Complex Human Disease Phenotypes?. <b>2016</b> , 19, 282-4   |      | 2         |
| 867 | Exposing the exposures responsible for type 2 diabetes and obesity. <b>2016</b> , 354, 69-73   |      | 138       |
| 866 | Quantum physics: Destruction of discrete charge. <i>Nature</i> , <b>2016</b> , 536, 38-9   | 50.4 |           |
| 865 | An Ecosystem to Support Traditional Clinical Investigation: Lessons From Aging, Exercise, Blood Pressure, and Women. <b>2016</b> , 68, 855-6             |      |           |
| 864 | Type 2 Diabetes Genes Gleaned by Making a ECell Screen Routine. <i>Diabetes</i> , <b>2016</b> , 65, 3541-3543  | 0.9  |           |
| 863 | An alternative effector gene at the type 2 diabetes-associated TCF7L2 locus?. <i>Diabetologia</i> , <b>2016</b> , 59, 2292-2294                          | 10.3 | 7         |
| 862 | Never Waste a Good Crisis: Confronting Reproducibility in Translational Research. <b>2016</b> , 24, 348-360  |      | 80        |
| 861 | The Difficult Journey from Genome-wide Association Studies to Pathophysiology: The Melatonin Receptor 1B (MT2) Paradigm. <b>2016</b> , 24, 345-347       |      | 13        |
| 860 | Genetic Background Limits Generalizability of Genotype-Phenotype Relationships. <b>2016</b> , 91, 1253-1259  |      | 143       |

| 859 | Personalised nutrition: What makes you so 'special?. <b>2016</b> , 41, 353-359   | 27  |
|-----|--|-----|
| 858 | Therapeutics Targeting FGF Signaling Network in Human Diseases. <b>2016</b> , 37, 1081-1096  | 99  |
| 857 | The Application of Genomics in Diabetes: Barriers to Discovery and Implementation. <b>2016</b> , 39, 1858-1869   | 21  |
| 856 | Assessment of Human Tribbles Homolog 3 Genetic Variation (rs2295490) Effects on Type 2 Diabetes Patients with Glucose Control and Blood Pressure Lowering Treatment. <b>2016</b> , 13, 181-189 | 9   |
| 855 | Diabetes and data in many forms. <b>2016</b> , 36, 381-384   | 1   |
| 854 | Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. <b>2016</b> , 10, 71-77   | 14  |
| 853 | Exploring the genetic architecture of inflammatory bowel disease by whole-genome sequencing identifies association at ADCY7. <b>2017</b> , 49, 186-192   | 104 |
| 852 | The Metabolic Syndrome in Men study: a resource for studies of metabolic and cardiovascular diseases. <b>2017</b> , 58, 481-493  | 77  |
| 851 | Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , <b>2017</b> , 542, 186-190 50.4   | 412 |
| 850 | Decreased STARD10 Expression Is Associated with Defective Insulin Secretion in Humans and Mice. <b>2017</b> , 100, 238-256   | 50  |
| 849 | Polygenic risk scores in familial Alzheimer disease. <b>2017</b> , 88, 1180-1186   | 41  |
| 848 | Painting a new picture of personalised medicine for diabetes. <i>Diabetologia</i> , <b>2017</b> , 60, 793-799 10.3   | 102 |
| 847 | Shortcuts to a functional adipose tissue: The role of small non-coding RNAs. <b>2017</b> , 12, 82-102  | 43  |
| 846 | Arsenic Exposure and Type 2 Diabetes: MicroRNAs as Mechanistic Links?. <b>2017</b> , 17, 18  | 20  |
| 845 | Functional annotation of sixty-five type-2 diabetes risk SNPs and its application in risk prediction.  Scientific Reports, <b>2017</b> , 7, 43709  4-9   | 3   |
| 844 | Genomics of Islet (Dys)function and Type 2 Diabetes. <b>2017</b> , 33, 244-255   | 44  |
| 843 | Centenarians as extreme phenotypes: An ecological perspective to get insight into the relationship between the genetics of longevity and age-associated diseases. <b>2017</b> , 165, 195-201   | 25  |
| 842 | Opportunities and challenges of whole-genome and -exome sequencing. <b>2017</b> , 18, 14   | 110 |

| 841 | Towards a systematic nationwide screening strategy for MODY. <i>Diabetologia</i> , <b>2017</b> , 60, 609-612   | 10.3  | 8            |
|-----|--|-------|--------------|
| 840 | A case report of hereditary neuropathy with liability to pressure palsies accompanied by type 2 diabetes mellitus and psoriasis. <b>2017</b> , 96, e6922               |       | 6            |
| 839 | Using genetics to inform new therapeutics for diabetes. <b>2017</b> , 12, 159-169  |       |              |
| 838 | High-Resolution Genetic Maps Identify Multiple Type 2 Diabetes Loci at Regulatory Hotspots in African Americans and Europeans. <b>2017</b> , 100, 803-816              |       | 14           |
| 837 | Diabetes, Pancreatogenic Diabetes, and Pancreatic Cancer. <i>Diabetes</i> , <b>2017</b> , 66, 1103-1110  | 0.9   | 178          |
| 836 | Epigenetic regulation of glucose metabolism. <b>2017</b> , 20, 266-271   |       | 5            |
| 835 | Human genetics as a model for target validation: finding new therapies for diabetes. <i>Diabetologia</i> , <b>2017</b> , 60, 960-970                                   | 10.3  | 15           |
| 834 | Genetics of Diabetic Kidney Disease-From the Worst of Nightmares to the Light of Dawn?. <b>2017</b> , 28, 389  | 9-393 | 13           |
| 833 | PCSK9 genetic variants and risk of type 2 diabetes: a mendelian randomisation study. <b>2017</b> , 5, 97-105   |       | 225          |
| 832 | N-acetylglucosamine: more than a silent partner in insulin resistance. <b>2017</b> , 27, 595-598   |       | 1            |
| 831 | Whole Exome Sequencing to Identify Genetic Variants Associated with Raised Atherosclerotic Lesions in Young Persons. <i>Scientific Reports</i> , <b>2017</b> , 7, 4091 | 4.9   | 10           |
| 830 | Metalloprotein entatic control of ligand-metal bonds quantified by ultrafast x-ray spectroscopy. <b>2017</b> , 356, 1276-1280  |       | 86           |
| 829 | Pharmacogenetics in type 2 diabetes: still a conundrum in clinical practice. <b>2017</b> , 12, 155-158   |       | 5            |
| 828 | Chromosome 10. <b>2017</b> , 1-43  |       | 1            |
| 827 | Type 2 Diabetes: Demystifying the Global Epidemic. <i>Diabetes</i> , <b>2017</b> , 66, 1432-1442   | 0.9   | 150          |
| 826 | How mice are indispensable for understanding obesity and diabetes genetics. <b>2017</b> , 24, 83-91  |       | 21           |
| 825 | Insulin Resistance and Mitochondrial Dysfunction. <i>Advances in Experimental Medicine and Biology</i> , <b>2017</b> , 982, 465-520                                    | 3.6   | 73           |
| 824 | An Expanded Genome-Wide Association Study of Type 2 Diabetes in Europeans. <i>Diabetes</i> , <b>2017</b> , 66, 288   | 85290 | <b>2</b> 414 |

| 823 | The impact of rare and low-frequency genetic variants in common disease. <b>2017</b> , 18, 77   |      | 174 |
|-----|---|------|-----|
| 822 | Mining the Genome for Therapeutic Targets. <i>Diabetes</i> , <b>2017</b> , 66, 1770-1778  | 0.9  | 11  |
| 821 | Association analyses of East Asian individuals and trans-ancestry analyses with European individuals reveal new loci associated with cholesterol and triglyceride levels. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, 1770-1784 | 5.6  | 90  |
| 820 | The genetic architecture of molecular traits. <b>2017</b> , 1, 25-31  |      | 3   |
| 819 | The case for too little melatonin signalling in increased diabetes risk. <i>Diabetologia</i> , <b>2017</b> , 60, 823-825  | 10.3 | 19  |
| 818 | A systematic review of genetic syndromes with obesity. <b>2017</b> , 18, 603-634  |      | 93  |
| 817 | A Low-Frequency Inactivating Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. <i>Diabetes</i> , <b>2017</b> , 66, 2019-2032   | 0.9  | 29  |
| 816 | The Q192R polymorphism of the paraoxonase-1 (PON1) gene is associated with susceptibility to gestational diabetes mellitus in the Greek population. <b>2017</b> , 33, 617-620   |      | 7   |
| 815 | Therapeutic Strategies for Mitochondrial Dysfunction and Oxidative Stress in Age-Related Metabolic Disorders. <b>2017</b> , 146, 13-46  |      | 32  |
| 814 | How Can Genetic Studies Help Us to Understand Links Between Birth Weight and Type 2 Diabetes?. <b>2017</b> , 17, 22   |      | 23  |
| 813 | Precision diabetes: learning from monogenic diabetes. <i>Diabetologia</i> , <b>2017</b> , 60, 769-777   | 10.3 | 162 |
| 812 | Genetics of T2DM in 2016: Biological and translational insights from T2DM genetics. <b>2017</b> , 13, 71-72   |      | 8   |
| 811 | Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <b>2017</b> , 49, 1560-1563  |      | 68  |
| 810 | Exome-wide association study of plasma lipids in >300,000 individuals. <b>2017</b> , 49, 1758-1766  |      | 310 |
| 809 | Gene Editing and Human Pluripotent Stem Cells: Tools for Advancing Diabetes Disease Modeling and Beta-Cell Development. <b>2017</b> , 17, 116   |      | 9   |
| 808 | CRP-level-associated polymorphism rs1205 within the CRP gene is associated with 2-hour glucose level: The SAPPHIRe study. <i>Scientific Reports</i> , <b>2017</b> , 7, 7987   | 4.9  | 8   |
| 807 | Integrating evolutionary and regulatory information with a multispecies approach implicates genes and pathways in obsessive-compulsive disorder. <b>2017</b> , 8, 774   |      | 41  |
| 806 | The genetic underpinnings of body fat distribution. <b>2017</b> , 12, 417-427   |      | 2   |

| 805 | The Genetics of Physical Activity. <b>2017</b> , 19, 119   | 18  |
|-----|--|-----|
| 804 | Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. <b>2017</b> , 49, 1747-1751  | 55  |
| 803 | A Loss-of-Function Splice Acceptor Variant in Is Protective for Type 2 Diabetes. <i>Diabetes</i> , <b>2017</b> , 66, 2903-2914   | 32  |
| 802 | Environmental/lifestyle factors in the pathogenesis and prevention of type 2 diabetes. <b>2017</b> , 15, 131   | 212 |
| 801 | Concepts, estimation and interpretation of SNP-based heritability. <b>2017</b> , 49, 1304-1310   | 217 |
| 800 | Genome-wide analysis of health-related biomarkers in the UK Household Longitudinal Study reveals novel associations. <i>Scientific Reports</i> , <b>2017</b> , 7, 11008                                | 49  |
| 799 | Non-parametric genetic prediction of complex traits with latent Dirichlet process regression models. <b>2017</b> , 8, 456  | 53  |
| 798 | Linkage disequilibrium-dependent architecture of human complex traits shows action of negative selection. <b>2017</b> , 49, 1421-1427  | 204 |
| 797 | Lipopolysaccharide-binding protein (LBP) reverses the amyloid state of fibrin seen in plasma of type 2 diabetics with cardiovascular co-morbidities. <i>Scientific Reports</i> , <b>2017</b> , 7, 9680 | 24  |
| 796 | Analysis of population-specific pharmacogenomic variants using next-generation sequencing data.  Scientific Reports, <b>2017</b> , 7, 8416  4.9  | 16  |
| 795 | Improving power for rare-variant tests by integrating external controls. 2017, 41, 610-619   | 6   |
| 794 | Findings of a 1303 Korean whole-exome sequencing study. <b>2017</b> , 49, e356   | 23  |
| 793 | Association analyses based on false discovery rate implicate new loci for coronary artery disease. <b>2017</b> , 49, 1385-1391   | 361 |
| 792 | Association of HSD11B1 gene polymorphisms with type 2 diabetes and metabolic syndrome in South Indian population. <b>2017</b> , 131, 142-148   | 10  |
| 791 | Future Directions of Genomics Research in Rheumatic Diseases. <b>2017</b> , 43, 481-487  | 5   |
| 790 | Transcribing Eell mitochondria in health and disease. <b>2017</b> , 6, 1040-1051   | 38  |
| 789 | Mechanisms of Type 2 Diabetes Risk Loci. <b>2017</b> , 17, 72  | 29  |
| 788 | Cloud-based interactive analytics for terabytes of genomic variants data. <b>2017</b> , 33, 3709-3715  | 7   |

## (2017-2017)

| 787              | T2DiACoD: A Gene Atlas of Type 2 Diabetes Mellitus Associated Complex Disorders. <i>Scientific Reports</i> , <b>2017</b> , 7, 6892  | 20 |
|------------------|---|----|
| 786              | Whole-Genome Sequencing in Common Respiratory Diseases. Ready, Set, Go!. <b>2017</b> , 196, 121-122   | 2  |
| 7 <sup>8</sup> 5 | -ancestry Fine Mapping and Molecular Assays Identify Regulatory Variants at the HDL-C GWAS Locus. <b>2017</b> , 7, 3217-3227  | 14 |
| 784              | Prioritising Causal Genes at Type 2 Diabetes Risk Loci. <b>2017</b> , 17, 76  | 21 |
| 783              | Endocrinology Meets Metabolomics: Achievements, Pitfalls, and Challenges. 2017, 28, 705-721   | 19 |
| 782              | Towards precision medicine for type 2 diabetes. <b>2017</b> , 8, 243  |    |
| 781              | Regenerative medicine and cell-based approaches to restore pancreatic function. <b>2017</b> , 14, 612-628   | 56 |
| 780              | Towards a personalized assessment of pancreatic function in diabetes. <b>2017</b> , 2, 275-285  |    |
| 779              | Personalized epigenetic management of diabetes. <b>2017</b> , 14, 531-549   | 5  |
| 778              | Fusion pore in exocytosis: More than an exit gate? A Etell perspective. <b>2017</b> , 68, 45-61   | 10 |
| 777              | A Decade of Genetic and Metabolomic Contributions to Type 2 Diabetes Risk Prediction. <b>2017</b> , 17, 135   | 13 |
| 776              | DNA methylation profiles in sibling pairs discordant for intrauterine exposure to maternal gestational diabetes. <b>2017</b> , 12, 825-832  | 21 |
| 775              | Using Personalized Medicine in the Management of Diabetes Mellitus. 2017, 37, 1131-1149   | 5  |
| 774              | A droplet-based microfluidic platform for kinetics-based detection of single nucleotide variation at room temperature with large discrimination factors. <b>2017</b> , 253, 731-737 | 8  |
| 773              | A Type 2 Diabetes-Associated Functional Regulatory Variant in a Pancreatic Islet Enhancer at the Locus. <i>Diabetes</i> , <b>2017</b> , 66, 2521-2530                               | 37 |
| 772              | The role of human host genetics in tuberculosis resistance. <b>2017</b> , 11, 721-737   | 14 |
| 771              | Prediction of gene expression with cis-SNPs using mixed models and regularization methods. <b>2017</b> , 18, 368  | 17 |
| 770              | Genome sequence of a diabetes-prone rodent reveals a mutation hotspot around the ParaHox gene cluster. <b>2017</b> , 114, 7677-7682   | 20 |

| 769             | 10 Years of GWAS Discovery: Biology, Function, and Translation. <b>2017</b> , 101, 5-22   |              | 1651 |
|-----------------|---|--------------|------|
| 768             | The genomic landscape of African populations in health and disease. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, R225-R236   | 5.6          | 43   |
| 767             | Increasing mapping precision of genome-wide association studies: to genotype and impute, sequence, or both?. <b>2017</b> , 18, 118  |              | 8    |
| 766             | Introduction of the DiaGene study: clinical characteristics, pathophysiology and determinants of vascular complications of type 2 diabetes. <i>Diabetology and Metabolic Syndrome</i> , <b>2017</b> , 9, 47   | 5.6          | 11   |
| 765             | A New Drug Target for Type 2 Diabetes. <b>2017</b> , 170, 12-14   |              | 20   |
| 764             | Friction at the BAR Leads to Membrane Breakup. <b>2017</b> , 170, 14-16   |              | 1    |
| 763             | Dissecting the genetics of complex traits using summary association statistics. <b>2017</b> , 18, 117-127   |              | 252  |
| 762             | Genome-wide association analyses using electronic health records identify new loci influencing blood pressure variation. <b>2017</b> , 49, 54-64  |              | 157  |
| 761             | Exome-chip association analysis reveals an Asian-specific missense variant in PAX4 associated with type 2 diabetes in Chinese individuals. <i>Diabetologia</i> , <b>2017</b> , 60, 107-115  | 10.3         | 11   |
| 760             | Polygenic score prediction captures nearly all common genetic risk for Alzheimer's disease. <b>2017</b> , 49, 214.e7-214.e11  |              | 101  |
| 759             | Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. <b>2017</b> , 4, 17017   | 9            | 22   |
| 758             | Genomics of Type 2 Diabetes Mellitus and Glycemic Traits. <b>2017</b> , 17, 140-144   |              |      |
| 757             | High Prevalence of Diabetes-Predisposing Variants in MODY Genes Among Danish Women With Gestational Diabetes Mellitus. <b>2017</b> , 1, 681-690   |              | 23   |
| 756             | Genetic aetiology of glycaemic traits: approaches and insights. <i>Human Molecular Genetics</i> , <b>2017</b> , 26, R17   | <u>2R</u> 18 | 48   |
| 755             | 2017 Roadmap for Innovation-ACC Health Policy Statement on Healthcare Transformation in the Era´of Digital Health, Big Data, and Precision Health: A Report of the American College of Cardiology Task Force on Health Policy Statements and Systems of Care. <b>2017</b> , 70, 2696-2718 |              | 61   |
| 754             | Risk prediction using common and rare genetic variants: Application to Type 2 diabetes. <b>2017</b> ,   |              | O    |
| 753             | Phenotypic analysis of 303 multiplex families with common epilepsies. <b>2017</b> , 140, 2144-2156  |              | 22   |
| 75 <sup>2</sup> | Semiparametric analysis of complex polygenic gene-environment interactions in case-control studies. <b>2017</b> , 104, 801-812  |              | 1    |

| 751 | Gene-Diet Interaction and Precision Nutrition in Obesity. <b>2017</b> , 18,   | 79               |
|-----|---|------------------|
| 75° | Diverse type 2 diabetes genetic risk factors functionally converge in a phenotype-focused gene network. <b>2017</b> , 13, e1005816  | 11               |
| 749 | Spectrum of mutations in monogenic diabetes genes identified from high-throughput DNA sequencing of 6888 individuals. <b>2017</b> , 15, 213   | 45               |
| 748 | Identification and characterization of a FOXA2-regulated transcriptional enhancer at a type 2 diabetes intronic locus that controls GCKR expression in liver cells. <b>2017</b> , 9, 63                               | 16               |
| 747 | The association between Alu hypomethylation and severity of type 2 diabetes mellitus. <b>2017</b> , 9, 93   | 19               |
| 746 | Identifying and mitigating batch effects in whole genome sequencing data. <b>2017</b> , 18, 351   | 26               |
| 745 | Genome-wide meta-analysis in Japanese populations identifies novel variants at the TMC6-TMC8 and SIX3-SIX2 loci associated with HbA. <i>Scientific Reports</i> , <b>2017</b> , 7, 16147                               | 25               |
| 744 | Genetics and Diabetes. <b>2017</b> , 659-675  |                  |
| 743 | LASER server: ancestry tracing with genotypes or sequence reads. <b>2017</b> , 33, 2056-2058  | 15               |
| 742 | Association of polymorphic markers of genes , and with type 2 diabetes mellitus in the Russian population. <b>2017</b> , 5, e3414   | 17               |
| 741 | The pathogenetic role of Etell mitochondria in type 2 diabetes. <b>2018</b> , 236, R145-R159  | 46               |
| 740 | Genetic architecture of obesity and related metabolic traits-recent insights from isolated populations. <b>2018</b> , 50, 74-78   | 3                |
| 739 | Progress in defining the genetic contribution to type 2 diabetes susceptibility. <b>2018</b> , 50, 41-51  | 15               |
| 738 | Genome-wide association studies in Crohn's disease: Past, present and future. <b>2018</b> , 7, e1001  | 45               |
| 737 | Identification of seven novel loci associated with amino acid levels using single-variant and gene-based tests in 8545 Finnish men from the METSIM study. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 1664-16 | 74 <sup>20</sup> |
| 736 | Islet proteomics reveals genetic variation in dopamine production resulting in altered insulin secretion. <b>2018</b> , 293, 5860-5877  | 22               |
| 735 | Precision medicine in diabetes prevention, classification and management. <b>2018</b> , 9, 998-1015   | 32               |
| 734 | Patterns of differential gene expression in a cellular model of human islet development, and relationship to type 2 diabetes predisposition. <i>Diabetologia</i> , <b>2018</b> , 61, 1614-1622                        | 9                |

| 733 | No novel, high penetrant gene might remain to be found in Japanese patients with unknown MODY. <b>2018</b> , 63, 821-829  |                 | 1   |
|-----|---|-----------------|-----|
| 732 | Implications of publicly available genomic data resources in searching for therapeutic targets of obesity and type 2 diabetes. <b>2018</b> , 50, 1-13                                   |                 | 2   |
| 731 | Medical relevance of protein-truncating variants across 337,205 individuals in the UK Biobank study. <b>2018</b> , 9, 1612  |                 | 61  |
| 730 | Sizing up whole-genome sequencing studies of common diseases. <b>2018</b> , 50, 635-637   |                 | 10  |
| 729 | Signatures of negative selection in the genetic architecture of human complex traits. <b>2018</b> , 50, 746-753   |                 | 178 |
| 728 | Integration of human adipocyte chromosomal interactions with adipose gene expression prioritizes obesity-related genes from GWAS. <b>2018</b> , 9, 1512                                 |                 | 41  |
| 727 | Mexican American and South Asian population-based cohorts reveal high prevalence of type 2 diabetes and crucial differences in metabolic phenotypes. <b>2018</b> , 6, e000436           |                 | 6   |
| 726 | Pharmacogenomics and big genomic data: from lab to clinic and back again. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, R72-R78   | <del>5</del> .6 | 19  |
| 725 | A Common Type 2 Diabetes Risk Variant Potentiates Activity of an Evolutionarily Conserved Islet Stretch Enhancer and Increases C2CD4A and C2CD4B Expression. <b>2018</b> , 102, 620-635 |                 | 34  |
| 724 | Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes. <b>2018</b> , 50, 559-571  |                 | 221 |
| 723 | The Extending Spectrum of NPC1-Related Human Disorders: From Niemann-Pick C1 Disease to Obesity. <b>2018</b> , 39, 192-220  |                 | 18  |
| 722 | Pathogenesis of Type 2 Diabetes Mellitus. <b>2018</b> , 1-74  |                 |     |
| 721 | Sequence-Based Analysis of Lipid-Related Metabolites in a Multiethnic Study. <b>2018</b> , 209, 607-616   |                 | 4   |
| 720 | Metabolomics insights into early type 2 diabetes pathogenesis and detection in individuals with normal fasting glucose. <i>Diabetologia</i> , <b>2018</b> , 61, 1315-1324               | 10.3            | 66  |
| 719 | Nutritional Genomics and Direct-to-Consumer Genetic Testing: An Overview. <b>2018</b> , 9, 128-135  |                 | 26  |
| 718 | NAFLD risk alleles in PNPLA3, TM6SF2, GCKR and LYPLAL1 show divergent metabolic effects.  Human Molecular Genetics, <b>2018</b> , 27, 2214-2223   | <del>5</del> .6 | 65  |
| 717 | Using Full Genomic Information to Predict Disease: Breaking Down the Barriers Between Complex and Mendelian Diseases. <b>2018</b> , 19, 289-301   |                 | 6   |
| 716 | Effect of genetic architecture on the prediction accuracy of quantitative traits in samples of unrelated individuals. <b>2018</b> , 120, 500-514  |                 | 32  |

| 715 | Cohort Profile: The Singapore Multi-Ethnic Cohort (MEC) study. 2018, 47, 699-699j  | 34  |
|-----|--|-----|
| 714 | AQR is a novel type 2 diabetes-associated gene that regulates signaling pathways critical for glucose metabolism. <b>2018</b> , 45, 111-120  | 11  |
| 713 | Power Analysis for Genetic Association Test (PAGEANT) provides insights to challenges for rare variant association studies. <b>2018</b> , 34, 1506-1513  | 10  |
| 712 | T2D Genome-Wide Association Study Risk SNPs Impact Locus Gene Expression and Proliferation in Human Islets. <i>Diabetes</i> , <b>2018</b> , 67, 872-884  | 28  |
| 711 | The contribution of family history to the burden of diagnosed diabetes, undiagnosed diabetes, and prediabetes in the United States: analysis of the National Health and Nutrition Examination Survey, 2009-2014. <b>2018</b> , 20, 1159-1166 | 11  |
| 710 | Reply: No evidence for rare TRAP1 mutations influencing the risk of idiopathic Parkinson's disease. <b>2018</b> , 141, e17   | 2   |
| 709 | Precision medicine in diabetes: an opportunity for clinical translation. <b>2018</b> , 1411, 140-152   | 22  |
| 708 | Cardiometabolic risk in obese children. <b>2018</b> , 1411, 166-183  | 80  |
| 707 | Epidemiology of diabetes and diabetic complications in China. <i>Diabetologia</i> , <b>2018</b> , 61, 1249-1260 10.3   | 159 |
| 706 | Maturity-onset diabetes of the young as a model for elucidating the multifactorial origin of type 2 diabetes mellitus. <b>2018</b> , 9, 704-712  | 28  |
| 705 | Physiologic Interpretation of GWAS Signals for Type 2 Diabetes. <b>2018</b> , 1706, 323-351  | 1   |
| 704 | Precision nutrition for prevention and management of type 2 diabetes. <b>2018</b> , 6, 416-426   | 99  |
| 703 | Inbred or Outbred? Genetic Diversity in Laboratory Rodent Colonies. 2018, 8, 679-686   | 12  |
| 702 | Identification of Disease Susceptibility Alleles in the Next Generation Sequencing Era. 2018, 1706, 3-16   | 3   |
| 701 | Animal models of obesity and diabetes mellitus. <b>2018</b> , 14, 140-162  | 330 |
| 700 | Identification of genetic elements in metabolism by high-throughput mouse phenotyping. <b>2018</b> , 9, 288  | 48  |
| 699 | Re-analysis of public genetic data reveals a rare X-chromosomal variant associated with type 2 diabetes. <b>2018</b> , 9, 321  | 50  |
| 698 | Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. <b>2018</b> , 115, 379-384   | 21  |

| 697 | Causal relationship of hepatic fat with liver damage and insulin resistance in nonalcoholic fatty liver. <b>2018</b> , 283, 356-370                                    | 140 |
|-----|--|-----|
| 696 | The era of GWAS is over - Commentary. <b>2018</b> , 24, 260-261  |     |
| 695 | Estimating and testing direct genetic effects in directed acyclic graphs using estimating equations. <b>2018</b> , 42, 174-186   | 2   |
| 694 | Loss-of-function variants in ADCY3 increase risk of obesity and type 2 diabetes. <b>2018</b> , 50, 172-174   | 97  |
| 693 | A network approach to exploring the functional basis of gene-gene epistatic interactions in disease susceptibility. <b>2018</b> , 34, 1741-1749                        | 10  |
| 692 | De novo mutations implicate novel genes in systemic lupus erythematosus. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 421-429                                   | 29  |
| 691 | Improved score statistics for meta-analysis in single-variant and gene-level association studies. <b>2018</b> , 42, 333-343  | 3   |
| 690 | Design of Arab Diabetes Gene-Centric Array (ADGCA) in population with an epidemic of Type 2 Diabetes: A population specific SNP evaluation. <b>2018</b> , 663, 157-164 | 4   |
| 689 | Profiling and Leveraging Relatedness in a Precision Medicine Cohort of 92,455 Exomes. <b>2018</b> , 102, 874-889   | 38  |
| 688 | Detecting phenotype-driven transitions in regulatory network structure. <b>2018</b> , 4, 16  | 18  |
| 687 | Genetic Drivers of Pancreatic Islet Function. <b>2018</b> , 209, 335-356   | 26  |
| 686 | Functional annotation of genomic variants in studies of late-onset Alzheimer's disease. <b>2018</b> , 34, 2724-2731  | 13  |
| 685 | Epigenome-wide association in adipose tissue from the METSIM cohort. <i>Human Molecular Genetics</i> , <b>2018</b> , 27, 1830-1846                                     | 22  |
| 684 | Cis- and Trans-Modifiers of Repeat Expansions: Blending Model Systems with Human Genetics. <b>2018</b> , 34, 448-465   | 15  |
| 683 | Estimation of indirect effect when the mediator is a censored variable. <b>2018</b> , 27, 3010-3025  | 6   |
| 682 | Cohort Profile: The Oxford Biobank. <b>2018</b> , 47, 21-21g   | 24  |
| 681 | Reversing the tide - diagnosis and prevention of T2DM in populations of African descent. <b>2018</b> , 14, 45-56   | 24  |
| 680 | Psychiatric Genomics: An Update and an Agenda. <b>2018</b> , 175, 15-27  | 328 |

| 679 | Pharmacoepigenetics and Toxicoepigenetics: Novel Mechanistic Insights and Therapeutic Opportunities. <b>2018</b> , 58, 161-185   |      | 36   |
|-----|--|------|------|
| 678 | Phenotypic Consequences of a Genetic Predisposition to Enhanced Nitric Oxide Signaling.  Circulation, <b>2018</b> , 137, 222-232   | 16.7 | 53   |
| 677 | Metabolic pathways at the crossroads of diabetes and inborn errors. <b>2018</b> , 41, 5-17   |      | 4    |
| 676 | A risk score including body mass index, glycated haemoglobin and triglycerides predicts future glycaemic control in people with type 2 diabetes. <i>Diabetes, Obesity and Metabolism</i> , <b>2018</b> , 20, 681-688             | ó.7  | 17   |
| 675 | Whole-exome sequencing in a Japanese family with highly aggregated diabetes identifies a candidate susceptibility mutation in ADAMTSL3. <b>2018</b> , 135, 143-149   |      | 5    |
| 674 | The molecular functions of hepatocyte nuclear factors - In and beyond the liver. <b>2018</b> , 68, 1033-1048   |      | 98   |
| 673 | Systems biology of the IMIDIA biobank from organ donors and pancreatectomised patients defines a novel transcriptomic signature of islets from individuals with type 2 diabetes. <i>Diabetologia</i> , <b>2018</b> , 61, 641-657 | 10.3 | 84   |
| 672 | Genetic architecture: the shape of the genetic contribution to human traits and disease. <b>2018</b> , 19, 110-12  | 4    | 219  |
| 671 | Does insulin therapy matter? Determinants of diabetes care outcomes. <b>2018</b> , 12, 224-230   |      | 3    |
| 670 | Methods for meta-analysis of multiple traits using GWAS summary statistics. <b>2018</b> , 42, 134-145  |      | 30   |
| 669 | Global aetiology and epidemiology of type 2 diabetes mellitus and its complications. <b>2018</b> , 14, 88-98   |      | 1622 |
| 668 | Genetic prediction of type 2 diabetes using deep neural network. <b>2018</b> , 93, 822-829   |      | 8    |
| 667 | Genetic Approaches to the Study of Gene Variants and Their Impact on the Pathophysiology of Type 2 Diabetes. <b>2018</b> , 56, 22-55   |      | 17   |
| 666 | Postpartum glucose intolerance: an updated overview. <b>2018</b> , 59, 481-494   |      | 29   |
| 665 | A Family-Based Rare Haplotype Association Method for Quantitative Traits. <b>2018</b> , 83, 175-195  |      | 3    |
| 664 | Combining controls can improve power in two-stage association studies. <b>2018</b> , 19, 89  |      |      |
| 663 | Genes associated with Type 2 Diabetes and vascular complications. <b>2018</b> , 10, 178-196  |      | 27   |
| 662 | . 2018,  |      | 2    |

| 661 | Shared genetic risk contributes to type 1 and type 2 diabetes etiology. <i>Human Molecular Genetics</i> , 2018,  | 27  |
|-----|--|-----|
| 660 | Imputation-Aware Tag SNP Selection To Improve Power for Large-Scale, Multi-ethnic Association Studies. <b>2018</b> , 8, 3255-3267  | 17  |
| 659 | Circadian dysrhythmia-linked diabetes mellitus: Examining melatonin's roles in prophylaxis and management. <b>2018</b> , 9, 99-114   | 15  |
| 658 | Recent developments in statistical methods for GWAS and high-throughput sequencing association studies of complex traits. <b>2018</b> , 2, 132-159   | 3   |
| 657 | Precision in personalized prediction-based medicine. <b>2018</b> , 15, 467-470   |     |
| 656 | Evidence for genetic contribution to the increased risk of type 2 diabetes in schizophrenia. <b>2018</b> , 8, 252  | 34  |
| 655 | Genetics of Obesity in Diverse Populations. <b>2018</b> , 18, 145  | 16  |
| 654 | Methods and Tools in Genome-wide Association Studies. <b>2018</b> , 1819, 93-136   | 7   |
| 653 | Epigenetics of chronic inflammatory diseases. <b>2019</b> , 12, 1-14   | 32  |
| 652 | Singleton Variants Dominate the Genetic Architecture of Human Gene Expression. 2018,   | 3   |
| 651 | Non-Coding RNA in Pancreas and ECell Development. <b>2018</b> , 4,   | 24  |
| 650 | Genetic polymorphisms of diabetes-related genes, their interaction with diabetes status, and breast cancer incidence and mortality: The Long Island Breast Cancer Study Project. <b>2019</b> , 58, 436-446 | 6   |
| 649 | An Enrichment Analysis for Cardiometabolic Traits Suggests Non-Random Assignment of Genes to microRNAs. <b>2018</b> , 19,  | O   |
| 648 | Chromatin interactions and expression quantitative trait loci reveal genetic drivers of multimorbidities. <b>2018</b> , 9, 5198  | 33  |
| 647 | Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. <b>2018</b> , 50, 1600-1607  | 72  |
| 646 | Fine-mapping type 2 diabetes loci to single-variant resolution using high-density imputation and islet-specific epigenome maps. <b>2018</b> , 50, 1505-1513  | 675 |
| 645 | Turning Vice into Virtue: Using Batch-Effects to Detect Errors in Large Genomic Data Sets. <b>2018</b> , 10, 2697-270  | )86 |
| 644 | Type 2 diabetes genetic loci informed by multi-trait associations point to disease mechanisms and subtypes: A soft clustering analysis. <b>2018</b> , 15, e1002654   | 180 |

| 643 | A Global Overview of Precision Medicine in Type 2 Diabetes. <i>Diabetes</i> , <b>2018</b> , 67, 1911-1922   | 0.9  | 52   |
|-----|---|------|------|
| 642 | Epigenetics Variation and Pathogenesis in Diabetes. <b>2018</b> , 18, 121   |      | 17   |
| 641 | A type 2 diabetes disease module with a high collective influence for Cdk2 and PTPLAD1 is localized in endosomes. <b>2018</b> , 13, e0205180  |      | 1    |
| 640 | The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , <b>2018</b> , 562, 203-209  | 50.4 | 2108 |
| 639 | The Eell in diabetes mellitus. <b>2018</b> , 14, 694-704  |      | 49   |
| 638 | Advances in our understanding of the genetics of childhood neurodevelopmental disorders. <b>2018</b> , 21, 171-172  |      | 5    |
| 637 | A reference haplotype panel for genome-wide imputation of short tandem repeats. <b>2018</b> , 9, 4397   |      | 19   |
| 636 | Ethnicity-Specific Association Between Ghrelin Leu72Met Polymorphism and Type 2 Diabetes Mellitus Susceptibility: An Updated Meta-Analysis. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 541 | 4.5  | 3    |
| 635 | Targeted genotyping of variable number tandem repeats with adVNTR. 2018, 28, 1709-1719  |      | 26   |
| 634 | Pathogenesis of Type 2 Diabetes Mellitus. <b>2018</b> , 181-253   |      | 5    |
| 633 | Low-Frequency and Rare-Coding Variation Contributes to Multiple Sclerosis Risk. <b>2018</b> , 175, 1679-1687.   | e7   | 72   |
| 632 | Functional Variant in the GCKR Gene Affects Lactate Levels Differentially in the Fasting State and During Hyperglycemia. <i>Scientific Reports</i> , <b>2018</b> , 8, 15989                     | 4.9  | 3    |
| 631 | Two Novel Candidate Genes for Insulin Secretion Identified by Comparative Genomics of Multiple Backcross Mouse Populations. <b>2018</b> , 210, 1527-1542  |      | 10   |
| 630 | Exome sequencing-based identification of novel type 2 diabetes risk allele loci in the Qatari population. <b>2018</b> , 13, e0199837  |      | 3    |
| 629 | Type 2 Diabetes-Associated Genetic Variants Regulate Chromatin Accessibility in Human Islets. <i>Diabetes</i> , <b>2018</b> , 67, 2466-2477   | 0.9  | 31   |
| 628 | Prevention of type 2 diabetes-success story that is waiting for next steps. <b>2018</b> , 72, 1260-1266   |      | 6    |
| 627 | Islet prohormone processing in health and disease. <i>Diabetes, Obesity and Metabolism</i> , <b>2018</b> , 20 Suppl 2, 64-76  | 6.7  | 29   |
| 626 | Identification of novel variants associated with osteoporosis, type 2 diabetes and potentially pleiotropic loci using pleiotropic cFDR method. <b>2018</b> , 117, 6-14                          |      | 11   |

| 625                      | Type 2 diabetes mellitus: distribution of genetic markers in Kazakh population. 2018, 13, 377-388  | 4                       |
|--------------------------|--|-------------------------|
| 624                      | Pathophysiology of Type 2 Diabetes in Koreans. <b>2018</b> , 33, 9-16  | 8                       |
| 623                      | A Systems Perspective of Complex Diseases: From Reductionism to Integration. <b>2018</b> , 17-36   |                         |
| 622                      | Identification of Novel Candidate Markers of Type 2 Diabetes and Obesity in Russia by Exome Sequencing with a Limited Sample Size. <i>Genes</i> , <b>2018</b> , 9,   | 14                      |
| 621                      | Hematopoietically expressed homeobox gene is associated with type 2 diabetes in KK Cg-A/J mice and a Taiwanese Han Chinese population. <b>2018</b> , 16, 185-191   | 6                       |
| 620                      | Common and Rare Coding Genetic Variation Underlying the Electrocardiographic PR Interval. <b>2018</b> , 11, e002037  | 11                      |
| 619                      | From genome-wide associations to candidate causal variants by statistical fine-mapping. <b>2018</b> , 19, 491-504  | 289                     |
| 618                      | Rare-Variant Studies to Complement Genome-Wide Association Studies. <b>2018</b> , 19, 97-112   | 15                      |
| 617                      | The ADRA2A rs553668 variant is associated with type 2 diabetes and five variants were associated at nominal significance levels in a population-based case-control study from Mexico City. <b>2018</b> , 669, 28-34  | 8                       |
|                          |  |                         |
| 616                      | The personal and clinical utility of polygenic risk scores. <b>2018</b> , 19, 581-590  | 582                     |
| 616                      | The personal and clinical utility of polygenic risk scores. <b>2018</b> , 19, 581-590  Network Analysis as a Grand Unifier in Biomedical Data Science. <b>2018</b> , 1, 153-180  | 582<br>17               |
|                          |  |                         |
| 615                      | Network Analysis as a Grand Unifier in Biomedical Data Science. <b>2018</b> , 1, 153-180   | 17                      |
| 615<br>614               | Network Analysis as a Grand Unifier in Biomedical Data Science. <b>2018</b> , 1, 153-180  Reagent Validation to Facilitate Experimental Reproducibility. <b>2018</b> , 81, e40  Genotype imputation for Han Chinese population using Haplotype Reference Consortium as   | 17<br>4                 |
| 615<br>614<br>613        | Network Analysis as a Grand Unifier in Biomedical Data Science. <b>2018</b> , 1, 153-180  Reagent Validation to Facilitate Experimental Reproducibility. <b>2018</b> , 81, e40  Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. <b>2018</b> , 137, 431-436   | 17<br>4<br>9            |
| 615<br>614<br>613        | Network Analysis as a Grand Unifier in Biomedical Data Science. 2018, 1, 153-180  Reagent Validation to Facilitate Experimental Reproducibility. 2018, 81, e40  Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. 2018, 137, 431-436  Genetics of migraine. 2018, 148, 493-503   | 17<br>4<br>9            |
| 615<br>614<br>613<br>612 | Network Analysis as a Grand Unifier in Biomedical Data Science. 2018, 1, 153-180  Reagent Validation to Facilitate Experimental Reproducibility. 2018, 81, e40  Genotype imputation for Han Chinese population using Haplotype Reference Consortium as reference. 2018, 137, 431-436  Genetics of migraine. 2018, 148, 493-503  Drug-induced hyperglycaemia and diabetes: pharmacogenomics perspectives. 2018, 41, 725-736  Nonsynonymous Variants in and Are Associated With Type 2 Diabetes in an East Asian Population. | 17<br>4<br>9<br>22<br>8 |

| 607 | Reproducibility in Biomedical Research. <b>2018</b> , 1-66   |     | 1   |
|-----|--|-----|-----|
| 606 | Advances in the Genetics of Youth-Onset Type 2 Diabetes. <b>2018</b> , 18, 57  |     | 15  |
| 605 | Transcription factor-7-like 2 () gene acts downstream of the / kinase to control mTOR signaling, [] cell growth, and insulin secretion. <b>2018</b> , 293, 14178-14189   |     | 15  |
| 604 | Identification of novel high-impact recessively inherited type 2 diabetes risk variants in the Greenlandic population. <i>Diabetologia</i> , <b>2018</b> , 61, 2005-2015   | ).3 | 11  |
| 603 | Genetic basis of early-onset, maturity-onset diabetes of the young-like diabetes in Japan and features of patients without mutations in the major MODY genes: Dominance of maternal inheritance. <b>2018</b> , 19, 1164-1172 |     | 12  |
| 602 | Nonalcoholic Fatty Liver Disease as a High-Value Predictor of Postoperative Hyperglycemia and Its Associated Complications in Major Abdominal Surgery. <b>2018</b> , 227, 419-429.e6   |     | 4   |
| 601 | BoostMe accurately predicts DNA methylation values in whole-genome bisulfite sequencing of multiple human tissues. <b>2018</b> , 19, 390   |     | 21  |
| 600 | Genetic interaction effects reveal lipid-metabolic and inflammatory pathways underlying common metabolic disease risks. <b>2018</b> , 11, 54   |     | 7   |
| 599 | Using whole genome scores to compare three clinical phenotyping methods in complex diseases.  Scientific Reports, 2018, 8, 11360  4:9  | 9   | 7   |
| 598 | Type 2 diabetes risk alleles in PAM impact insulin release from human pancreatic Etells. <b>2018</b> , 50, 1122-113  | 31  | 35  |
| 597 | Dietary and genetic risk scores and incidence of type 2 diabetes. <b>2018</b> , 13, 13   |     | 22  |
| 596 | Genome-wide association analyses identify 143 risk variants and putative regulatory mechanisms for type 2 diabetes. <b>2018</b> , 9, 2941  |     | 262 |
| 595 | High-Throughput Approaches onto Uncover (Epi)Genomic Architecture of Type 2 Diabetes. <i>Genes</i> , 2018, 9,  | 2   | 10  |
| 594 | Transcriptional Regulation of Glucose Metabolism: The Emerging Role of the HMGA1 Chromatin Factor. <i>Frontiers in Endocrinology</i> , <b>2018</b> , 9, 357  | 7   | 20  |
| 593 | Understanding human fetal pancreas development using subpopulation sorting, RNA sequencing and single-cell profiling. <b>2018</b> , 145,   |     | 42  |
| 592 | Impact of KCNQ1, CDKN2A/2B, CDKAL1, HHEX, MTNR1B, SLC30A8, TCF7L2, and UBE2E2 on risk of developing type 2 diabetes in Thai population. <b>2018</b> , 19, 93   |     | 19  |
| 591 | Views Of Primary Care Providers On Testing Patients For Genetic Risks For Common Chronic Diseases. <b>2018</b> , 37, 793-800   |     | 36  |
| 590 | A Study on the Association Between Polymorphisms in the Cytochrome P450 Family 17 Subfamily A Member 1 Gene Region and Type 2 Diabetes Mellitus in Han Chinese. <i>Frontiers in Endocrinology</i> , 5.7 <b>2018</b> , 9, 323 | 7   | 4   |

| 589              | Genetic variants in long noncoding RNA H19 and MEG3 confer risk of type 2 diabetes in an Iranian population. <b>2018</b> , 675, 265-271  |      | 32   |
|------------------|--|------|------|
| 588              | What Can Diabetes-Associated Genetic Variation in TCF7L2 Teach Us About the Pathogenesis of Type 2 Diabetes?. <b>2018</b> , 16, 383-389  |      | 9    |
| 587              | A coding and non-coding transcriptomic perspective on the genomics of human metabolic disease. <b>2018</b> , 46, 7772-7792   |      | 22   |
| 586              | Identification and functional analysis of glycemic trait loci in the China Health and Nutrition Survey. <b>2018</b> , 14, e1007275   |      | 25   |
| 585              | An Exome-wide Association Study for Type 2 Diabetes-Attributed End-Stage Kidney Disease in African Americans. <b>2018</b> , 3, 867-878   |      | 9    |
| 5 <sup>8</sup> 4 | A Hepatocyte FOXN3-Ecell Glucagon Axis Regulates Fasting Glucose. 2018, 24, 312-319  |      | 6    |
| 583              | The Genetics and Development of Scoliosis. 2018,   |      | 6    |
| 582              | Identification of a missense variant in the WFS1 gene that causes a mild form of Wolfram syndrome and is associated with risk for type 2 diabetes in Ashkenazi Jewish individuals. <i>Diabetologia</i> , <b>2018</b> , 61, 2180-2188 | 10.3 | 19   |
| 581              | Possible role of TCF7L2 in the pathogenesis of type 2 diabetes mellitus. <b>2018</b> , 32, 830-834   |      | 9    |
| 580              | Genetics of Diabetes and Diabetic Complications. 2018, 1-60  |      |      |
| 579              | Pathway-based approach using hierarchical components of rare variants to analyze multiple phenotypes. <b>2018</b> , 19, 79   |      | 6    |
| 578              | Pilot genome-wide association study identifying novel risk loci for type 2 diabetes in a Maya population. <b>2018</b> , 677, 324-331   |      | 9    |
| 577              | Genetically Altered Mice as an Approach for the Investigation of Obesity and Metabolic Disease. <b>2018</b> , 233-255  |      |      |
| 576              | Genome-wide polygenic scores for common diseases identify individuals with risk equivalent to monogenic mutations. <b>2018</b> , 50, 1219-1224   |      | 1073 |
| 575              | Genes that make you fat, but keep you healthy. <b>2018</b> , 284, 450-463  |      | 25   |
| 574              | Toll-like Receptor 4 Pathway Polymorphisms Interact with Pollution to Influence Asthma Diagnosis and Severity. <i>Scientific Reports</i> , <b>2018</b> , 8, 12713  | 4.9  | 12   |
| 573              | The research data management platform (RDMP): A novel, process driven, open-source tool for the management of longitudinal cohorts of clinical data. <b>2018</b> , 7,  |      | 6    |
| 572              | Type 2 diabetes-associated variants of the MT melatonin receptor affect distinct modes of signaling. <b>2018</b> , 11,   |      | 33   |

| 571 | The value of genetic risk scores in precision medicine for diabetes. <b>2018</b> , 3, 279-281   | 14  |
|-----|---|-----|
| 570 | Applicability of Precision Medicine Approaches to Managing Hypertension in Rural Populations. <b>2018</b> , 8,  | 5   |
| 569 | Zebrafish as a Model for Obesity and Diabetes. <b>2018</b> , 6, 91  | 98  |
| 568 | Cohort Profile: Genetics of Diabetes Audit and Research in Tayside Scotland (GoDARTS). <b>2018</b> , 47, 380-381j   | 37  |
| 567 | Genomic insights into the causes of type 2 diabetes. <b>2018</b> , 391, 2463-2474   | 64  |
| 566 | Common Disease Is More Complex Than Implied by the Core Gene Omnigenic Model. <b>2018</b> , 173, 1573-1580  | 151 |
| 565 | Genetic studies of gestational duration and preterm birth. 2018, 52, 33-47  | 24  |
| 564 | Genetic inactivation of ANGPTL4 improves glucose homeostasis and is associated with reduced risk of diabetes. <b>2018</b> , 9, 2252   | 71  |
| 563 | Human Genetics of Obesity and Type 2 Diabetes Mellitus: Past, Present, and Future. <b>2018</b> , 11, e002090  | 41  |
| 562 | Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. <b>2018</b> , 14, e1007329  | 41  |
| 561 | IBD risk loci are enriched in multigenic regulatory modules encompassing putative causative genes. <b>2018</b> , 9, 2427  | 95  |
| 560 | Cardiovascular disease: The rise of the genetic risk score. <b>2018</b> , 15, e1002546  | 81  |
| 559 | Body Composition and Genetic Lipodystrophy Risk Score Associate With Nonalcoholic Fatty Liver Disease and Liver Fibrosis. <b>2019</b> , 3, 1073-1084                                      | 9   |
| 558 | Genetic Predisposition to Type 2 Diabetes and Risk of Subclinical Atherosclerosis and Cardiovascular Diseases Among 160,000 Chinese Adults. <i>Diabetes</i> , <b>2019</b> , 68, 2155-2164 | 20  |
| 557 | Recent advances and perspectives in next generation sequencing application to the genetic research of type 2 diabetes. <b>2019</b> , 10, 376-395  | 8   |
| 556 | GNAS gene is an important regulator of insulin secretory capacity in pancreatic Etells. 2019, 715, 144028   | 14  |
| 555 | Modeling Monogenic Diabetes using Human ESCs Reveals Developmental and Metabolic Deficiencies Caused by Mutations in HNF1A. <b>2019</b> , 25, 273-289.e5                                  | 35  |
| 554 | How Recent Advances in Genomics Improve Precision Diagnosis and Personalized Care of Maturity-Onset Diabetes of the Young. <b>2019</b> , 19, 79   | 10  |

| 553 | The Locus: A Genetic Window Into the Pathogenesis of Type 1 and Type 2 Diabetes. <b>2019</b> , 42, 1624-162  | !9  | 23  |
|-----|--|-----|-----|
| 552 | Pathway analysis of rare variants for the clustered phenotypes by using hierarchical structured components analysis. <b>2019</b> , 12, 100   |     | 5   |
| 551 | Beta-Cell Dedifferentiation in Type 2 Diabetes: Concise Review. <b>2019</b> , 37, 1267-1272  |     | 17  |
| 550 | Type 2 Diabetes: Multiple Genes, Multiple Diseases. <b>2019</b> , 19, 55   |     | 28  |
| 549 | On Distributed Collaboration for Biomedical Analyses. <b>2019</b> ,  |     | 2   |
| 548 | ZRANB3 is an African-specific type 2 diabetes locus associated with beta-cell mass and insulin response. <b>2019</b> , 10, 3195  |     | 46  |
| 547 | A multivariable approach for risk markers from pooled molecular data with only partial overlap. <b>2019</b> , 20, 128  |     |     |
| 546 | The Genetic Epidemiology of Type 2 Diabetes: Opportunities for Health Translation. <b>2019</b> , 19, 62  |     | 16  |
| 545 | Quality of dietary fat and genetic risk of type 2 diabetes: individual participant data meta-analysis. <b>2019</b> , 366, l4292  |     | 23  |
| 544 | Evaluating the Potential of Younger Cases and Older Controls Cohorts to Improve Discovery Power in Genome-Wide Association Studies of Late-Onset Diseases. <b>2019</b> , 9,                                  |     | 3   |
| 543 | Epigenetics and Type 2 Diabetes Risk. <b>2019</b> , 19, 47   |     | 14  |
| 542 | Human pancreatic islet three-dimensional chromatin architecture provides insights into the genetics of type 2 diabetes. <b>2019</b> , 51, 1137-1148  |     | 111 |
| 541 | Phytochemical constituents, antioxidant and antidiabetic activities of different extracts of the leaves, stem and root barks of Alstonia boonei: an in vitro and in silico study. <b>2019</b> , 166, 444-456 |     | 6   |
| 540 | Age-Linked Non-Transmissible Diseases. <b>2019</b> , 59-82   |     |     |
| 539 | Genome-wide Association Study of Change in Fasting Glucose over time in 13,807 non-diabetic European Ancestry Individuals. <i>Scientific Reports</i> , <b>2019</b> , 9, 9439                                 | 4.9 | 3   |
| 538 | T2D Risk Genes: Exome Sequencing Goes Straight to the Source. <b>2019</b> , 30, 10-11  |     | 2   |
| 537 | Genetics, adaptation to environmental changes and archaic admixture in the pathogenesis of diabetes mellitus in Indigenous Australians. <b>2019</b> , 20, 321-332  |     | 2   |
| 536 | Diabetic kidney diseases revisited: A new perspective for a new era. <b>2019</b> , 30, 250-263   |     | 54  |

| 535 | Genome-Wide Association Studies. <b>2019</b> ,  | O  |
|-----|---|----|
| 534 | Double or hybrid diabetes: A systematic review on disease prevalence, characteristics and risk factors. <b>2019</b> , 9, 33   | 39 |
| 533 | Dietary Fat and the Genetic Risk of Type 2 Diabetes. <b>2019</b> , 19, 109  | 3  |
| 532 | The Role of Genetic Variant rs13266634 in SLC30A8/ZnT8 in Post-Operative Hyperglycemia after Major Abdominal Surgery. <b>2019</b> ,   |    |
| 531 | Topological data analysis can extract sub-groups with high incidence rates of Type 2 diabetes. <b>2019</b> , 22, 44   |    |
| 530 | Ultrarare variants drive substantial cis heritability of human gene expression. <b>2019</b> , 51, 1349-1355   | 46 |
| 529 | (Epi)genomic heterogeneity of pancreatic islet function and failure in type 2 diabetes. <b>2019</b> , 27S, S15-S24  | 7  |
| 528 | "Omics" and "epi-omics" underlying the Eell adaptation to insulin resistance. <b>2019</b> , 27S, S42-S48  | 9  |
| 527 | Biomarkers for type 2 diabetes. <b>2019</b> , 27S, S139-S146  | 42 |
| 526 | Network medicine-travelling with the insulin receptor: Encounter of the second type. <b>2019</b> , 13, 14-20  | Ο  |
| 525 | Rapid and room temperature detection of single nucleotide variation with enhanced discrimination by crowding assisted allele specific extension. <b>2019</b> , 55, 12052-12055                  | 1  |
| 524 | Genetic Risk Scores for Diabetes Diagnosis and Precision Medicine. <b>2019</b> , 40, 1500-1520  | 94 |
| 523 | Large-Scale "OMICS" Studies to Explore the Physiopatholgy of HIV-1 Infection. <i>Frontiers in Genetics</i> , <b>2019</b> , 10, 799  | 3  |
| 522 | The Role of Pharmacogenomics in Diabetes. <b>2019</b> , 247-269   |    |
| 521 | Inferring the potentially complex genetic architectures of adaptation, sexual dimorphism and genotype by environment interactions by partitioning of mean phenotypes. <b>2019</b> , 32, 369-379 | 1  |
| 520 | ARL15 overexpression attenuates high glucose-induced impairment of insulin signaling and oxidative stress in human umbilical vein endothelial cells. <b>2019</b> , 220, 127-135                 | 7  |
| 519 | Jackknife Model Averaging Prediction Methods for Complex Phenotypes with Gene Expression Levels by Integrating External Pathway Information. <b>2019</b> , 2019, 2807470                        | 6  |
| 518 | The Burmese cat as a genetic model of type 2 diabetes in humans. <b>2019</b> , 50, 319-325  | 9  |
|     |   |    |

| 517 | Immune-related somatic mutation genes are enriched in PDACs with diabetes. 2019, 12, 1147-1154   |      | 4   |
|-----|--|------|-----|
| 516 | Geographic Variation and Bias in the Polygenic Scores of Complex Diseases and Traits in Finland. <b>2019</b> , 104, 1169-1181  |      | 50  |
| 515 | Inferring the Nature of Missing Heritability in Human Traits Using Data from the GWAS Catalog. <b>2019</b> , 212, 891-904  |      | 16  |
| 514 | Type 2 diabetes: a multifaceted disease. <i>Diabetologia</i> , <b>2019</b> , 62, 1107-1112   | 10.3 | 55  |
| 513 | Systemic Lupus Erythematosus. <b>2019</b> , 1-17   |      |     |
| 512 | The Biology of Senescence. <b>2019</b> ,   |      |     |
| 511 | Exome sequencing of 20,791 cases of type 2 diabetes and 24,440 controls. <i>Nature</i> , <b>2019</b> , 570, 71-76  | 50.4 | 129 |
| 510 | Adipocyte Metabolism and Insulin Signaling Perturbations: Insights from Genetics. <b>2019</b> , 30, 396-406  |      | 9   |
| 509 | Pancreatic islet chromatin accessibility and conformation reveals distal enhancer networks of type 2 diabetes risk. <b>2019</b> , 10, 2078   |      | 41  |
| 508 | Benefits and limitations of genome-wide association studies. <b>2019</b> , 20, 467-484   |      | 516 |
| 507 | Milk in the prevention and management of type 2 diabetes: The potential role of milk proteins. <b>2019</b> , 35, e3187   |      | 9   |
| 506 | Diagnostic high-throughput sequencing of 2396 patients with bleeding, thrombotic, and platelet disorders. <b>2019</b> , 134, 2082-2091   |      | 70  |
| 505 | Exome chip-driven association study of lipidemia in >14,000 Koreans and evaluation of genetic effect on identified variants between different ethnic groups. <b>2019</b> , 43, 617-628 |      | 2   |
| 504 | Diabetes: Is There a Future for Pharmacogenomics Guided Treatment?. <b>2019</b> , 106, 329-337   |      | 18  |
| 503 | Post-selection estimation and testing following aggregate association tests. <b>2019</b> , 81, 547-573   |      | 5   |
| 502 | Trans Effects on Gene Expression Can Drive Omnigenic Inheritance. <b>2019</b> , 177, 1022-1034.e6  |      | 183 |
| 501 | The Continuing Evolution of Precision Health in Type 2 Diabetes: Achievements and Challenges. <b>2019</b> , 19, 16   |      | 2   |
| 500 | Genomic Medicine-Progress, Pitfalls, and Promise. <b>2019</b> , 177, 45-57   |      | 75  |

| 499 | The Genetic Basis of Metabolic Disease. <b>2019</b> , 177, 146-161  |     | 51  |  |
|-----|---|-----|-----|--|
| 498 | A semiparametric efficient estimator in case-control studies for gene-environment independent models. <b>2019</b> , 173, 38-50  |     | 2   |  |
| 497 | "Wasting away": Diabetes, food insecurity, and medical insecurity in the Somali Region of Ethiopia. <b>2019</b> , 228, 155-163  |     | 13  |  |
| 496 | Cohort Profile: The Henan Rural Cohort: a prospective study of chronic non-communicable diseases. <b>2019</b> , 48, 1756-1756j  |     | 119 |  |
| 495 | Identification of Functional Gene Modules Associated With STAT-Mediated Antiviral Responses to White Spot Syndrome Virus in Shrimp. <b>2019</b> , 10, 212   |     | 5   |  |
| 494 | Association of variants in HTRA1 and NOTCH3 with MRI-defined extremes of cerebral small vessel disease in older subjects. <b>2019</b> , 142, 1009-1023  |     | 21  |  |
| 493 | Discovering metabolic disease gene interactions by correlated effects on cellular morphology. <b>2019</b> , 24, 108-119   |     | 6   |  |
| 492 | Omics: Potential Role in Early Phase Drug Development. <b>2019</b> , 309-347  |     |     |  |
| 491 | The Contribution of Low-Frequency and Rare Coding Variation to Susceptibility to Type 2 Diabetes. <b>2019</b> , 19, 25  |     | 7   |  |
| 490 | Etiology and Pathogenesis of Latent Autoimmune Diabetes in Adults (LADA) Compared to Type 2 Diabetes. <b>2019</b> , 10, 320   |     | 25  |  |
| 489 | Roadmap for a precision-medicine initiative in the Nordic region. <b>2019</b> , 51, 924-930   |     | 12  |  |
| 488 | Noninvasive Self-diagnostic Device for Tear Collection and Glucose Measurement. <i>Scientific Reports</i> , <b>2019</b> , 9, 4747   | 4.9 | 13  |  |
| 487 | Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data. <b>2019</b> , 11, 19  |     | 18  |  |
| 486 | Point mutations in the PDX1 transactivation domain impair human Etell development and function. <b>2019</b> , 24, 80-97   |     | 27  |  |
| 485 | Deficiency of ZnT8 Promotes Adiposity and Metabolic Dysfunction by Increasing Peripheral Serotonin Production. <i>Diabetes</i> , <b>2019</b> , 68, 1197-1209  | 0.9 | 11  |  |
| 484 | Pancreatic Pericytes in Glucose Homeostasis and Diabetes. <i>Advances in Experimental Medicine and Biology</i> , <b>2019</b> , 1122, 27-40  | 3.6 | 3   |  |
| 483 | Tobacco and type 2 diabetes: is the association explained by genetic factors?. <b>2019</b> , 48, 926-933  |     | 2   |  |
| 482 | Could the high consumption of high glycaemic index carbohydrates and sugars, associated with the nutritional transition to the Western type of diet, be the common cause of the obesity epidemic and the worldwide increasing incidences of Type 1 and Type 2 diabetes?. <b>2019</b> , 125, 41-50 |     | 14  |  |

| 481 | Genetic landscape of chronic obstructive pulmonary disease identifies heterogeneous cell-type and phenotype associations. <b>2019</b> , 51, 494-505                                      |      | 119 |
|-----|--|------|-----|
| 480 | Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <b>2019</b> , 51, 452-469  |      | 44  |
| 479 | The Korea Biobank Array: Design and Identification of Coding Variants Associated with Blood Biochemical Traits. <i>Scientific Reports</i> , <b>2019</b> , 9, 1382                        | 4.9  | 82  |
| 478 | Quantification of frequency-dependent genetic architectures in 25 UK Biobank traits reveals action of negative selection. <b>2019</b> , 10, 790  |      | 55  |
| 477 | PAS-SNP: iOS App with GWAS SNP-Disease Database for Personalized Genomics Research: PAS-SNP for GWAS SNP-Disease. <b>2019</b> ,  |      |     |
| 476 | Association Between Long-term Exposure to PM2.5 and Incidence of Type 2 Diabetes in Taiwan: A National Retrospective Cohort Study. <b>2019</b> , 30 Suppl 1, S67-S75                     |      | 16  |
| 475 | Pancreatic Islet Transcriptional Enhancers and Diabetes. <b>2019</b> , 19, 145   |      | O   |
| 474 | Future Preventive Gene Therapy of Polygenic Diseases from a Population Genetics Perspective. <b>2019</b> , 20,   |      | 1   |
| 473 | Habenular TCF7L2 links nicotine addiction to diabetes. <i>Nature</i> , <b>2019</b> , 574, 372-377  | 50.4 | 47  |
| 472 | Profiling the Oral Microbiome and Plasma Biochemistry of Obese Hyperglycemic Subjects in Qatar. <b>2019</b> , 7,   |      | 7   |
| 471 | PAX4 R192H is associated with younger onset of Type 2 diabetes in East Asians in Singapore. <b>2019</b> , 33, 53-58  |      | 2   |
| 470 | Current perspectives in assessing humoral immunity after measles vaccination. <b>2019</b> , 18, 75-87  |      | 30  |
| 469 | DNA Sequence Variation in Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. <i>Diabetes</i> , <b>2019</b> , 68, 226-234 | 0.9  | 12  |
| 468 | Mediation analysis in a case-control study when the mediator is a censored variable. <b>2019</b> , 38, 1213-122  | 29   | 2   |
| 467 | Systems Genomics of Thigh Adipose Tissue From Asian Indian Type-2 Diabetics Revealed Distinct Protein Interaction Hubs. <i>Frontiers in Genetics</i> , <b>2018</b> , 9, 679              | 4.5  | 4   |
| 466 | Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic ICell Identity and Function. <b>2019</b> , 26, 788-801.e6   |      | 28  |
| 465 | The harmonic mean -value for combining dependent tests. <b>2019</b> , 116, 1195-1200   |      | 94  |
| 464 | Histone Deacetylase HDAC8 and Insulin Resistance. <b>2019</b> , 405-421  |      |     |

| 463 | Established and emerging strategies to crack the genetic code of obesity. <b>2019</b> , 20, 212-240  | 17  |
|-----|--|-----|
| 462 | Kidney Transplant Management. <b>2019</b> ,  |     |
| 461 | Implementation of Genomic Medicine. <b>2019</b> , 369-380  |     |
| 460 | Gallstone Disease and Type 2 Diabetes Risk: A Mendelian Randomization Study. <b>2019</b> , 70, 610-620   | 11  |
| 459 | Discovery of common and rare genetic risk variants for colorectal cancer. <b>2019</b> , 51, 76-87  | 177 |
| 458 | Starvation in the Midst of Plenty: Reflections on the History and Biology of Insulin and Leptin. <b>2019</b> , 40, 1-16  | 26  |
| 457 | Sweet fish: Fish models for the study of hyperglycemia and diabetes. <b>2019</b> , 11, 193-203   | 18  |
| 456 | Big data management challenges in health research-a literature review. <b>2019</b> , 20, 156-167   | 31  |
| 455 | Two novel susceptibility loci for type 2 diabetes mellitus identified by longitudinal exome-wide association studies in a Japanese population. <b>2019</b> , 111, 34-42                    | 4   |
| 454 | Missing heritability of complex diseases: case solved?. <b>2020</b> , 139, 103-113   | 44  |
| 453 | Methylglyoxal, a Highly Reactive Dicarbonyl Compound, in Diabetes, Its Vascular Complications, and Other Age-Related Diseases. <b>2020</b> , 100, 407-461                                  | 116 |
| 452 | Type 2 Diabetes. <b>2020</b> ,   | 2   |
| 451 | Nutrients and Gene Expression in Type 2 Diabetes. <b>2020</b> , 441-445  |     |
| 450 | Orphan G-protein coupled receptor 183 (GPR183) potentiates insulin secretion and prevents glucotoxicity-induced Etell dysfunction. <b>2020</b> , 499, 110592                               | 7   |
| 449 | Interaction Between Type 2 Diabetes Prevention Strategies and Genetic Determinants of Coronary Artery Disease on Cardiometabolic Risk Factors. <i>Diabetes</i> , <b>2020</b> , 69, 112-120 | 9   |
| 448 | Using What We Already Have: Uncovering New Drug Repurposing Strategies in Existing Omics Data. <b>2020</b> , 60, 333-352   | 21  |
| 447 | Construction of a Plasmonic Chip for Metabolic Analysis in Cervical Cancer Screening and Evaluation. <b>2020</b> , 4, 1900469  | 44  |
| 446 | Genetics and Chronic Kidney Disease. <b>2020</b> , 375-396   |     |

| 445 | Genetic determinants of bone mass and osteoporotic fracture. 2020, 1615-1630   | 1       |
|-----|--|---------|
| 444 | Combining sequence data from multiple studies: Impact of analysis strategies on rare variant calling and association results. <b>2020</b> , 44, 41-51                        | 1       |
| 443 | Population genetic simulation study of power in association testing across genetic architectures and study designs. <b>2020</b> , 44, 90-103                                 | 5       |
| 442 | Behavioural cardiovascular risk factors and prevalence of diabetes in subjects with familial hypercholesterolaemia. <b>2020</b> , 27, 1649-1660                              | 4       |
| 441 | Emerging roles of Eell mitochondria in type-2-diabetes. <b>2020</b> , 71, 100843   | 15      |
| 440 | Flavonoids and type 2 diabetes: Evidence of efficacy in clinical and animal studies and delivery strategies to enhance their therapeutic efficacy. <b>2020</b> , 152, 104629 | 52      |
| 439 | Melatonin Effects on Glucose Metabolism: Time To Unlock the Controversy. <b>2020</b> , 31, 192-204   | 46      |
| 438 | A brief history of human disease genetics. <i>Nature</i> , <b>2020</b> , 577, 179-189  | ).4 181 |
| 437 | Computational network biology: Data, models, and applications. <b>2020</b> , 846, 1-66   | 54      |
| 436 | The Melanocortin 4 Receptor p.Ile269Asn Mutation Is Associated with Childhood and Adult Obesity in Mexicans. <b>2020</b> , 105,  | 6       |
| 435 | Genetics' Piece of the PI: Inferring the Origin of Complex Traits and Diseases from Proteome-Wide Protein-Protein Interaction Dynamics. <b>2020</b> , 42, e1900169           |         |
| 434 | Genetic variation in rs7903146 correlating with peripheral arterial disease in long-standing type 2 diabetes. <b>2020</b> , 17, 1479164119888475                             | 2       |
| 433 | Pathogenic variants in actionable MODY genes are associated with type 2 diabetes. <b>2020</b> , 2, 1126-1134   | 9       |
| 432 | Divergent genes in gerbils: prevalence, relation to GC-biased substitution, and phenotypic relevance. <b>2020</b> , 20, 134  | O       |
| 431 | Genomics in Personalized Nutrition: Can You "Eat for Your Genes"?. <b>2020</b> , 12,   | 19      |
| 430 | MethHaplo: combining allele-specific DNA methylation and SNPs for haplotype region identification. <b>2020</b> , 21, 451   | 2       |
|     |  |         |
| 429 | Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease. <b>2020</b> , 52, 1169-1177          | 51      |

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| 427                             | Analyzing Functional Pathways and constructing gene-gene network for Narcolepsy based on candidate genes. <b>2020</b> , 17, 1508-1514   | О  |
|---------------------------------|---|--|
| 426                             | Heterogeneous Effects of Calorie Content and Nutritional Components Underlie Dietary Influence on Pancreatic Cancer Susceptibility. <b>2020</b> , 32, 107880  | 1  |
| 425                             | [Diabetes and pancreatic cancer - state of the art]. 2020, 162, 42-46   |  |
| 424                             | Epigenetics in Etell adaptation and type 2 diabetes. <b>2020</b> , 55, 125-131  | 4  |
| 423                             | Improved Semiparametric Analysis of Polygenic Gene <b>E</b> nvironment Interactions in Case <b>C</b> ontrol Studies. <b>2020</b> , 1  |  |
| 422                             | Disentangling the heterogeneity of adulthood-onset non-autoimmune diabetes: a little closer but lot more to do. <b>2020</b> , 55, 157-164   | 3  |
| 421                             | Persistent or Transient Human ICell Dysfunction Induced by Metabolic Stress: Specific Signatures and Shared Gene Expression with Type 2 Diabetes. <b>2020</b> , 33, 108466  | 22                                       |
| 420                             | Polymorphisms of the Gene Encoding Cytochrome b-245 Beta Chain of NADPH Oxidase: Relationship with Redox Homeostasis Markers and Risk of Type 2 Diabetes Mellitus. <b>2020</b> , 56, 856-862  | 3  |
| 419                             | Genetic variants in glutamate cysteine ligase confer protection against type 2 diabetes. <b>2020</b> , 47, 5793-5805  | 7  |
|                                 |   |  |
| 418                             | Pathophysiology of Type 2 Diabetes Mellitus. <b>2020</b> , 21,  | 222                                      |
| 418<br>417                      | Pathophysiology of Type 2 Diabetes Mellitus. <b>2020</b> , 21,  Canalization and Robustness in Human Genetics and Disease. <b>2020</b> , 54, 189-211  | 6  |
|                                 |   |  |
| 417                             | Canalization and Robustness in Human Genetics and Disease. <b>2020</b> , 54, 189-211  |  |
| 417<br>416                      | Canalization and Robustness in Human Genetics and Disease. <b>2020</b> , 54, 189-211  Diabetesclusters: Diabetessubgruppen und Folgeerkrankungen. <b>2020</b> , 16, 635-640  Beta cell dysfunction in diabetes: the islet microenvironment as an unusual suspect. <i>Diabetologia</i> ,   | 6  |
| 417<br>416<br>415               | Canalization and Robustness in Human Genetics and Disease. 2020, 54, 189-211  Diabetesclusters: Diabetessubgruppen und Folgeerkrankungen. 2020, 16, 635-640  Beta cell dysfunction in diabetes: the islet microenvironment as an unusual suspect. <i>Diabetologia</i> , 2020, 63, 2076-2085   | 21                                       |
| 417<br>416<br>415<br>414        | Canalization and Robustness in Human Genetics and Disease. 2020, 54, 189-211  Diabetesclusters: Diabetessubgruppen und Folgeerkrankungen. 2020, 16, 635-640  Beta cell dysfunction in diabetes: the islet microenvironment as an unusual suspect. <i>Diabetologia</i> , 2020, 63, 2076-2085  Human and molecular genetics shed lights on fatty liver disease and diabetes conundrum. 2020, 3, e00179  | <ul><li>6</li><li>21</li><li>5</li></ul> |
| 417<br>416<br>415<br>414<br>413 | Canalization and Robustness in Human Genetics and Disease. 2020, 54, 189-211  Diabetesclusters: Diabetessubgruppen und Folgeerkrankungen. 2020, 16, 635-640  Beta cell dysfunction in diabetes: the islet microenvironment as an unusual suspect. <i>Diabetologia</i> , 2020, 63, 2076-2085  Human and molecular genetics shed lights on fatty liver disease and diabetes conundrum. 2020, 3, e00179  Precision Health and Nursing: Seeing the Familiar in the Foreign. 2020, 52, 199-208  A method for scoring the cell type-specific impacts of noncoding variants in personal genomes. | 6<br>21<br>5<br>2                        |

| 409 | Unsupervised Clustering of Missense Variants in HNF1A Using Multidimensional Functional Data Aids Clinical Interpretation. <b>2020</b> , 107, 670-682       | 9  |
|-----|---|----|
| 408 | Identification of type 2 diabetes loci in 433,540 East Asian individuals. <i>Nature</i> , <b>2020</b> , 582, 240-245 50.4                                   | 89 |
| 407 | Genetic predisposition in type 2 diabetes: A promising approach toward a personalized management of diabetes. <b>2020</b> , 98, 525-547                     | 16 |
| 406 | Smoking-by-genotype interaction in type 2 diabetes risk and fasting glucose. <b>2020</b> , 15, e0230815   | 4  |
| 405 | Circulating Protein Signatures and Causal Candidates for Type 2 Diabetes. <i>Diabetes</i> , <b>2020</b> , 69, 1843-18530.9                                  | 27 |
| 404 | Review article: the emerging role of genetics in precision medicine for patients with non-alcoholic steatohepatitis. <b>2020</b> , 51, 1305-1320            | 38 |
| 403 | A novel approach to modeling multifactorial diseases using Ensemble Bayesian Rule classifiers. <b>2020</b> , 107, 103455                                    | 0  |
| 402 | Identifying novel associations in GWAS by hierarchical Bayesian latent variable detection of differentially misclassified phenotypes. <b>2020</b> , 21, 178 | 3  |
| 401 | From personalised nutrition to precision medicine: the rise of consumer genomics and digital health. <b>2020</b> , 79, 300-310                              | 5  |
| 400 | Comparison of sirtuin 1 level and related blood factors in diabetic and healthy subjects. <b>2020</b> , 26, 17-21   | 2  |
| 399 | Cohort profile: the Singapore diabetic cohort study. <b>2020</b> , 10, e036443  | 2  |
| 398 | Importance of Genetic Studies of Cardiometabolic Disease in Diverse Populations. <b>2020</b> , 126, 1816-1840   | 7  |
| 397 | Association between genetic risk scores and risk of narcolepsy: a case-control study. <b>2020</b> , 8, 103  | Ο  |
| 396 | The influence of rare variants in circulating metabolic biomarkers. <b>2020</b> , 16, e1008605  | 3  |
| 395 | Dietary SCFAs Immunotherapy: Reshaping the Gut Microbiota in Diabetes. <i>Advances in Experimental Medicine and Biology</i> , <b>2021</b> , 1307, 499-519   | 6  |
| 394 | Transcription Factor RREB1: from Target Genes towards Biological Functions. <b>2020</b> , 16, 1463-1473   | 14 |
| 393 | Systematic Review of Polygenic Risk Scores for Type 1 and Type 2 Diabetes. <b>2020</b> , 21,  | 15 |
| 392 | Sequencing and imputation in GWAS: Cost-effective strategies to increase power and genomic coverage across diverse populations. <b>2020</b> , 44, 537-549   | 10 |

## (2020-2020)

| 391 | Identification and genomic analysis of pedigrees with exceptional longevity identifies candidate rare variants. <b>2020</b> , 143, 104972  | 5   |
|-----|--|-----|
| 390 | Molecular genetic approaches to dissect complex behaviors in zebrafish. <b>2020</b> , 223-244  | Ο   |
| 389 | A Complex Systems Model of Breast Cancer Etiology: The Paradigm II Conceptual Model. <b>2020</b> , 29, 1720-1730   | 5   |
| 388 | A Long Non-coding RNA, , Is an Effector Transcript at the Chromosome 8p23.1- Metabolic Traits and Type 2 Diabetes Risk Locus. <i>Frontiers in Genetics</i> , <b>2020</b> , 11, 615                 | 5   |
| 387 | Microevolutionary Dynamics of Chicken Genomes under Divergent Selection for Adiposity. <b>2020</b> , 23, 101193  | 1   |
| 386 | Insights into pancreatic islet cell dysfunction from type 2 diabetes mellitus genetics. <b>2020</b> , 16, 202-212  | 50  |
| 385 | Intolerance of loud sounds in childhood: Is there an intergenerational association with grandmaternal smoking in pregnancy?. <b>2020</b> , 15, e0229323  | 4   |
| 384 | Polygenic risk score as a key factor in cardiovascular clinical prediction models. <b>2020</b> , 73, 608-610   |     |
| 383 | Mechanisms of diabetic cardiomyopathy and potential therapeutic strategies: preclinical and clinical evidence. <b>2020</b> , 17, 585-607   | 139 |
| 382 | Toward Genetic Prediction of Nonalcoholic Fatty Liver Disease Trajectories: PNPLA3 and Beyond. <b>2020</b> , 158, 1865-1880.e1   | 42  |
| 381 | Combined analysis of whole-exon sequencing and lncRNA sequencing in type 2 diabetes mellitus patients with obesity. <b>2020</b> , 24, 2451-2463  | 2   |
| 380 | A Dual Reporter EndoC-H1 Human Ecell Line for Efficient Quantification of Calcium Flux and Insulin Secretion. <b>2020</b> , 161,   | 5   |
| 379 | The derived allele of a novel intergenic variant at chromosome 11 associates with lower body mass index and a favorable metabolic phenotype in Greenlanders. <b>2020</b> , 16, e1008544            | 1   |
| 378 | From Genetic Association to Molecular Mechanisms for Islet-cell Dysfunction in Type 2 Diabetes. <b>2020</b> , 432, 1551-1578   | 16  |
| 377 | Genome-wide rare variant analysis for thousands of phenotypes in over 70,000 exomes from two cohorts. <b>2020</b> , 11, 542  | 47  |
| 376 | Pleiotropic Effects of a KCNQ1 Variant on Lipid Profiles and Type 2 Diabetes: A Family-Based Study in China. <b>2020</b> , 2020, 8278574   | 1   |
| 375 | Genome-wide association study identifies novel risk variants from RPS6KA1, CADPS, VARS, and DHX58 for fasting plasma glucose in Arab population. <i>Scientific Reports</i> , <b>2020</b> , 10, 152 | 9   |
| 374 | Neurocognitive impairment in type 2 diabetes: evidence for shared genetic aetiology. <i>Diabetologia</i> , <b>2020</b> , 63, 977-986   | 1   |

| 373                             | Nutrition and its role in epigenetic inheritance of obesity and diabetes across generations. <b>2020</b> , 31, 119-133   |     | 16 |
|---------------------------------|--|-----|----|
| 372                             | Association of variants with hemoglobin A1c and impact on diabetes diagnosis in East Asian individuals. <b>2020</b> , 8,   |     | 7  |
| 371                             | Telomere Maintenance Genes are associated with Type 2 Diabetes Susceptibility in Northwest Indian Population Group. <i>Scientific Reports</i> , <b>2020</b> , 10, 6444   | 4.9 | 4  |
| 370                             | Automated gene data integration with Databio. <b>2020</b> , 13, 195  |     | O  |
| 369                             | Modeling different types of diabetes using human pluripotent stem cells. <b>2021</b> , 78, 2459-2483   |     | 8  |
| 368                             | Recapitulating Evolutionary Divergence in a Single Cis-Regulatory Element Is Sufficient to Cause Expression Changes of the Lens Gene Tdrd7. <b>2021</b> , 38, 380-392  |     | 1  |
| 367                             | Functional evaluation of 16 SCHAD missense variants: Only amino acid substitutions causing congenital hyperinsulinism of infancy lead to loss-of-function phenotypes in vitro. <b>2021</b> , 44, 240-252   |     | O  |
| 366                             | The obesity paradox and diabetes. <b>2021</b> , 26, 1057-1068  |     | 6  |
| 365                             | Human genetic analyses of organelles highlight the nucleus in age-related trait heritability.  |     | 1  |
|                                 | December Chiffic in the Cott Missacking and Burk December 1 District and District a |     |    |
| 364                             | Progressive Shifts in the Gut Microbiome Reflect Prediabetes and Diabetes Development in a Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , <b>2020</b> , 11, 602326  | 5.7 | 2  |
| 364<br>363                      |  | 5:7 | 38 |
|                                 | Treatment-Naive Mexican Cohort. Frontiers in Endocrinology, <b>2020</b> , 11, 602326   | 5.7 |    |
| 363                             | Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , <b>2020</b> , 11, 602326  Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <b>2021</b> , 22, 49  | 5-7 | 38 |
| 363<br>362                      | Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , <b>2020</b> , 11, 602326  Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <b>2021</b> , 22, 49  Epigenetic and Developmental Basis of Risk of Obesity and Metabolic Disease. <b>2021</b> , 289-313  gene polymorphisms and susceptibility to type 2 diabetes: evidence from a meta-regression and   | 5-7 | 38 |
| 363<br>362<br>361               | Treatment-Naive Mexican Cohort. <i>Frontiers in Endocrinology</i> , <b>2020</b> , 11, 602326  Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. <b>2021</b> , 22, 49  Epigenetic and Developmental Basis of Risk of Obesity and Metabolic Disease. <b>2021</b> , 289-313  gene polymorphisms and susceptibility to type 2 diabetes: evidence from a meta-regression and meta-analysis based on 47 studies. <b>2021</b> , 20, 845-867  Whole Genome Sequence Association Analysis of Fasting Glucose and Fasting Insulin Levels in   | 5-7 | 38 |
| 363<br>362<br>361<br>360        | Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. 2021, 22, 49  Epigenetic and Developmental Basis of Risk of Obesity and Metabolic Disease. 2021, 289-313  gene polymorphisms and susceptibility to type 2 diabetes: evidence from a meta-regression and meta-analysis based on 47 studies. 2021, 20, 845-867  Whole Genome Sequence Association Analysis of Fasting Glucose and Fasting Insulin Levels in Diverse Cohorts from the NHLBI TOPMed Program.  Considerations in using human pluripotent stem cellElerived pancreatic beta cells to treat type 1   | 5-7 | 38 |
| 363<br>362<br>361<br>360<br>359 | Exploiting the GTEx resources to decipher the mechanisms at GWAS loci. 2021, 22, 49  Epigenetic and Developmental Basis of Risk of Obesity and Metabolic Disease. 2021, 289-313  gene polymorphisms and susceptibility to type 2 diabetes: evidence from a meta-regression and meta-analysis based on 47 studies. 2021, 20, 845-867  Whole Genome Sequence Association Analysis of Fasting Glucose and Fasting Insulin Levels in Diverse Cohorts from the NHLBI TOPMed Program.  Considerations in using human pluripotent stem cellderived pancreatic beta cells to treat type 1 diabetes. 2021, 173-203  Factors associated with gastro-duodenal ulcer in compensated type 2 diabetic patients: a Romanian   | 5-7 | 38 |

| 355 | Who will benefit from bariatric surgery for diabetes? A protocol for an observational cohort study. <b>2021</b> , 11, e042355   |     | 1  |
|-----|---|-----|----|
| 354 | Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations.  |     | О  |
| 353 | Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a regulator of insulin secretion. <b>2021</b> , 34, 108703                                     |     | 1  |
| 352 | Lack of association between BDNF rs6265 polymorphism and risk of type 2 diabetes: A protocol for meta-analysis and trial sequential analysis. <b>2021</b> , 100, e23305 |     |    |
| 351 | Identification of low-frequency variants of UGT1A3 associated with bladder cancer risk by next-generation sequencing. <b>2021</b> , 40, 2382-2394                       |     | 3  |
| 350 | Interaction between dietary branched-chain amino acids and genetic risk score on the risk of type 2 diabetes in Chinese. <b>2021</b> , 16, 4                            |     | 2  |
| 349 | Loss of Znt8 function in diabetes mellitus: risk or benefit?. <b>2021</b> , 476, 2703-2718  |     | 2  |
| 348 | Model-based assessment of replicability for genome-wide association meta-analysis. <b>2021</b> , 12, 1964   |     | 3  |
| 347 | Impact of pre- and post-variant filtration strategies on imputation. Scientific Reports, 2021, 11, 6214   | 4.9 | 1  |
| 346 | Exome Chip Analysis of 14,026 Koreans Reveals Known and Newly Discovered Genetic Loci Associated with Type 2 Diabetes Mellitus. <b>2021</b> , 45, 231-240               |     | 1  |
| 345 | Whole-genome sequencing of African Americans implicates differential genetic architecture in inflammatory bowel disease. <b>2021</b> , 108, 431-445                     |     | 0  |
| 344 | Enhancer-Gene Interaction Analyses Identified the Epidermal Growth Factor Receptor as a Susceptibility Gene for Type 2 Diabetes Mellitus. <b>2021</b> , 45, 241-250     |     | 1  |
| 343 | A regulatory variant at 3q21.1 confers an increased pleiotropic risk for hyperglycemia and altered bone mineral density. <b>2021</b> , 33, 615-628.e13                  |     | 7  |
| 342 | RegVar: Tissue-specific Prioritization of Noncoding Regulatory Variants.  |     |    |
| 341 | Modulating the Microbiota as a Therapeutic Intervention for Type 2 Diabetes. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 632335                               | 5.7 | 15 |
| 340 | CRISPR-based genome editing in primary human pancreatic islet cells. <b>2021</b> , 12, 2397   |     | 7  |
| 339 | Single-cell chromatin accessibility identifies pancreatic islet cell type- and state-specific regulatory programs of diabetes risk. <b>2021</b> , 53, 455-466           |     | 18 |
| 338 | Genetic architecture of type 2 diabetes and its shared genetic component with low birth weight in African Americans. <b>2021</b> , 24, 326-332                          |     | 1  |

337 Diabetes and Renin-Angiotensin-Aldosterone System: Pathophysiology and Genetics.

| 336 | Multi-omics analysis identifies CpGs near G6PC2 mediating the effects of genetic variants on fasting glucose. <i>Diabetologia</i> , <b>2021</b> , 64, 1613-1625   | 10.3 | 3  |
|-----|---|------|----|
| 335 | Alternative exon splicing and differential expression in pancreatic islets reveals candidate genes and pathways implicated in early diabetes development. <b>2021</b> , 32, 153-172                         |      | 0  |
| 334 | Clinical trials with plants in diabetes mellitus therapy: a systematic review. <b>2021</b> , 14, 735-747  |      | 7  |
| 333 | Genetic variants in the gene are associated with increased BMI and insulin levels in nondiabetic Chilean population. <b>2021</b> , 65, 305-314  |      | 0  |
| 332 | Genetics of canine diabetes mellitus part 2: Current understanding and future directions. <b>2021</b> , 270, 105612   |      | 1  |
| 331 | Progress in Defining the Genetic Contribution to Type 2 Diabetes in Individuals of East Asian Ancestry. <b>2021</b> , 21, 17  |      | 2  |
| 330 | Whole Alga, Algal Extracts, and Compounds as Ingredients of Functional Foods: Composition and Action Mechanism Relationships in the Prevention and Treatment of Type-2 Diabetes Mellitus. <b>2021</b> , 22, |      | 4  |
| 329 | The Human Islet: Mini-Organ With Mega-Impact. <b>2021</b> , 42, 605-657   |      | 7  |
| 328 | Human Pluripotent Stem Cells Go Diabetic: A Glimpse on Monogenic Variants. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 648284   | 5.7  | 2  |
| 327 | Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. <b>2021</b> , 17, e1009531  |      | 4  |
| 326 | Mergeomics 2.0: a web server for multi-omics data integration to elucidate disease networks and predict therapeutics. <b>2021</b> , 49, W375-W387   |      | 4  |
| 325 | Non-Alcoholic Fatty Liver Disease: Metabolic, Genetic, Epigenetic and Environmental Risk Factors. <b>2021</b> , 18,   |      | 13 |
| 324 | The population frequency of human mitochondrial DNA variants is highly dependent upon mutational bias.  |      |    |
| 323 | Leveraging Genomic Associations in Precision Digital Care for Weight Loss: Cohort Study. <b>2021</b> , 23, e25  | 5401 | 2  |
| 322 | A murine model of the human CREBRFR457Q obesity-risk variant does not influence energy or glucose homeostasis in response to nutritional stress.  |      |    |
| 321 | Stakeholder engagement to ensure the sustainability of biobanks: a survey of potential users of biobank services. <b>2021</b> ,   |      | O  |
| 320 | DNA Methylation Patterning and the Regulation of Beta Cell Homeostasis. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 651258  | 5.7  | 7  |

| 319 | Interaction between TCF7L2 rs7903146 Genotype, HbA1c Levels, and the Periodontal Status of Dental Patients. <b>2021</b> , 15, 495-501   | Ο  |
|-----|---|----|
| 318 | Natural anticoagulants: A missing link in mild to moderate bleeding tendencies. <b>2021</b> , 27, 701-709   | 3  |
| 317 | Association of HLA-B Gene Polymorphisms with Type 2 Diabetes in Pashtun Ethnic Population of Khyber Pakhtunkhwa, Pakistan. <b>2021</b> , 2021, 6669731  | 1  |
| 316 | Polygenic Risk Score of Adolescent Idiopathic Scoliosis for Potential Clinical Use. <b>2021</b> , 36, 1481-1491   | 1  |
| 315 | Genome Editing Human Pluripotent Stem Cells to Model ECell Disease and Unmask Novel Genetic Modifiers. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 682625                           | O  |
| 314 | Genome engineering and disease modeling programmable nucleases for insulin gene therapy; promises of CRISPR/Cas9 technology. <b>2021</b> , 13, 485-502  | 2  |
| 313 | RNA m6A reader IMP2/IGF2BP2 promotes pancreatic Etell proliferation and insulin secretion by enhancing PDX1 expression. <b>2021</b> , 48, 101209  | 9  |
| 312 | Knowledge discovery in genetics of diabetes in Iran, a roadmap for future researches <b>2021</b> , 20, 1785-1791  | 1  |
| 311 | Gaining insight into metabolic diseases from human genetic discoveries. <b>2021</b> , 37, 1081-1094   | 1  |
| 310 | Systems Biology Analysis of Human Genomes Points to Key Pathways Conferring Spina Bifida Risk.  |    |
| 309 | Analysis of rare coding variants in 200,000 exome-sequenced subjects reveals novel genetic risk factors for type 2 diabetes. <b>2021</b> , e3482  | 1  |
| 308 | Altered islet prohormone processing: a cause or consequence of diabetes?. <b>2022</b> , 102, 155-208  | 3  |
| 307 | Highly multiplexed rapid DNA detection with single-nucleotide specificity via convective PCR in a portable device. <b>2021</b> , 5, 702-712   | 10 |
| 306 | Screening for monogenic subtypes of gestational diabetes in a high prevalence island population - A whole exome sequencing study. <b>2021</b> , e3486   | O  |
| 305 | Maturity Onset Diabetes of the Young-New Approaches for Disease Modelling. <b>2021</b> , 22,  | 4  |
| 304 | Non-Coding RNAs: Novel Players in Insulin Resistance and Related Diseases. <b>2021</b> , 22,  | 2  |
| 303 | Functional Role of miR-155 in the Pathogenesis of Diabetes Mellitus and Its Complications. <b>2021</b> , 7,   | 8  |
| 302 | Genetic Risk Score for Type 2 Diabetes and Traits Related to Glucose-Insulin Homeostasis in Youth: The Exploring Perinatal Outcomes Among Children (EPOCH) Study. <b>2021</b> , 44, 2018-2024 | 1  |

301 Genome-wide association studies: assessing trait characteristics in model and crop plants. **2021**, 78, 5743-5754<sub>10</sub>

| 300 | REPRINT OF: CLASSIFICATION OF DIABETES MELLITUS. <b>2021</b> , 108972  | 5  |
|-----|--|----|
| 299 | Re-Programming Autoreactive T Cells Into T-Regulatory Type 1 Cells for the Treatment of Autoimmunity. <b>2021</b> , 12, 684240   | О  |
| 298 | Effect of dietary fat intake and genetic risk on glucose and insulin-related traits in Brazilian young adults <b>2021</b> , 20, 1337-1347  | 1  |
| 297 | New Insights Into Mitochondrial Dysfunction at Disease Susceptibility Loci in the Development of Type 2 Diabetes. <i>Frontiers in Endocrinology</i> , <b>2021</b> , 12, 694893                               | 1  |
| 296 | No Casual Relationship Between T2DM and the Risk of Infectious Diseases: A Two-Sample Mendelian Randomization Study. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 720874                                 | O  |
| 295 | The Link between Type 2 Diabetes Mellitus and the Polymorphisms of Glutathione-Metabolizing Genes Suggests a New Hypothesis Explaining Disease Initiation and Progression. <b>2021</b> , 11,                 | 3  |
| 294 | Genetics of Type 2 Diabetes: Opportunities for Precision Medicine: JACC Focus Seminar. <b>2021</b> , 78, 496-512   | 2  |
| 293 | Lower Dietary Intake of Plant Protein Is Associated with Genetic Risk of Diabetes-Related Traits in Urban Asian Indian Adults. <b>2021</b> , 13,   | 1  |
| 292 | A meta-analysis of the genome-wide association studies on two genetically correlated phenotypes (self-reported headache and self-reported migraine) identifies four new risk loci for headaches (N=397,385). | Ο  |
| 291 | Multi-Trait Genomic Risk Stratification for Type 2 Diabetes. <b>2021</b> , 8, 711208   | 1  |
| 290 | Identification of direct transcriptional targets of NFATC2 that promote Lell proliferation. <b>2021</b> , 131,   | 1  |
| 289 | Anticipation of Precision Diabetes and Promise of Integrative Multi-Omics. 2021, 50, 559-574   |    |
| 288 | Human genetic analyses of organelles highlight the nucleus in age-related trait heritability. <b>2021</b> , 10,  | 1  |
| 287 | Discovery and implications of polygenicity of common diseases. <b>2021</b> , 373, 1468-1473  | 13 |
| 286 | A murine model of the human CREBRFR457Q obesity-risk variant does not influence energy or glucose homeostasis in response to nutritional stress. <b>2021</b> , 16, e0251895                                  | 1  |
| 285 | The importance of increasing population diversity in genetic studies of type 2 diabetes and related glycaemic traits. <i>Diabetologia</i> , <b>2021</b> , 64, 2653-2664                                      | О  |
| 284 | What Regulates Basal Insulin Secretion and Causes Hyperinsulinemia?. <i>Diabetes</i> , <b>2021</b> , 70, 2174-2182 0.9   | 4  |

| 283 | Type 2 Diabetes and Dietary Carbohydrate Intake of Adolescents and Young Adults: What Is the Impact of Different Choices?. <b>2021</b> , 13,  | О   |
|-----|---|-----|
| 282 | Exome Sequencing of 5 Families with Severe Early-Onset Periodontitis. <b>2021</b> , 220345211029266   | 1   |
| 281 | Functional characterization of T2D-associated SNP effects on baseline and ER stress-responsive I cell transcriptional activation. <b>2021</b> , 12, 5242                            | 1   |
| 280 | An Update on the Epidemiology of Type 2 Diabetes: A Global Perspective. <b>2021</b> , 50, 337-355   | 17  |
| 279 | Does NAFLD mediate the relationship between obesity and type 2 diabetes risk? evidence from the multi-ethnic study of atherosclerosis (MESA). <b>2021</b> , 63, 15-21               | 2   |
| 278 | Combinatorial analytics: An essential tool for the delivery of precision medicine and precision agriculture. <b>2021</b> , 1, 100003  | 1   |
| 277 | Circulating long non-coding RNAs NKILA, NEAT1, MALAT1, and MIAT expression and their association in type 2 diabetes mellitus. <b>2021</b> , 9,                                      | 8   |
| 276 | Weighted burden analysis in 200,000 exome-sequenced subjects characterises rare variant effects on risk of type 2 diabetes.   | 0   |
| 275 | Exercise as a complementary medicine intervention in type 2 diabetes mellitus: A systematic review with narrative and qualitative synthesis of evidence. <b>2021</b> , 15, 273-286  | 8   |
| 274 | Pathophysiology of Obesity and Diabetes. <b>2021</b> , 29-42  | 3   |
| 273 | Investigating rare pathogenic/likely pathogenic exonic variation in bipolar disorder. 2021, 26, 5239-5250   | 3   |
| 272 | The First Genome-Wide Association Study for Type 2 Diabetes in Youth: The Progress in Diabetes Genetics in Youth (ProDiGY) Consortium. <i>Diabetes</i> , <b>2021</b> , 70, 996-1005 | 8   |
| 271 | Genetics of Small Vessel Disease. <b>2017</b> , 263-279   | 1   |
| 270 | Genetic Determinants and Pharmacogenetics of Osteoporosis and Osteoporotic Fracture. <b>2020</b> , 485-506  | 3   |
| 269 | Genome-Wide Association Study for Type 2 Diabetes. <b>2019</b> , 49-86  | 1   |
| 268 | PAM haploinsufficiency does not accelerate the development of diet- and human IAPP-induced diabetes in mice. <i>Diabetologia</i> , <b>2020</b> , 63, 561-576                        | 3   |
| 267 | Genetic variant effects on gene expression in human pancreatic islets and their implications for T2D. <b>2020</b> , 11, 4912  | 30  |
| 266 | Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <b>2018</b> , 50, 26-41                         | 186 |

| 265                           | Dissecting the genetics of complex traits using summary association statistics.  | 6                 |
|-------------------------------|--|-------------------|
| 264                           | Insights into the genetic epidemiology of CrohnB and rare diseases in the Ashkenazi Jewish population.   | 2                 |
| 263                           | Linkage disequilibrium dependent architecture of human complex traits reveals action of negative selection.  | 9                 |
| 262                           | A network-based approach to eQTL interpretation and SNP functional characterization.   | 4                 |
| 261                           | Convergence of dispersed regulatory mutations predicts driver genes in prostate cancer.  | 4                 |
| 260                           | Power Analysis Provides Bounds for Genetic Architecture and Insights to Challenges for Rare<br>Variant Association Studies.  | 1                 |
| 259                           | Imputation aware tag SNP selection to improve power for multi-ethnic association studies.  | 1                 |
| 258                           | Integrative cross tissue analysis of gene expression identifies novel type 2 diabetes genes.   | 7                 |
| 257                           | Psychiatric Genomics: An Update and an Agenda.   | 3                 |
| 256                           | Refining the accuracy of validated target identification through coding variant fine-mapping in type 2 diabetes.   | 4                 |
|                               |  | , , ,             |
| 255                           | Widespread signatures of negative selection in the genetic architecture of human complex traits.   | 7                 |
| <sup>2</sup> 55               |  |                   |
|                               | Widespread signatures of negative selection in the genetic architecture of human complex traits.  Quantification of frequency-dependent genetic architectures and action of negative selection in 25   | 7                 |
| 254                           | Widespread signatures of negative selection in the genetic architecture of human complex traits.  Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits.  Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a new regulator of   | 7                 |
| 254<br>253                    | Widespread signatures of negative selection in the genetic architecture of human complex traits.  Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits.  Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a new regulator of insulin secretion.  Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk   | 7 18 2            |
| <sup>254</sup> <sup>253</sup> | Widespread signatures of negative selection in the genetic architecture of human complex traits.  Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits.  Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a new regulator of insulin secretion.  Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes.  Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in   | 7 18 2            |
| 254<br>253<br>252<br>251      | Widespread signatures of negative selection in the genetic architecture of human complex traits.  Quantification of frequency-dependent genetic architectures and action of negative selection in 25 UK Biobank traits.  Chromatin 3D interaction analysis of the STARD10 locus unveils FCHSD2 as a new regulator of insulin secretion.  Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes.  Pancreatic progenitor epigenome maps prioritize type 2 diabetes risk genes with roles in development.  Rare Non-coding Variation Identified by Large Scale Whole Genome Sequencing Reveals | 7<br>18<br>2<br>1 |

| 247 | Targeted Genotyping of Variable Number Tandem Repeats with adVNTR.  | 5  |
|-----|---|----|
| 246 | 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 |
| 245 | Clustering of Type 2 Diabetes Genetic Loci by Multi-Trait Associations Identifies Disease Mechanisms and Subtypes.                                    | 5  |
| 244 | Developing a network view of type 2 diabetes risk pathways through integration of genetic, genomic and functional data.                               | 4  |
| 243 | Protein-Coding Variants Implicate Novel Genes Related to Lipid Homeostasis Contributing to Body Fat Distribution.                                     | 1  |
| 242 | Expanded genetic landscape of chronic obstructive pulmonary disease reveals heterogeneous cell type and phenotype associations.                       | O  |
| 241 | Genetic discovery and translational decision support from exome sequencing of 20,791 type 2 diabetes cases and 24,440 controls from five ancestries.  | 2  |
| 240 | Inferring the nature of missing heritability in human traits.   | 1  |
| 239 | EndoC-H1 multi-genomic profiling defines gene regulatory programs governing human pancreatic Lell identity and function.                              | 1  |
| 238 | Human pancreatic islet 3D chromatin architecture provides insights into the genetics of type 2 diabetes.  | 7  |
| 237 | Trans effects on gene expression can drive omnigenic inheritance.   | 5  |
| 236 | Geographic variation and bias in polygenic scores of complex diseases and traits in Finland.  | 5  |
| 235 | Sequencing and Imputation in GWAS: Cost-Effective Strategies to Increase Power and Genomic Coverage Across Diverse Populations.                       | 2  |
| 234 | An open resource of structural variation for medical and population genetics.   | 33 |
| 233 | A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease.   | 4  |
| 232 | Influence of genetic variants on gene expression in human pancreatic islets Implications for type 2 diabetes.   | 9  |
| 231 | Identification of type 2 diabetes loci in 433,540 East Asian individuals.   | 4  |
| 230 | Genome-wide rare variant analysis for thousands of phenotypes in 54,000 exomes.   | 3  |

| 229 | Single cell chromatin accessibility reveals pancreatic islet cell type- and state-specific regulatory programs of diabetes risk.   | 18              |
|-----|--|-----------------|
| 228 | An integrated platform to systematically identify causal variants and genes for polygenic human traits.  | 8               |
| 227 | Exploiting the GTEx resources to decipher the mechanisms at GWAS loci.   | 21              |
| 226 | Novel association of rs58542926 genotype with increased serum tyrosine levels and decreased apoB-100 particles in Finns. <b>2017</b> , 58, 1471-1481                               | 35              |
| 225 | A CRISPR/Cas9 genome editing pipeline in the EndoC-H1 cell line to study genes implicated in beta cell function. <b>2019</b> , 4, 150  | 12              |
| 224 | A CRISPR/Cas9 genome editing pipeline in the EndoC-H1 cell line to study genes implicated in beta cell function. <b>2019</b> , 4, 150  | 12              |
| 223 | Common, low-frequency, and rare genetic variants associated with lipoprotein subclasses and triglyceride measures in Finnish men from the METSIM study. <b>2017</b> , 13, e1007079 | 33              |
| 222 | Enrichment of minor allele of SNPs and genetic prediction of type 2 diabetes risk in British population. <b>2017</b> , 12, e0187644  | 11              |
| 221 | Genetic Aspects of Latent Autoimmune Diabetes in Adults: A Mini-Review. <b>2019</b> , 15, 194-198  | 7               |
| 220 | Association of PPARG Gene Polymorphisms Pro12Ala with Type 2 Diabetes Mellitus: A<br>Meta-analysis. <b>2019</b> , 15, 277-283  | 5               |
| 219 | Integrating functional ageing into daily clinical practice. <b>2019</b> , 4, 30-35   | 1               |
| 218 | Secretory granule protein chromogranin B (CHGB) forms an anion channel in membranes. <b>2018</b> , 1, e20180013  | <b>39</b> 5     |
| 217 | Gene Polymorphism and Their Risk Association With Type 2 Diabetes Mellitus. 2019, 7, 33-37   | 1               |
| 216 | Identification of potential markers for type 2 diabetes mellitus via bioinformatics analysis. <b>2020</b> , 22, 1868-188   | 82 <sub>5</sub> |
| 215 | Genetic Testing for Type 2 Diabetes in High-Risk Children: the Case for Primordial Prevention. 3, e20695   | 2               |
| 214 | Longitudinal Study of Diabetic Differences between International Migrants and Natives among the Asian Population. <b>2020</b> , 28, 110-118  | 2               |
| 213 | Age-related late-onset disease heritability patterns and implications for genome-wide association studies. <b>2019</b> , 7, e7168  | 9               |
| 212 | The population frequency of human mitochondrial DNA variants is highly dependent upon mutational bias. <b>2021</b> , 10,   | O               |

| 211 | Mediation model with a categorical exposure and a censored mediator with application to a genetic study. <b>2021</b> , 16, e0257628                           |     | Ο |
|-----|---|-----|---|
| 210 | Copine 3 "CPNE3" is a novel regulator for insulin secretion and glucose uptake in pancreatic Etells. <i>Scientific Reports</i> , <b>2021</b> , 11, 20692      | 4.9 | 3 |
| 209 | Mutations and variants of ONECUT1 in diabetes. <b>2021</b> , 27, 1928-1940  |     | 6 |
| 208 | Exploring the Epigenetic Regulatory Role of m6A-Associated SNPs in Type 2 Diabetes Pathogenesis. <b>2021</b> , 14, 1369-1378                                  |     | O |
| 207 | The broad pathogenetic role of TCF7L2 in human diseases beyond type 2 diabetes. <b>2021</b> , 237, 301  |     | 2 |
| 206 | Predicting causal variants affecting expression using whole genome sequence and RNA-seq from multiple human tissues.  |     | 2 |
| 205 | Genome sequence of a diabetes-prone desert rodent reveals a mutation hotspot around the ParaHox gene cluster.   |     | 1 |
| 204 | Histone Deacetylase HDAC8 and Insulin Resistance. <b>2017</b> , 1-16  |     |   |
| 203 | Causal analyses, statistical efficiency and phenotypic precision through Recall-by-Genotype study design.   |     | 2 |
| 202 | A comprehensive reanalysis of publicly available GWAS datasets reveals an X chromosome rare regulatory variant associated with high risk for type 2 diabetes. |     |   |
| 201 | De novo mutations implicate novel genes with burden of rare variants in Systemic Lupus Erythematosus.   |     |   |
| 200 | Phenotype-driven transitions in regulatory network structure.   |     |   |
| 199 | Non-Parametric Genetic Prediction of Complex Traits with Latent Dirichlet Process Regression Models.  |     |   |
| 198 | Type 2 Diabetes Risk Alleles Reveal a Role for Peptidylglycine Alpha-amidating Monooxygenase in Beta Cell Function.   |     | 2 |
| 197 | The harmonic mean p-value for combining dependent tests.  |     | 1 |
| 196 | Turning vice into virtue: Using Batch-Effects to Detect Errors in Large Genomic Datasets.   |     | 1 |
| 195 | Improved Score Statistics for Meta-analysis in Single-variant and Gene-level Association Studies.   |     |   |
| 194 | Chromatin accessibility profiling uncovers genetic- and T2D disease state-associated changes in cis-regulatory element use in human islets.                   |     | 2 |

193 Epigenome-wide association in adipose tissue from the METSIM cohort.

| 192 | Genetics of Diabetes and Diabetic Complications. <b>2018</b> , 81-139  | 1 |
|-----|--|---|
| 191 | Current Understanding of Genetic Factors in Idiopathic Scoliosis. 2018, 139-157  |   |
| 190 | Novel susceptibility loci and genetic regulation mechanisms for type 2 diabetes.   | 1 |
| 189 | A reference haplotype panel for genome-wide imputation of short tandem repeats.  | 2 |
| 188 | Low frequency and rare coding variation contributes to multiple sclerosis risk.  |   |
| 187 | Low-frequency variant functional architectures reveal strength of negative selection across coding and non-coding annotations.                                 | 1 |
| 186 | Pancreatic islet chromatin accessibility and conformation defines distal enhancer networks of type 2 diabetes risk.  | 2 |
| 185 | Shared genetic contribution to type 1 and type 2 diabetes risk.  | 2 |
| 184 | Chromatin interactions and expression quantitative trait loci reveal genetic drivers of multimorbidities.  |   |
| 183 | Age-related late-onset disease heritability patterns and implications for genome-wide association studies.   | 1 |
| 182 | Jackknife model averaging prediction methods for complex phenotypes with gene expression levels by integrating external pathway information.                   |   |
| 181 | Kidney Transplantation and Diabetic Nephropathy. <b>2019</b> , 451-467   |   |
| 180 | Diabetes in Kidney Transplant Recipients. <b>2019</b> , 113-131  | 1 |
| 179 | Partitioning the genetic architecture of amyotrophic lateral sclerosis.  |   |
| 178 | Integration of a Large-Scale Genetic Analysis Workbench Increases the Accessibility of a High-Performance Pathway-Based Analysis Method. <b>2018</b> , 16, e39 |   |
| 177 | The Future of and Beyond GWAS. <b>2019</b> , 193-209   |   |
| 176 | Identifying novel associations in GWAS by hierarchical Bayesian latent variable detection of differentially misclassified phenotypes.                          |   |

| 175 | Genetic Variants Associated with the Development of Type 2 Diabetes: Approaches to Their Identification. <b>2019</b> , 74, 44-53                           |   |
|-----|--|---|
| 174 | A Transdisciplinary Approach to Classify Thyroid Levels in Patients. <b>2019</b> , 47, 20180527  |   |
| 173 | A Novel Type 2 Diabetes Locus in sub-Saharan Africans, ZRANB3, is Implicated in Beta Cell Proliferation.   |   |
| 172 | Deep serum proteomics reveal biomarkers and causal candidates for type 2 diabetes.   | 2 |
| 171 | Population genetic simulation study of power in association testing across genetic architectures and study designs.  |   |
| 170 | Progressive shifts in the gut microbiome reflect prediabetes and diabetes development in a treatment-naive Mexican cohort.                                 | O |
| 169 | Evaluating the Potential of Younger Cases and Older Controls Cohorts to Improve Discovery Power in Genome-wide Association Studies of Late-onset Diseases. |   |
| 168 | Future Preventive Gene Therapy of Polygenic Diseases from a Population Genetics Perspective.   |   |
| 167 | Automated Gene Data Integration with Databio.  |   |
| 166 | Etell dedifferentiation is associated with epithelial-mesenchymal transition triggered by miR-7-mediated repression of mSwi/Snf complex.                   | O |
| 165 | Whole-Exome Sequencing (WES) for Illumina Short Read Sequencers Using Solution-Based Capture. <b>2020</b> , 2076, 85-108                                   | 2 |
| 164 | Population-specific and transethnic genome-wide analyses reveal distinct and shared genetic risks of coronary artery disease.                              |   |
| 163 | Unsupervised clustering of missense variants in the HNF1A gene using multidimensional functional data aids clinical interpretation.                        |   |
| 162 | A Bayesian method for rare variant analysis using functional annotations and its application to Autism.  |   |
| 161 | Legislative regulation and use of genetic information in the Russian Federation and abroad. <b>2019</b> , XIV,   |   |
| 160 | Membrane insertion of chromogranin B for granule maturation in regulated secretion.  | O |
| 159 | Genetik menschlicher Erkrankungen. <b>2020</b> , 725-812   |   |
| 158 | Estimating the causal effect of genetic liability to prevalent disease on hospital costs using Mendelian Randomization.                                    |   |

| 157 | La puntuacifi de riesgo poligfiico como factor clave en los modelos de prediccifi clítica cardiovascular. <b>2020</b> , 73, 608-610   |     |   |
|-----|---|-----|---|
| 156 | Gain of function of Malate Dehydrogenase 2 (MDH2) and familial hyperglycemia. 2021,   |     | 1 |
| 155 | DNA Methylation and Type 2 Diabetes: Novel Biomarkers for Risk Assessment?. <b>2021</b> , 22,   |     | 2 |
| 154 | Prediction of primary venous thromboembolism based on clinical and genetic factors within the U.K. Biobank. <i>Scientific Reports</i> , <b>2021</b> , 11, 21340   | 4.9 | Ο |
| 153 | "Treasure Your Exceptions"-Studying Human Extreme Phenotypes to Illuminate Metabolic Health and Disease: The 2019 Banting Medal for Scientific Achievement Lecture. <i>Diabetes</i> , <b>2021</b> , 70, 29-38 | 0.9 | 1 |
| 152 | Maternal High-Fiber Diet Protects Offspring against Type 2 Diabetes. <b>2020</b> , 13,  |     | Ο |
| 151 | Overview of Genomic Heterogeneity in Statistical Genetics. <b>2020</b> , 53-97  |     |   |
| 150 | CHAPTER 6:Detection of Disease-associated Mutations and Biomarkers Using Next-generation Sequencing. <b>2020</b> , 117-136  |     |   |
| 149 | Functional characterization of thousands of type 2 diabetes-associated and chromatin-modulating variants under steady state and endoplasmic reticulum stress.   |     | 0 |
| 148 | A long noncoding RNA, LOC157273, is the effector transcript at the chromosome 8p23.1-PPP1R3B metabolic traits and type 2 diabetes risk locus.   |     |   |
| 147 | Prediction of Venous Thromboembolism Based on Clinical and Genetic Factors.   |     | 1 |
| 146 | Identification and genomic analysis of pedigrees with exceptional longevity identifies candidate rare variants.   |     |   |
| 145 | Recapitulating evolutionary divergence in a single cis-regulatory element is sufficient to cause expression changes of the lens gene Tdrd7.   |     |   |
| 144 | Donut PCR: a rapid, portable, multiplexed, and quantitative DNA detection platform with single-nucleotide specificity.  |     |   |
| 143 | Maternal High Fiber Diet Protects Offspring Against Type 2 Diabetes.  |     | 0 |
| 142 | A new approach of dissecting genetic effects for complex traits.  |     | Ο |
| 141 | Could personalised risk prediction for type 2 diabetes using polygenic risk scores direct prevention, enhance diagnostics, or improve treatment?. 5, 206  |     | 0 |
| 140 | A weighted empirical Bayes risk prediction model using multiple traits. <b>2020</b> , 19,   |     |   |
|     |   |     |   |

139 Whole-Exome sequencing identifies a Type 2 Diabetes candidate mutation in PTPRF.

| Outgroup Machine Learning Approach Identifies Single Nucleotide Variants in Noncoding DNA Associated with Autism Spectrum Disorder. 2019, 24, 260-271  370 Dietary induction and reversal of obesity and insulin resistance is associated with changes in Fgf21 DNA methylation in liver of mice. 2021, 100, 108907  371 Environmental risk factors of type 2 diabetes-an exposome approach. Diabetologia, 2021, 1 10.3 5  372 Deletion of ABCB10 in beta-cells protects from high-fat diet induced insulin resistance. 2021, 55, 101403  373 A combined polygenic score of 21,293 rare and 22 common variants significantly improves diabetes diagnosis based on hemoglobin A1C levels.  373 Lipotoxicity and ECell Failure in Type 2 Diabetes: Oxidative Stress Linked to NADPH Oxidase and ER Stress. 2021, 10.  374 Aglobal analysis on the differential regulation of RNA binding proteins (RBPs) by TNFfbs potential modulators of metabolic syndromes. 2022, 2, 100037  375 Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  376 Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  377 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  378 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations. 2022, 18, e1009628  379 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  370 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  370 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional prolapse. 2022, 10, e15163  371 Prediction of a 10-year risk of type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022, 10, e15163  372 Plasma miR-21 as a potential predicto |     |  |      |   |
|--|-----|--|------|---|
| Environmental risk factors of type 2 diabetes-an exposome approach. Diabetologia, 2021, 1  136 Environmental risk factors of type 2 diabetes-an exposome approach. Diabetologia, 2021, 1  137 Deletion of ABCB10 in beta-cells protects from high-fat diet induced insulin resistance. 2021, 55, 101403  138 A combined polygenic score of 21,293 rare and 22 common variants significantly improves diabetes diagnosis based on hemoglobin A1C levels.  139 Lipotoxicity and ECell Failure in Type 2 Diabetes: Oxidative Stress Linked to NADPH Oxidase and ER Stress. 2021, 10.  130 A global analysis on the differential regulation of RNA binding proteins (RBPs) by TNFibs potential modulators of metabolic syndromes. 2022, 2, 100037  131 Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  130 Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  129 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  128 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  129 The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  120 Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  121 Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 138 |  |      | 4 |
| Deletion of ABCB10 in beta-cells protects from high-fat diet induced insulin resistance. 2021, 55, 101403  A combined polygenic score of 21,293 rare and 22 common variants significantly improves diabetes diagnosis based on hemoglobin A1C levels.  Lipotoxicity and ECell Failure in Type 2 Diabetes: Oxidative Stress Linked to NADPH Oxidase and ER Stress 2021, 10,  A global analysis on the differential regulation of RNA binding proteins (RBPs) by TNFBs potential modulators of metabolic syndromes. 2022, 2, 100037  Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 137 |  |      | 2 |
| A combined polygenic score of 21,293 rare and 22 common variants significantly improves diabetes diagnosis based on hemoglobin A1C levels.  Lipotoxicity and ECell Failure in Type 2 Diabetes: Oxidative Stress Linked to NADPH Oxidase and ER Stress 2021, 10,  A global analysis on the differential regulation of RNA binding proteins (RBPs) by TNFBs potential modulators of metabolic syndromes. 2022, 2, 100037  Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163  | 136 | Environmental risk factors of type 2 diabetes-an exposome approach. <i>Diabetologia</i> , <b>2021</b> , 1        | 10.3 | 5 |
| diagnosis based on hemoglobin A1C levels.  Lipotoxicity and ECell Failure in Type 2 Diabetes: Oxidative Stress Linked to NADPH Oxidase and ER Stress 2021, 10,  A global analysis on the differential regulation of RNA binding proteins (RBPs) by TNFt potential modulators of metabolic syndromes. 2022, 2, 100037  Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  O  The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 135 | Deletion of ABCB10 in beta-cells protects from high-fat diet induced insulin resistance. <b>2021</b> , 55, 10140 | )3   |   |
| A global analysis on the differential regulation of RNA binding proteins (RBPs) by TNFBs potential modulators of metabolic syndromes. 2022, 2, 100037  O Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  O Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  O Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 134 |  |      | О |
| potential modulators of metabolic syndromes. 2022, 2, 100037  131 Scales for assessing the genetic risk of developing type 2 diabetes mellitus. 2021, 24, 115  130 Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  129 Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  128 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  127 The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  126 Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  127 Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163  | 133 |  |      | 1 |
| Genome-wide association study of 1,391 plasma metabolites in 6,136 Finnish men identifies 303 novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  128 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  127 The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  126 Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 132 |  |      | O |
| novel signals and provides biological insights into human diseases.  Prediction of a 10-year risk of type 2 diabetes mellitus in the Turkish population: A cross-sectional study. 2021, 100, e27721  128 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  127 The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  128 Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  129 Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 131 | Scales for assessing the genetic risk of developing type 2 diabetes mellitus. <b>2021</b> , 24, 115              |      | 1 |
| study. 2021, 100, e27721  128 Using population-specific add-on polymorphisms to improve genotype imputation in underrepresented populations 2022, 18, e1009628  127 The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  126 Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163  | 130 |  |      |   |
| underrepresented populations 2022, 18, e1009628  The polymorphisms of extracellular matrix-remodeling genes are associated with pelvic organ prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163   | 129 |  |      | 1 |
| prolapse 2022,  Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,  Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus 2022, 10, e15163  | 128 |  |      | O |
| Plasma miR-21 as a potential predictor in prediabetic individuals with a positive family history of type 2 diabetes mellitus <b>2022</b> , 10, e15163  | 127 |  |      | О |
| type 2 diabetes mellitus <b>2022</b> , 10, e15163  | 126 | Type 2 diabetes mellitus in sub-Saharan Africa: challenges and opportunities 2022,                               |      | 2 |
| 124 Human population genomics approach in food metabolism. <b>2022</b> , 433-449   | 125 |  |      | О |
|  | 124 | Human population genomics approach in food metabolism. <b>2022</b> , 433-449                                     |      |   |
| Epigenetic scores for the circulating proteome as tools for disease prediction <b>2022</b> , 11,   | 123 | Epigenetic scores for the circulating proteome as tools for disease prediction 2022, 11,                         |      | 2 |
| Evaluation of Evidence for Pathogenicity Demonstrates that BLK, KLF11 and PAX4 Should not be  122 Included in Diagnostic Testing for MODY <i>Diabetes</i> , <b>2022</b> ,  | 122 |  | 0.9  | 2 |

| 121 | Common variants in genes involved in islet amyloid polypeptide (IAPP) processing and the degradation pathway are associated with T2DM risk: A Chinese population study <b>2022</b> , 109235 | O |
|-----|---|---|
| 120 | Mutations in G6PC2 gene with increased risk for development of type 2 diabetes: Understanding via computational approach <b>2022</b> , 130, 351-373   | 1 |
| 119 | Editorial: Beta-Cell Fate: From Gene Circuits to Disease Mechanisms Frontiers in Genetics, 2022, 13, 822449   |   |
| 118 | The role of liver fat in cardiometabolic diseases is highlighted by genome-wide association study of MRI-derived measures of body composition.  |   |
| 117 | Diabetes and Ischemic Stroke: An Old and New Relationship an Overview of the Close Interaction between These Diseases <b>2022</b> , 23,   | 2 |
| 116 | Role of metabolizing MTHFR gene polymorphism (rs1801133) and its mRNA expression among<br>Type 2 Diabetes. 1  |   |
| 115 | Damaging missense variants in IGF1R implicate a role for IGF-1 resistance in the aetiology of type 2 diabetes.  | О |
| 114 | HNF1A Mutations and Beta Cell Dysfunction in Diabetes <b>2022</b> , 23,   | 1 |
| 113 | Insights Into Genome-Wide Association Study for Diabetes: A Bibliometric and Visual Analysis From 2001 to 2021 <i>Frontiers in Endocrinology</i> , <b>2022</b> , 13, 817620                 | 1 |
| 112 | BayesRB: a markov chain Monte Carlo-based polygenic genetic risk score algorithm for dichotomous traits.  |   |
| 111 | Genome-wide association studies of metabolites in Finnish men identify disease-relevant loci <b>2022</b> , 13, 1644   | 5 |
| 110 | Identification of genetic effects underlying type 2 diabetes in South Asian and European populations <b>2022</b> , 5, 329   | 2 |
| 109 | Inflammatory cytokines rewire the proinsulin interaction network in human islets.   |   |
| 108 | Transethnic meta-analysis of exome-wide variants identifies new loci associated with male-specific metabolic syndrome <b>2022</b> , 1   |   |
| 107 | PAM variants were associated with type 2 diabetes mellitus risk in the Chinese population <b>2022</b> , 1   |   |
| 106 | Human pancreatic islet miRNA-mRNA networks of altered miRNAs due to glycemic status <b>2022</b> , 25, 103995  | 1 |
| 105 | The impact of educational attainment, intelligence and intellectual disability on schizophrenia: a Swedish population-based register and genetic study <b>2022</b> ,                        | О |
| 104 | The Association between Fasting Glucose and Sugar Sweetened Beverages Intake Is Greater in Latin Americans with a High Polygenic Risk Score for Type 2 Diabetes Mellitus <b>2021</b> , 14,  | 1 |

## (2019-2021)

| 103 | Systems biology analysis of human genomes points to key pathways conferring spina bifida risk <b>2021</b> , 118,  | 3 |
|-----|---|---|
| 102 | RegVar: Tissue-specific Prioritization of Noncoding Regulatory Variants 2021,   |   |
| 101 | A genome-wide association study identifies novel candidate genes for susceptibility to diabetes mellitus in non-obese cats. <b>2021</b> , 16, e0259939  | O |
| 100 | Association between RAC1 gene variation, redox homeostasis and type 2 diabetes mellitus <b>2022</b> , e13792  | 2 |
| 99  | Additive and Interactive Genetically Contextual Effects of HbA1c on cg19693031 Methylation in Type 2 Diabetes <i>Genes</i> , <b>2022</b> , 13,  | 0 |
| 98  | Genetics of chronic obstructive pulmonary disease: understanding the pathobiology and heterogeneity of a complex disorder <b>2022</b> ,   | 7 |
| 97  | Burden of Type 2 Diabetes and Associated Cardiometabolic Traits and Their Heritability Estimates in Endogamous Ethnic Groups of India: Findings From the INDIGENIUS Consortium <i>Frontiers in Endocrinology</i> , <b>2022</b> , 13, 847692 | O |
| 96  | Image_1.tif. <b>2021</b> ,  |   |
| 95  | lmage_2.tif. <b>2021</b> ,  |   |
| 94  | Table_1.xls. <b>2019</b> ,  |   |
| 93  | Table_2.xls. <b>2019</b> ,  |   |
| 92  | Table_3.xls. <b>2019</b> ,  |   |
| 91  | Table_4.doc. <b>2019</b> ,  |   |
| 90  | Table_5.docx. <b>2019</b> ,   |   |
| 89  | image_1.TIF. <b>2018</b> ,  |   |
| 88  | table_1.DOC. <b>2018</b> ,  |   |
| 87  | table_2.DOCX. <b>2018</b> ,   |   |
| 86  | Data_Sheet_1.CSV. <b>2019</b> ,   |   |

| 85 | Data_Sheet_10.ZIP. <b>2019</b> ,  |      |   |
|----|---|------|---|
| 84 | Data_Sheet_2.ZIP. <b>2019</b> ,   |      |   |
| 83 | Data_Sheet_3.ZIP. <b>2019</b> ,   |      |   |
| 82 | Data_Sheet_4.ZIP. <b>2019</b> ,   |      |   |
| 81 | Data_Sheet_5.ZIP. <b>2019</b> ,   |      |   |
| 80 | Data_Sheet_6.CSV. <b>2019</b> ,   |      |   |
| 79 | Data_Sheet_7.CSV. <b>2019</b> ,   |      |   |
| 78 | Data_Sheet_8.CSV. <b>2019</b> ,   |      |   |
| 77 | Data_Sheet_9.ZIP. <b>2019</b> ,   |      |   |
| 76 | Treating equivalent cases differently: A comparative analysis of substance use disorder and type 2 diabetes in Norwegian treatment guidelines <i>Journal of Evaluation in Clinical Practice</i> , <b>2022</b> , | 2.5  | 1 |
| 75 | Contribution of rare variants in monogenic diabetes-genes to early-onset type 2 diabetes <i>Diabetes and Metabolism</i> , <b>2022</b> , 101353  | 5.4  | 0 |
| 74 | Health impact of seven herpesviruses on (pre)diabetes incidence and HbA: results from the KORA cohort <i>Diabetologia</i> , <b>2022</b> , 1   | 10.3 | 1 |
| 73 | Ethnic-Specific Type 2 Diabetes Risk Factor PAX4 R192H Is Associated with Attention-Specific Cognitive Impairment in Chinese with Type 2 Diabetes <i>Journal of Alzheimerys Disease</i> , <b>2022</b> ,         | 4.3  |   |
| 72 | Precision Nutrition for Type 2 Diabetes. <b>2022</b> , 233-249  |      |   |
| 71 | Complementary Experimental Methods in Genetics Open Up New Avenues of Research to Elucidate the Pathogenesis of Periodontitis. <i>Advances in Experimental Medicine and Biology</i> , <b>2022</b> , 209-227     | 3.6  |   |
| 70 | Psychosocial Effects of Receiving Genome-Wide Polygenic Risk Information Concerning Type 2 Diabetes and Coronary Heart Disease: A Randomized Controlled Trial. <i>Frontiers in Genetics</i> , 13,               | 4.5  | O |
| 69 | The missing heritability in type 1 diabetes mellitus. <i>Diabetes, Obesity and Metabolism</i> ,   | 6.7  | 0 |
| 68 | Achievements, prospects and challenges in precision care for monogenic insulin-deficient and insulin-resistant diabetes. <i>Diabetologia</i> ,  | 10.3 | 0 |

67 PAX4 loss of function alters human endocrine cell development and influences diabetes risk.

| 66 | Loss of RREB1 in pancreatic beta cells reduces cellular insulin content and affects endocrine cell gene expression.  |      |   |
|----|--|------|---|
| 65 | The genetics of type 2 diabetes in youth: Where we are and the road ahead. <i>Journal of Pediatrics</i> , <b>2022</b> ,  | 3.6  |   |
| 64 | Risk assessment for hip and knee osteoarthritis using polygenic risk scores. <i>Arthritis and Rheumatology</i> ,   | 9.5  | O |
| 63 | mGWAS-Explorer: Linking SNPs, Genes, Metabolites, and Diseases for Functional Insights. <i>Metabolites</i> , <b>2022</b> , 12, 526   | 5.6  | 0 |
| 62 | A Genome-Wide Association Study of Prediabetes Status Change. Frontiers in Endocrinology, 13,  | 5.7  |   |
| 61 | Macronutrient intake modulates impact of EcoRI polymorphism of ApoB gene on lipid profile and inflammatory markers in patients with type 2 diabetes. <i>Scientific Reports</i> , <b>2022</b> , 12,                     | 4.9  |   |
| 60 | Overview of Transcriptomic Research on Type 2 Diabetes: Challenges and Perspectives. <i>Genes</i> , <b>2022</b> , 13, 1176   | 4.2  | 2 |
| 59 | Heterogeneous Development of Ecell Populations In Diabetes-Resistant and -Susceptible Mice. <i>Diabetes</i> ,  | 0.9  |   |
| 58 | Genetics and Epigenetics in Personalized Nutrition: Evidence, Expectations, and Experiences.  Molecular Nutrition and Food Research, 2200077   | 5.9  |   |
| 57 | Polygenic Risk Scores for Cardiovascular Disease: A Scientific Statement From the American Heart Association. <i>Circulation</i> ,   | 16.7 | 1 |
| 56 | Comparative genomic analyses of multiple backcross mouse populations suggest SGCG as a novel potential obesity-modifier gene. <i>Human Molecular Genetics</i> ,  | 5.6  | O |
| 55 | Estimating the causal effect of liability to disease on healthcare costs using Mendelian Randomization. <i>Economics and Human Biology</i> , <b>2022</b> , 46, 101154  | 2.6  | 0 |
| 54 | Investigating causality in the association between DNA methylation and prevalent T2D using a bidirectional two-sample Mendelian Randomization.   |      |   |
| 53 | Full epistatic interaction maps retrieve part of missing heritability and improve phenotypic prediction.   |      |   |
| 52 | hsa-miR-607, lncRNA TUG1 and hsa_circ_0071106 can be combined as biomarkers in type 2 diabetes mellitus. <i>Experimental Biology and Medicine</i> , 153537022211106  | 3.7  | О |
| 51 | Combined effect of pancreatic lipid content and gene variants (TCF7L2, WFS1 and 11BHSD1) on B-cell function in Middle Aged Women in a Post Hoc Analysis. <i>Diabetology and Metabolic Syndrome</i> , <b>2022</b> , 14, | 5.6  |   |
| 50 | Rare loss of function variants in the hepatokine gene INHBE protect from abdominal obesity. <b>2022</b> , 13,  |      | O |

| 49 | Next-generation sequencing technologies in diabetes research. <b>2022</b> , 7, 100097  | O |
|----|--|---|
| 48 | Whole genome sequence association analysis of fasting glucose and fasting insulin levels in diverse cohorts from the NHLBI TOPMed program. <b>2022</b> , 5,        | 1 |
| 47 | The genetic interactions between non-alcoholic fatty liver disease and cardiovascular diseases. 13,  | 2 |
| 46 | Research progress on the mechanism of beta-cell apoptosis in type 2 diabetes mellitus. 13,   | O |
| 45 | Nontargeted and Targeted Metabolomic Profiling Reveals Novel Metabolite Biomarkers of Incident Diabetes in African Americans.                                      | 0 |
| 44 | Periodontitis and implant complications in diabetes.   | 4 |
| 43 | Inflammatory cytokines rewire the proinsulin interaction in human islets.  | О |
| 42 | Rare genetic variants explain missing heritability in smoking.   | O |
| 41 | Diabetes mellitus [Begutachtung. <b>2022</b> , 1-10  | 0 |
| 40 | Multidimensional Early Prediction Score for Drug-Resistant Epilepsy. <b>2022</b> , 18, 553   | O |
| 39 | Genetic risk score is associated with T2DM and diabetes complications risks. <b>2023</b> , 849, 146921   | 0 |
| 38 | Increasing number of long-lived ancestors associates with up to a decade of healthspan extension and a healthy metabolomic profile in mid-life.                    | O |
| 37 | How dysregulation of the immune system promotes diabetes mellitus and cardiovascular risk complications. 9,  | 0 |
| 36 | Common and distinct genetic architecture of age at diagnosis of diabetes in South Indian and European populations.   | O |
| 35 | Nutrigenomics: Insights and Implications for Genome-Based Nutrition. <b>2022</b> , 207-230   | 0 |
| 34 | A combined polygenic score of 21,293 rare and 22 common variants improves diabetes diagnosis based on hemoglobin A1C levels.                                       | 1 |
| 33 | Using Data to Improve the Management of Diabetes: The Tayside Experience.  | 0 |
| 32 | Genetic variants for prediction of gestational diabetes mellitus and modulation of susceptibility by a nutritional intervention based on a Mediterranean diet. 13, | О |

| 31 | The contribution of functional HNF1A variants and polygenic susceptibility to risk of type 2 diabetes in ancestrally diverse populations.  | 0 |
|----|--|---|
| 30 | Sex-specific genetic loci linked to early and late onset type 2 diabetes.  | Ο |
| 29 | Advances in multi-omics study of biomarkers of glycolipid metabolism disorder. 2022, 20, 5935-5951   | O |
| 28 | The contribution of common and rare genetic variants to variation in metabolic traits in 288,137 East Asians. <b>2022</b> , 13,  | O |
| 27 | Damaging missense variants in IGF1R implicate a role for IGF-1 resistance in the etiology of type 2 diabetes. <b>2022</b> , 100208   | O |
| 26 | A novel splice-affecting HNF1A variant with large population impact on diabetes in Greenland. <b>2022</b> , 100529   | O |
| 25 | The link between liver fat and cardiometabolic diseases is highlighted by genome-wide association study of MRI-derived measures of body composition. <b>2022</b> , 5,  | 0 |
| 24 | The Application of High-Throughput Approaches in Identifying Novel Therapeutic Targets and Agents to Treat Diabetes. 2200151   | Ο |
| 23 | A Meta-Analysis of the Genome-Wide Association Studies on Two Genetically Correlated Phenotypes Suggests Four New Risk Loci for Headaches.   | Ο |
| 22 | Investigation of the Relationship between the rs8192688 Polymorphism of the FABP-4 Gene and Cardiovascular Disease Susceptibility in Type 2 Diabetic Patients in Ilam Province, Iran. <b>2022</b> , 30, 97-104 | 0 |
| 21 | Insight into genetic, biological, and environmental determinants of sexual-dimorphism in type 2 diabetes and glucose-related traits. 9,  | Ο |
| 20 | Polygenic risk scores for the prediction of cardiometabolic disease.   | 1 |
| 19 | Leveraging the Genetic Correlation between Traits Improves the Detection of Epistasis in Genome-wide Association Studies.  | 0 |
| 18 | Uncovering the gene regulatory network of type 2 diabetes through multi-omic data integration. <b>2022</b> , 20,   | O |
| 17 | The mechanisms of chromogranin B-regulated Cl[homeostasis. <b>2022</b> , 50, 1659-1672   | 0 |
| 16 | Natural variation of respiration-related traits in plants.   | O |
| 15 | Loss of RREB1 in pancreatic beta cells reduces cellular insulin content and affects endocrine cell gene expression.  | 0 |
| 14 | Pharmakogenetik neuer Glukosespiegelsenker: eine Chance fildie Przisionsmedizin?.  | 0 |

| 13 | Germline loss-of-functionPAMvariants are enriched in subjects with pituitary hypersecretion.  | O |
|----|---|---|
| 12 | The Type 2 Diabetes Knowledge Portal: An open access genetic resource dedicated to type 2 diabetes and related traits. <b>2023</b> , 35, 695-710.e6   | O |
| 11 | Identification of pathogenic GCK variants in patients with common type 2 diabetes can lead to discontinuation of pharmacological treatment. <b>2023</b> , 35, 100972  | O |
| 10 | Geneanvironment interactions in the associations of PFAS exposure with insulin sensitivity and beta-cell function in a Faroese cohort followed from birth to adulthood. <b>2023</b> , 226, 115600                               | O |
| 9  | Does the quality of street greenspace matter? Examining the associations between multiple greenspace exposures and chronic health conditions of urban residents in a rapidly urbanising Chinese city. <b>2023</b> , 222, 115344 | О |
| 8  | Variants in the Control Region of Mitochondrial Genome Associated with type 2 Diabetes in a Cohort of Mexican Mestizos. <b>2023</b> , 54, 113-123   | O |
| 7  | DNA methylation profiling reveals novel pathway implicated in cardiovascular diseases of diabetes. 14,  | O |
| 6  | FALCON systematically interrogates free fatty acid biology and identifies a novel mediator of lipotoxicity.   | O |
| 5  | Rare and Common Variants in GALNT3 May Affect Bone Mass Independently of Phosphate Metabolism.  | O |
| 4  | Machine Learning Model Based on Insulin Resistance Metagenes Underpins Genetic Basis of Type 2 Diabetes. <b>2023</b> , 13, 432  | O |
| 3  | Molecular Genetics of Abnormal Redox Homeostasis in Type 2 Diabetes Mellitus. <b>2023</b> , 24, 4738  | 0 |
| 2  | Leu72Met Polymorphism in Ghrelin Gene: A Potential Risk Factor for Hypertension in Type 2<br>Diabetes Patients. Volume 16, 557-564  | O |
| 1  | FALCON systematically interrogates free fatty acid biology and identifies a novel mediator of lipotoxicity. <b>2023</b> ,   | 0 |