John Blangero

List of Publications by Year in descending order

410 papers	38,570 citations	7251 80 h-index	4511 177 g-index
452 all docs	452 docs citations	452 times ranked	48424 citing authors

#	Article	IF	Citations
1	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	1.4	9
2	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	3.0	29
3	Rare coding variants in 35 genes associate with circulating lipid levelsâ€"A multi-ancestry analysis of 170,000 exomes. American Journal of Human Genetics, 2022, 109, 81-96.	2.6	24
4	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	1.2	2
5	Ancestral diversity improves discovery and fine-mapping of genetic loci for anthropometric traitsâ€"The Hispanic/Latino Anthropometry Consortium. Human Genetics and Genomics Advances, 2022, 3, 100099.	1.0	3
6	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	4.7	36
7	Burden of Type 2 Diabetes and Associated Cardiometabolic Traits and Their Heritability Estimates in Endogamous Ethnic Groups of India: Findings From the INDIGENIUS Consortium. Frontiers in Endocrinology, 2022, 13, 847692.	1.5	4
8	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. Frontiers in Endocrinology, 2022, 13, 863893.	1.5	7
9	Influence of the Human Lipidome on Epicardial Fat Volume in Mexican American Individuals. Frontiers in Cardiovascular Medicine, 2022, 9, .	1.1	3
10	Comprehensive genetic analysis of the human lipidome identifies loci associated with lipid homeostasis with links to coronary artery disease. Nature Communications, 2022, 13, .	5.8	30
11	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	1.3	12
12	Searching for Imaging Biomarkers of Psychotic Dysconnectivity. Biological Psychiatry: Cognitive Neuroscience and Neuroimaging, 2021, 6, 1135-1144.	1.1	2
13	Genetic influence on cognitive development between childhood and adulthood. Molecular Psychiatry, 2021, 26, 656-665.	4.1	28
14	A White Matter Connection of Schizophrenia and Alzheimerâ€™s Disease. Schizophrenia Bulletin, 2021, 47, 197-206.	2.3	35
15	Using the Schmahmann Syndrome Scale to Assess Cognitive Impairment in Young Adults with Metabolic Syndrome: a Hypothesis-Generating Report. Cerebellum, 2021, 20, 295-299.	1.4	1
16	Serum carotenoids and Pediatric Metabolic Index predict insulin sensitivity in Mexican American children. Scientific Reports, 2021, 11, 871.	1.6	6
17	Further evidence supporting a potential role for ADH1B in obesity. Scientific Reports, 2021, 11, 1932.	1.6	11
18	Genetic influences on externalizing psychopathology overlap with cognitive functioning and show developmental variation. European Psychiatry, 2021, 64, e29.	0.1	6

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19	Efficient Generation of Functional Hepatocytes from Human Induced Pluripotent Stem Cells for Disease Modeling and Disease Gene Discovery. Methods in Molecular Biology, 2021, , 85-101.	0.4	2
20	Transcriptomic Profiling of Fibropapillomatosis in Green Sea Turtles (Chelonia mydas) From South Texas. Frontiers in Immunology, 2021, 12, 630988.	2.2	10
21	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	13.7	1,069
22	Disease Modeling and Disease Gene Discovery in Cardiomyopathies: A Molecular Study of Induced Pluripotent Stem Cell Generated Cardiomyocytes. International Journal of Molecular Sciences, 2021, 22, 3311.	1.8	5
23	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	2.4	24
24	Robust, flexible, and scalable tests for Hardyâ€“Weinberg equilibrium across diverse ancestries. Genetics, 2021, 218, .	1.2	6
25	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	5.8	17
26	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	2.6	28
27	Determinants of penetrance and variable expressivity in monogenic metabolic conditions across 77,184 exomes. Nature Communications, 2021, 12, 3505.	5.8	49
28	Identifying the Lipidomic Effects of a Rare Loss-of-Function Deletion in ANGPTL3. Circulation Genomic and Precision Medicine, 2021, 14, e003232.	1.6	3
29	Association of HIV-1 Infection and Antiretroviral Therapy With Type 2 Diabetes in the Hispanic Population of the Rio Grande Valley, Texas, USA. Frontiers in Medicine, 2021, 8, 676979.	1.2	2
30	Population sequencing data reveal a compendium of mutational processes in the human germ line. Science, 2021, 373, 1030-1035.	6.0	43
31	Genetic Overlap Profiles of Cognitive Ability in Psychotic and Affective Illnesses: A Multisite Study of Multiplex Pedigrees. Biological Psychiatry, 2021, 90, 373-384.	0.7	5
32	Whole-genome sequencing in diverse subjects identifies genetic correlates of leukocyte traits: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 1836-1851.	2.6	14
33	APOC3 genetic variation, serum triglycerides, and risk of coronary artery disease in Asian Indians, Europeans, and other ethnic groups. Lipids in Health and Disease, 2021, 20, 113.	1.2	12
34	Multi-phenotype genome-wide association studies of the Norfolk Island isolate implicate pleiotropic loci involved in chronic kidney disease. Scientific Reports, 2021, 11, 19425.	1.6	1
35	Associations of cannabis use disorder with cognition, brain structure, and brain function in African Americans. Human Brain Mapping, 2021, 42, 1727-1741.	1.9	9
36	Genetic determinants of metabolic biomarkers and their associations with cardiometabolic traits in Hispanic/Latino adolescents. Pediatric Research, 2021, , .	1.1	0

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37	Genz and Mendell-Elston Estimation of the High-Dimensional Multivariate Normal Distribution. Algorithms, 2021, 14, 296.	1.2	1
38	Association of Smoking, Alcohol Consumption, Blood Pressure, Body Mass Index, and Glycemic Risk Factors With Age-Related Macular Degeneration. JAMA Ophthalmology, 2021, 139, 1299.	1.4	29
39	Comparing empirical kinship derived heritability for imaging genetics traits in the UK biobank and human connectome project. NeuroImage, 2021, 245, 118700.	2.1	2
40	The G505A Nonsynonymous Single-Nucleotide Polymorphism (SNP) in TAFI, the Gene Encoding Thrombin-Activatable Fibrinolysis Inhibitor (TAFI) Is Pleiotropically Associated with TAFI Antigen Levels and Coronary Heart Disease (CHD) in Mexican Americans of South Texas. Blood, 2021, 138, 3217-3217.	0.6	0
41	On the Role of Hemostasis Variables in Cardiometabolic Outcomes. Blood, 2021, 138, 4266-4266.	0.6	1
42	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	4.1	49
43	Cognitive impairment from early to middle adulthood in patients with affective and nonaffective psychotic disorders. Psychological Medicine, 2020, 50, 48-57.	2.7	13
44	Quantitative HLAâ€classâ€II/factor VIII (FVIII) peptidomic variation in dendritic cells correlates with the immunogenic potential of therapeutic FVIII proteins in hemophilia A. Journal of Thrombosis and Haemostasis, 2020, 18, 201-216.	1.9	3
45	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	6.0	54
46	Role of miRNA-mRNA Interaction in Neural Stem Cell Differentiation of Induced Pluripotent Stem Cells. International Journal of Molecular Sciences, 2020, 21, 6980.	1.8	6
47	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	13.7	376
48	Trauma in Affective and Nonaffective Psychosis: AssociationsÂand Dissociations With Cognitive FunctioningÂin Childhood and Adulthood. Biological Psychiatry, 2020, 87, S458.	0.7	0
49	The reliability and heritability of cortical folds and their genetic correlations across hemispheres. Communications Biology, 2020, 3, 510.	2.0	42
50	Dynamic incorporation of multiple in silico functional annotations empowers rare variant association analysis of large whole-genome sequencing studies at scale. Nature Genetics, 2020, 52, 969-983.	9.4	146
51	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	5.8	39
52	Rapid, Phase-free Detection of Long Identity-by-Descent Segments Enables Effective Relationship Classification. American Journal of Human Genetics, 2020, 106, 453-466.	2.6	42
53	Influence of Processing Pipeline on Cortical Thickness Measurement. Cerebral Cortex, 2020, 30, 5014-5027.	1.6	41
54	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	6.0	450

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55	Imaging local genetic influences on cortical folding. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7430-7436.	3.3	24
56	Minimal Relationship between Local Gyrification and General Cognitive Ability in Humans. Cerebral Cortex, 2020, 30, 3439-3450.	1.6	6
57	Heritability of 596 lipid species and genetic correlation with cardiovascular traits in the Busselton Family Heart Study. Journal of Lipid Research, 2020, 61, 537-545.	2.0	29
58	Neurocognitive impairment in type 2 diabetes: evidence for shared genetic aetiology. Diabetologia, 2020, 63, 977-986.	2.9	8
59	Genotype phasing in pedigrees using whole-genome sequence data. European Journal of Human Genetics, 2020, 28, 790-803.	1.4	3
60	Highly efficient induced pluripotent stem cell reprogramming of cryopreserved lymphoblastoid cell lines. Journal of Biological Methods, 2020, 7, e124.	1.0	11
61	Acanthosis nigricans as a composite marker of cardiometabolic risk and its complex association with obesity and insulin resistance in Mexican American children. PLoS ONE, 2020, 15, e0240467.	1.1	10
62	Disentangling the Effects of HLA DRB1*15:01 and DQB1*06:02 to Establish the True HLA Risk Allele for Inhibitor Development in the Treatment of Hemophilia A. Blood, 2020, 136, 1-2.	0.6	0
63	Specific Correction of the Intron-22 Inverted Factor VIII Gene in Autologous Blood Outgrowth Endothelial Cells from Patients with Severe Hemophilia A. Blood, 2020, 136, 30-31.	0.6	1
64	N-Linked Glycans on Therapeutic Factor VIII (FVIII) Proteins Attenuate Immunogenicity Potential: Evidence from Independent HLA-Class-II/FVIII (HLAcII/FVIII) Peptidomes. Blood, 2020, 136, 29-30.	0.6	0
65	Title is missing!. , 2020, 15, e0240467.		0
66	Title is missing!. , 2020, 15, e0240467.		0
67	Title is missing!. , 2020, 15, e0240467.		0
68	Title is missing!. , 2020, 15, e0240467.		0
69	Rediscovering the value of families for psychiatric genetics research. Molecular Psychiatry, 2019, 24, 523-535.	4.1	43
70	Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. Molecular Psychiatry, 2019, 24, 1920-1932.	4.1	44
71	T178. The Utility of Connectivity Phenotypes as Successful Biomarkers for Psychosis Diagnoses. Biological Psychiatry, 2019, 85, S198-S199.	0.7	0
72	Rare DEGS1 variant significantly alters de novo ceramide synthesis pathway. Journal of Lipid Research, 2019, 60, 1630-1639.	2.0	16

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73	O55. The Genetic Factors Influencing Externalizing Psychopathology Overlap With Those Influencing Neurocognition and Show Developmental Variation. Biological Psychiatry, 2019, 85, S128.	0.7	0
74	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.4	5
75	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	2.6	44
76	45. The Effect of Sex and BMI on the Genetic Overlap Between Plasma-Based Interleukins (-6 and -8) and Suicide Attempt. Biological Psychiatry, 2019, 85, S19.	0.7	0
77	Evidence for genetic correlation between human cerebral white matter microstructure and inflammation. Human Brain Mapping, 2019, 40, 4180-4191.	1.9	16
78	Exome sequencing of 20,791Âcases of type 2 diabetes and 24,440Âcontrols. Nature, 2019, 570, 71-76.	13.7	248
79	A neural signature of metabolic syndrome. Human Brain Mapping, 2019, 40, 3575-3588.	1.9	26
80	Glycated Serum Protein Genetics and Pleiotropy with Cardiometabolic Risk Factors. Journal of Diabetes Research, 2019, 2019, 1-9.	1.0	6
81	Family-based analyses reveal novel genetic overlap between cytokine interleukin-8 and risk for suicide attempt. Brain, Behavior, and Immunity, 2019, 80, 292-299.	2.0	11
82	Whole-exome sequencing in multiplex preeclampsia families identifies novel candidate susceptibility genes. Journal of Hypertension, 2019, 37, 997-1011.	0.3	19
83	F145. Extremely Weak Relationship Between Gyrification and Intelligence. Biological Psychiatry, 2019, 85, S269.	0.7	0
84	Crossover interference and sex-specific genetic maps shape identical by descent sharing in close relatives. PLoS Genetics, 2019, 15, e1007979.	1.5	46
85	Use of >100,000 NHLBI Trans-Omics for Precision Medicine (TOPMed) Consortium whole genome sequences improves imputation quality and detection of rare variant associations in admixed African and Hispanic/Latino populations. PLoS Genetics, 2019, 15, e1008500.	1.5	203
86	Genetic Research on Ocular Health and Disease in a Population from Nepal. Essentials in Ophthalmology, 2019, , 75-84.	0.0	3
87	Efficient Variant Set Mixed Model Association Tests for Continuous and Binary Traits in Large-Scale Whole-Genome Sequencing Studies. American Journal of Human Genetics, 2019, 104, 260-274.	2.6	103
88	A QTL on chromosome 3q23 influences processing speed in humans. Genes, Brain and Behavior, 2019, 18, e12530.	1.1	1
89	Genomic kinship construction to enhance genetic analyses in the human connectome project data. Human Brain Mapping, 2019, 40, 1677-1688.	1.9	14
90	Human Cortical Thickness Organized into Genetically-determined Communities across Spatial Resolutions. Cerebral Cortex, 2019, 29, 106-118.	1.6	18

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91	UniMÃ³vil: A Mobile Health Clinic Providing Primary Care to the Colonias of the Rio Grande Valley, South Texas. Frontiers in Public Health, 2019, 7, 215.	1.3	16
92	1337-P: Prediction of Insulin Sensitivity Using Serum Carotenoid Concentrations and Pediatric Metabolic Index in Mexican-American Children. Diabetes, 2019, 68, 1337-P.	0.3	0
93	2093-P: Acanthosis Nigricans as a Composite Marker of Cardiometabolic Risk and Its Complex Association with Obesity and Insulin Resistance in Mexican-American Children. Diabetes, 2019, 68, .	0.3	0
94	1770-P: Further Evidence Supporting a Potential Role for ADH1B in Obesity. Diabetes, 2019, 68, .	0.3	0
95	1639-P: Effect of Educational Status on Fasting Glucose and HbA1c Concentrations Independent of Income and Population Differences in Indian Populations. Diabetes, 2019, 68, .	0.3	0
96	1717-P: Burden of Type 2 Diabetes and Its Genetic Determinants in Indian Populations: Findings from the INDIGENIUS Consortium. Diabetes, 2019, 68, 1717-P.	0.3	2
97	The Dendritic Cell HLA-Class-II/Therapeutic Factor VIII (FVIII) Peptidome Is Influenced in Unanticipated Ways By the B-Domain of FVIII and the FVIII Chaperon Protein, Von Willebrand Factor: The Outrigger and Glycosylation-Umbrella (GUMB) Hypotheses. Blood, 2019, 134, 161-161.	0.6	0
98	On the Role of F8 Sequence Mismatch and Class-II Human Leukocyte Antigen Binding in the Development of Neutralizing Antibodies ("Inhibitors") Directed Against Therapeutic Factor VIII Proteins (tFVIIIs): Evidence from the PATH Study. Blood, 2019, 134, 2393-2393.	0.6	0
99	microRNA and mRNA interactions in induced pluripotent stem cell reprogramming of lymphoblastoid cell lines. American Journal of Stem Cells, 2019, 8, 28-37.	0.4	0
100	Assessment of Cognition and Personality as Potential Endophenotypes in the Western Australian Family Study of Schizophrenia. Schizophrenia Bulletin, 2018, 44, 908-921.	2.3	12
101	Genetic and environmental (physical fitness and sedentary activity) interaction effects on cardiometabolic risk factors in Mexican American children and adolescents. Genetic Epidemiology, 2018, 42, 378-393.	0.6	7
102	Neurodegenerative disease biomarkers AÎ²_{1â€“40}, AÎ²_{1â€“42}, tau, and pâ€tau₁₈₁ in the vervet monkey cerebrospinal fluid: RelationÂto normal aging, genetic influences, and cerebral amyloid angiopathy. Brain and Behavior, 2018, 8, e00903.	1.0	45
103	Whole genome sequencing of 91 multiplex schizophrenia families reveals increased burden of rare, exonic copy number variation in schizophrenia probands and genetic heterogeneity. Schizophrenia Research, 2018, 197, 337-345.	1.1	16
104	Exome Sequencing Identifies Genetic Variants Associated with Circulating Lipid Levels in Mexican Americans: The Insulin Resistance Atherosclerosis Family Study (IRASFS). Scientific Reports, 2018, 8, 5603.	1.6	9
105	Induced Pluripotent Stem Cells in Disease Modeling and Gene Identification. Methods in Molecular Biology, 2018, 1706, 17-38.	0.4	32
106	A genetic association study of carotid intima-media thickness (CIMT) and plaque in Mexican Americans and European Americans with rheumatoid arthritis. Atherosclerosis, 2018, 271, 92-101.	0.4	11
107	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	3.3	28
108	Data on genetic associations of carotid atherosclerosis markers in Mexican American and European American rheumatoid arthritis subjects. Data in Brief, 2018, 17, 820-829.	0.5	1

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109	Deficits in visual working-memory capacity and general cognition in African Americans with psychosis. Schizophrenia Research, 2018, 193, 100-106.	1.1	5
110	Pleiotropy of cardiometabolic syndrome with obesity-related anthropometric traits determined using empirically derived kinships from the Busselton Health Study. Human Genetics, 2018, 137, 45-53.	1.8	10
111	Genome-wide linkage scan for loci influencing plasma triglyceride levels. BMC Proceedings, 2018, 12, 52.	1.8	7
112	Contribution of Inbred Singletons to Variance Component Estimation of Heritability and Linkage. Human Heredity, 2018, 83, 92-99.	0.4	0
113	Modeling methylation data as an additional genetic variance component. BMC Proceedings, 2018, 12, 29.	1.8	16
114	Reliability of genomic predictions of complex human phenotypes. BMC Proceedings, 2018, 12, 51.	1.8	7
115	Heritability and genetic associations of triglyceride and HDL-C levels using pedigree-based and empirical kinships. BMC Proceedings, 2018, 12, 34.	1.8	5
116	Gestational Age and the Cord Blood Lipidomic Profile in Late Preterm and Term Infants. Neonatology, 2018, 114, 215-222.	0.9	5
117	Inferring Identical-by-Descent Sharing of Sample Ancestors Promotes High-Resolution Relative Detection. American Journal of Human Genetics, 2018, 103, 30-44.	2.6	34
118	Comparison of heritability estimates on resting state fMRI connectivity phenotypes using the ENIGMA analysis pipeline. Human Brain Mapping, 2018, 39, 4893-4902.	1.9	45
119	Fast and powerful genome wide association of dense genetic data with high dimensional imaging phenotypes. Nature Communications, 2018, 9, 3254.	5.8	6
120	Disentangling the genetic overlap between cholesterol and suicide risk. Neuropsychopharmacology, 2018, 43, 2556-2563.	2.8	18
121	Heritability estimates on resting state fMRI data using ENIGMA analysis pipeline. , 2018, , .		20
122	The Role of Class II Human Leukocyte Antigens (cII-HLAs) in Determining the Immunogenic Potential of Therapeutic Factor VIII Proteins in Hemophilia Patients: The "Gate Keeper" Hypothesis. Blood, 2018, 132, 5022-5022.	0.6	1
123	Genetics of Factor VIII Inhibitor Development in Hemophilia Patients: Novel Statistical Approaches in the PATH Study. Blood, 2018, 132, 1199-1199.	0.6	0
124	Shared Genetic Factors Influence Head Motion During MRI and Body Mass Index. Cerebral Cortex, 2017, 27, 5539-5546.	1.6	67
125	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	5.8	250
126	The Processing-Speed Impairment in Psychosis Is More Than Just Accelerated Aging. Schizophrenia Bulletin, 2017, 43, sbw168.	2.3	29

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127	Analysis of Whole Exome Sequencing with Cardiometabolic Traits Using Family-Based Linkage and Association in the IRAS Family Study. Annals of Human Genetics, 2017, 81, 49-58.	0.3	6
128	Serum phosphatidylinositol as a biomarker for bipolar disorder liability. Bipolar Disorders, 2017, 19, 107-115.	1.1	20
129	Lipidomics in the Study of Hypertension in Metabolic Syndrome. Current Hypertension Reports, 2017, 19, 7.	1.5	21
130	Evaluating a CLL susceptibility variant in ITGB2 in families with multiple subtypes of hematological malignancies. Blood, 2017, 130, 86-88.	0.6	11
131	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
132	Multiethnic genome-wide meta-analysis of ectopic fat depots identifies loci associated with adipocyte development and differentiation. Nature Genetics, 2017, 49, 125-130.	9.4	116
133	Genetics of serum carotenoid concentrations and their correlation with obesity-related traits in Mexican American children. American Journal of Clinical Nutrition, 2017, 106, 52-58.	2.2	16
134	Epigenetic Age Acceleration Assessed with Human White-Matter Images. Journal of Neuroscience, 2017, 37, 4735-4743.	1.7	24
135	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.3	47
136	Fast Genomeâ€Wide QTL Association Mapping on Pedigree and Population Data. Genetic Epidemiology, 2017, 41, 174-186.	0.6	10
137	Exome array analysis suggests an increased variant burden in families with schizophrenia. Schizophrenia Research, 2017, 185, 9-16.	1.1	18
138	Genetic variation and gene expression across multiple tissues and developmental stages in a nonhuman primate. Nature Genetics, 2017, 49, 1714-1721.	9.4	57
139	A Loss-of-Function Splice Acceptor Variant in IGF2 Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.3	52
140	Benchmarking Relatedness Inference Methods with Genome-Wide Data from Thousands of Relatives. Genetics, 2017, 207, 75-82.	1.2	81
141	Whole genome sequencing in psychiatric disorders: the WGSPD consortium. Nature Neuroscience, 2017, 20, 1661-1668.	7.1	122
142	TRAK2, a novel regulator of ABCA1 expression, cholesterol efflux and HDL biogenesis. European Heart Journal, 2017, 38, 3579-3587.	1.0	27
143	Genetic correlation of the plasma lipidome with type 2 diabetes, prediabetes and insulin resistance in Mexican American families. BMC Genetics, 2017, 18, 48.	2.7	10
144	Human subcortical brain asymmetries in 15,847 people worldwide reveal effects of age and sex. Brain Imaging and Behavior, 2017, 11, 1497-1514.	1.1	144

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145	The genetic basis of the comorbidity between cannabis use and major depression. Addiction, 2017, 112, 113-123.	1.7	28
146	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	2.4	31
147	ADAM19: A Novel Target for Metabolic Syndrome in Humans and Mice. Mediators of Inflammation, 2017, 2017, 1-9.	1.4	9
148	Genome-wide physical activity interactions in adiposity â€• A meta-analysis of 200,452 adults. PLoS Genetics, 2017, 13, e1006528.	1.5	158
149	Utility of Lymphoblastoid Cell Lines for Induced Pluripotent Stem Cell Generation. Stem Cells International, 2016, 2016, 1-20.	1.2	18
150	Association of Urinary Phthalates with Self-Reported Eye Affliction/Retinopathy in Individuals with Diabetes: National Health and Nutrition Examination Survey, 2001â€“2010. Journal of Diabetes Research, 2016, 2016, 1-10.	1.0	2
151	Lack of Association betweenSLC30A8Variants and Type 2 Diabetes in Mexican American Families. Journal of Diabetes Research, 2016, 2016, 1-9.	1.0	7
152	Progressive Bidirectional Age-Related Changes in Default Mode Network Effective Connectivity across Six Decades. Frontiers in Aging Neuroscience, 2016, 8, 137.	1.7	6
153	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	13.7	952
154	The Quantitative-MFG Test: A Linear Mixed Effect Model to Detect Maternal-Offspring Gene Interactions. Annals of Human Genetics, 2016, 80, 63-80.	0.3	3
155	Transcriptomics in type 2 diabetes: Bridging the gap between genotype and phenotype. Genomics Data, 2016, 8, 25-36.	1.3	37
156	GWAS and transcriptional analysis prioritize ITPR1 and CNTN4 for a serum uric acid 3p26 QTL in Mexican Americans. BMC Genomics, 2016, 17, 276.	1.2	13
157	The Arg59Trp variant in ANGPTL8 (betatrophin) is associated with total and HDL-cholesterol in American Indians and Mexican Americans and differentially affects cleavage of ANGPTL3. Molecular Genetics and Metabolism, 2016, 118, 128-137.	0.5	33
158	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	7.1	213
159	Quantitative physical activity assessment of children and adolescents in a rural population from <scp>E</scp>astern <scp>N</scp>epal. American Journal of Human Biology, 2016, 28, 129-137.	0.8	2
160	Methylation ofSOCS3is inversely associated with metabolic syndrome in an epigenome-wide association study of obesity. Epigenetics, 2016, 11, 699-707.	1.3	68
161	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	5.8	68
162	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	5.8	74

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163	Conceptualizing Major Depression. , 2016, , 487-501.		0
164	Genetic Variants in Toll-Like Receptor 4 Gene and Their Association Analysis with Estimated Glomerular Filtration Rate in Mexican American Families. CardioRenal Medicine, 2016, 6, 301-306.	0.7	3
165	Omics-squared: human genomic, transcriptomic and phenotypic data for genetic analysis workshop 19. BMC Proceedings, 2016, 10, 71-77.	1.8	17
166	Finding potential cis-regulatory loci using allele-specific chromatin accessibility as weights in a kernel-based variance component test. BMC Proceedings, 2016, 10, 103-108.	1.8	2
167	Independent test assessment using the extreme value distribution theory. BMC Proceedings, 2016, 10, 245-249.	1.8	1
168	A variance component method for integrated pathway analysis of gene expression data. BMC Proceedings, 2016, 10, 337-342.	1.8	1
169	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. Multiple Sclerosis Journal, 2016, 22, 1655-1664.	1.4	44
170	Lipidomic risk score independently and cost-effectively predicts risk of future type 2 diabetes: results from diverse cohorts. Lipids in Health and Disease, 2016, 15, 67.	1.2	44
171	Genome- and epigenome-wide association study of hypertriglyceridemic waist in Mexican American families. Clinical Epigenetics, 2016, 8, 6.	1.8	52
172	Recurrent major depression and right hippocampal volume: A bivariate linkage and association study. Human Brain Mapping, 2016, 37, 191-202.	1.9	21
173	New loci for body fat percentage reveal link between adiposity and cardiometabolic disease risk. Nature Communications, 2016, 7, 10495.	5.8	245
174	Genome-wide meta-analysis uncovers novel loci influencing circulating leptin levels. Nature Communications, 2016, 7, 10494.	5.8	153
175	Transancestral fine-mapping of four type 2 diabetes susceptibility loci highlights potential causal regulatory mechanisms. Human Molecular Genetics, 2016, 25, 2070-2081.	1.4	21
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