Joanne E Curran

List of Publications by Year
in descending order

155 papers	10,787 citations	81900 39 h-index	42399 92 g-index
182 all docs	182 docs citations	182 times ranked	20992 citing authors

#	Article	IF	Citations
1	Sequencing of 53,831 diverse genomes from the NHLBI TOPMed Program. Nature, 2021, 590, 290-299.	27.8	1,069
2	The genetic architecture of type 2 diabetes. Nature, 2016, 536, 41-47.	27.8	952
3	Common genetic variants influence human subcortical brain structures. Nature, 2015, 520, 224-229.	27.8	772
4	Identification of common variants associated with human hippocampal and intracranial volumes. Nature Genetics, 2012, 44, 552-561.	21.4	594
5	The transcriptional landscape of age in human peripheral blood. Nature Communications, 2015, 6, 8570.	12.8	533
6	Discovery of expression QTLs using large-scale transcriptional profiling in human lymphocytes. Nature Genetics, 2007, 39, 1208-1216.	21.4	456
7	The genetic architecture of the human cerebral cortex. Science, 2020, 367, .	12.6	450
8	Inherited causes of clonal haematopoiesis in 97,691 whole genomes. Nature, 2020, 586, 763-768.	27.8	376
9	Multi-site genetic analysis of diffusion images and voxelwise heritability analysis: A pilot project of the ENIGMAâ€“DTI working group. NeuroImage, 2013, 81, 455-469.	4.2	354
10	Long-term neural and physiological phenotyping of a single human. Nature Communications, 2015, 6, 8885.	12.8	353
11	Plasma lipid profiling in a large population-based cohort. Journal of Lipid Research, 2013, 54, 2898-2908.	4.2	304
12	Novel genetic loci associated with hippocampal volume. Nature Communications, 2017, 8, 13624.	12.8	250
13	Plasma Lipid Profiling Shows Similar Associations with Prediabetes and Type 2 Diabetes. PLoS ONE, 2013, 8, e74341.	2.5	247
14	Heritability of fractional anisotropy in human white matter: A comparison of Human Connectome Project and ENIGMA-DTI data. NeuroImage, 2015, 111, 300-311.	4.2	227
15	Novel genetic loci underlying human intracranial volume identified through genome-wide association. Nature Neuroscience, 2016, 19, 1569-1582.	14.8	213
16	High Dimensional Endophenotype Ranking in the Search for Major Depression Risk Genes. Biological Psychiatry, 2012, 71, 6-14.	1.3	170
17	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.	21.4	146
18	Multi-site study of additive genetic effects on fractional anisotropy of cerebral white matter: Comparing meta and megaanalytical approaches for data pooling. NeuroImage, 2014, 95, 136-150.	4.2	127

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19	Testing the Hypothesis of Accelerated Cerebral White Matter Aging in Schizophrenia and Major Depression. Biological Psychiatry, 2013, 73, 482-491.	1.3	107
20	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.	6.2	103
21	Non-crossover gene conversions show strong GC bias and unexpected clustering in humans. ELife, 2015, 4, .	6.0	95
22	Plasma Lipidomic Profile Signature of Hypertension in Mexican American Families. Hypertension, 2013, 62, 621-626.	2.7	87
23	Benchmarking Relatedness Inference Methods with Genome-Wide Data from Thousands of Relatives. Genetics, 2017, 207, 75-82.	2.9	81
24	Influence of age, sex and genetic factors on the human brain. Brain Imaging and Behavior, 2014, 8, 143-152.	2.1	69
25	Prosaposin is a regulator of progranulin levels and oligomerization. Nature Communications, 2016, 7, 11992.	12.8	68
26	Shared Genetic Factors Influence Head Motion During MRI and Body Mass Index. Cerebral Cortex, 2017, 27, 5539-5546.	2.9	67
27	Data for Genetic Analysis Workshop 18: human whole genome sequence, blood pressure, and simulated phenotypes in extended pedigrees. BMC Proceedings, 2014, 8, S2.	1.6	65
28	Genetic basis of neurocognitive decline and reduced white-matter integrity in normal human brain aging. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19006-19011.	7.1	62
29	Endogenous factor VIII synthesis from the intron 22â€“inverted F8 locus may modulate the immunogenicity of replacement therapy for hemophilia A. Nature Medicine, 2013, 19, 1318-1324.	30.7	59
30	Human Plasma Lipidome Is Pleiotropically Associated With Cardiovascular Risk Factors and Death. Circulation: Cardiovascular Genetics, 2014, 7, 854-863.	5.1	56
31	Genetic determinants of mitochondrial content. Human Molecular Genetics, 2007, 16, 1504-1514.	2.9	54
32	Association of Copy Number Variation of the 15q11.2 BP1-BP2 Region With Cortical and Subcortical Morphology and Cognition. JAMA Psychiatry, 2020, 77, 420.	11.0	54
33	Genome- and epigenome-wide association study of hypertriglyceridemic waist in Mexican American families. Clinical Epigenetics, 2016, 8, 6.	4.1	52
34	A Loss-of-Function Splice Acceptor Variant in IGF2 Is Protective for Type 2 Diabetes. Diabetes, 2017, 66, 2903-2914.	0.6	52
35	Dose response of the 16p11.2 distal copy number variant on intracranial volume and basal ganglia. Molecular Psychiatry, 2020, 25, 584-602.	7.9	49
36	A Low-Frequency Inactivating AKT2 Variant Enriched in the Finnish Population Is Associated With Fasting Insulin Levels and Type 2 Diabetes Risk. Diabetes, 2017, 66, 2019-2032.	0.6	47

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37	Crossover interference and sex-specific genetic maps shape identical by descent sharing in close relatives. PLoS Genetics, 2019, 15, e1007979.	3.5	46
38	Genetic loci for Epstein-Barr virus nuclear antigen-1 are associated with risk of multiple sclerosis. Multiple Sclerosis Journal, 2016, 22, 1655-1664.	3.0	44
39	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.	3.0	44
40	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.	7.9	44
41	Impact of Rare and Common Genetic Variants on Diabetes Diagnosis by Hemoglobin A1c in Multi-Ancestry Cohorts: The Trans-Omics for Precision Medicine Program. American Journal of Human Genetics, 2019, 105, 706-718.	6.2	44
42	Shared Genetic Factors Influence Amygdala Volumes and Risk for Alcoholism. Neuropsychopharmacology, 2015, 40, 412-420.	5.4	43
43	Rediscovering the value of families for psychiatric genetics research. Molecular Psychiatry, 2019, 24, 523-535.	7.9	43
44	Rapid, Phase-free Detection of Long Identity-by-Descent Segments Enables Effective Relationship Classification. American Journal of Human Genetics, 2020, 106, 453-466.	6.2	42
45	Waist Circumference Independently Associates with the Risk of Insulin Resistance and Type 2 Diabetes in Mexican American Families. PLoS ONE, 2013, 8, e59153.	2.5	40
46	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
47	Genetic Effects on DNA Methylation and Its Potential Relevance for Obesity in Mexican Americans. PLoS ONE, 2013, 8, e73950.	2.5	37
48	Mendelian randomization supports bidirectional causality between telomere length and clonal hematopoiesis of indeterminate potential. Science Advances, 2022, 8, eabl6579.	10.3	36
49	Transcriptomic Identification of ADH1B as a Novel Candidate Gene for Obesity and Insulin Resistance in Human Adipose Tissue in Mexican Americans from the Veterans Administration Genetic Epidemiology Study (VAGES). PLoS ONE, 2015, 10, e0119941.	2.5	35
50	A White Matter Connection of Schizophrenia and Alzheimerâ€™s Disease. Schizophrenia Bulletin, 2021, 47, 197-206.	4.3	35
51	Inferring Identical-by-Descent Sharing of Sample Ancestors Promotes High-Resolution Relative Detection. American Journal of Human Genetics, 2018, 103, 30-44.	6.2	34
52	Genomeâ€wide significant localization for working and spatial memory: Identifying genes for psychosis using models of cognition. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2014, 165, 84-95.	1.7	32
53	Induced Pluripotent Stem Cells in Disease Modeling and Gene Identification. Methods in Molecular Biology, 2018, 1706, 17-38.	0.9	32
54	GenotypeÃ—age interaction in human transcriptional ageing. Mechanisms of Ageing and Development, 2012, 133, 581-590.	4.6	31

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55	Sequence data and association statistics from 12,940 type 2 diabetes cases and controls. Scientific Data, 2017, 4, 170179.	5.3	31
56	Genome-wide association analysis confirms and extends the association of SLC2A9 with serum uric acid levels to Mexican Americans. Frontiers in Genetics, 2013, 4, 279.	2.3	30
57	Common genetic variants and gene expression associated with white matter microstructure in the human brain. NeuroImage, 2014, 97, 252-261.	4.2	30
58	Discovering Schizophrenia Endophenotypes in Randomly Ascertained Pedigrees. Biological Psychiatry, 2015, 77, 75-83.	1.3	30
59	Genetic determinants of telomere length from 109,122 ancestrally diverse whole-genome sequences in TOPMed. Cell Genomics, 2022, 2, 100084.	6.5	29
60	Genetic epidemiology of cardiometabolic risk factors and their clustering patterns in Mexican American children and adolescents: the SAFARI Study. Human Genetics, 2013, 132, 1059-1071.	3.8	28
61	Mapping eQTLs in the Norfolk Island Genetic Isolate Identifies Candidate Genes for CVD Risk Traits. American Journal of Human Genetics, 2013, 93, 1087-1099.	6.2	28
62	Evaluating the contribution of rare variants to type 2 diabetes and related traits using pedigrees. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 379-384.	7.1	28
63	Whole-genome sequencing association analysis of quantitative red blood cell phenotypes: The NHLBI TOPMed program. American Journal of Human Genetics, 2021, 108, 874-893.	6.2	28
64	TRAK2, a novel regulator of ABCA1 expression, cholesterol efflux and HDL biogenesis. European Heart Journal, 2017, 38, 3579-3587.	2.2	27
65	Association of CREBRF variants with obesity and diabetes in Pacific Islanders from Guam and Saipan. Diabetologia, 2019, 62, 1647-1652.	6.3	26
66	Genetic Architecture of Carotid Artery Intima-Media Thickness in Mexican Americans. Circulation: Cardiovascular Genetics, 2013, 6, 211-221.	5.1	24
67	Epigenetic Age Acceleration Assessed with Human White-Matter Images. Journal of Neuroscience, 2017, 37, 4735-4743.	3.6	24
68	Imaging local genetic influences on cortical folding. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 7430-7436.	7.1	24
69	1q21.1 distal copy number variants are associated with cerebral and cognitive alterations in humans. Translational Psychiatry, 2021, 11, 182.	4.8	24
70	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.	6.2	24
71	Identification of Pleiotropic Genetic Effects on Obesity and Brain Anatomy. Human Heredity, 2013, 75, 136-143.	0.8	23
72	Genotype Ã— Adiposity Interaction Linkage Analyses Reveal a Locus on Chromosome 1 for Lipoprotein-Associated Phospholipase A2, a Marker of Inflammation and Oxidative Stress. American Journal of Human Genetics, 2007, 80, 168-177.	6.2	22

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73	Exome Sequence Data From Multigenerational Families Implicate AMPA Receptor Trafficking in Neurocognitive Impairment and Schizophrenia Risk. Schizophrenia Bulletin, 2016, 42, 288-300.	4.3	22
74	ADAM28 is elevated in humans with the metabolic syndrome and is a novel sheddase of human tumour necrosis factorâ€Î±. Immunology and Cell Biology, 2012, 90, 966-973.	2.3	21
75	Lipidomics in the Study of Hypertension in Metabolic Syndrome. Current Hypertension Reports, 2017, 19, 7.	3.5	21
76	Serum phosphatidylinositol as a biomarker for bipolar disorder liability. Bipolar Disorders, 2017, 19, 107-115.	1.9	20
77	Genome-wide genetic investigation of serological measures of common infections. European Journal of Human Genetics, 2015, 23, 1544-1548.	2.8	18
78	Utility of Lymphoblastoid Cell Lines for Induced Pluripotent Stem Cell Generation. Stem Cells International, 2016, 2016, 1-20.	2.5	18
79	Disentangling the genetic overlap between cholesterol and suicide risk. Neuropsychopharmacology, 2018, 43, 2556-2563.	5.4	18
80	Human Cortical Thickness Organized into Genetically-determined Communities across Spatial Resolutions. Cerebral Cortex, 2019, 29, 106-118.	2.9	18
81	Shared genetic variance between obesity and white matter integrity in Mexican Americans. Frontiers in Genetics, 2015, 6, 26.	2.3	17
82	Chromosome Xq23 is associated with lower atherogenic lipid concentrations and favorable cardiometabolic indices. Nature Communications, 2021, 12, 2182.	12.8	17
83	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.	4.7	16
84	Rare DEGS1 variant significantly alters de novo ceramide synthesis pathway. Journal of Lipid Research, 2019, 60, 1630-1639.	4.2	16
85	Evidence for genetic correlation between human cerebral white matter microstructure and inflammation. Human Brain Mapping, 2019, 40, 4180-4191.	3.6	16
86	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.	6.2	14
87	GWAS and transcriptional analysis prioritize ITPR1 and CNTN4 for a serum uric acid 3p26 QTL in Mexican Americans. BMC Genomics, 2016, 17, 276.	2.8	13
88	Plasma lipidome is independently associated with variability in metabolic syndrome in Mexican American families. Journal of Lipid Research, 2014, 55, 939-946.	4.2	12
89	Increased waist circumference is independently associated with hypothyroidism in Mexican Americans: replicative evidence from two large, population-based studies. BMC Endocrine Disorders, 2014, 14, 46.	2.2	12
90	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.	3.0	12

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91	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. Hypertension, 2022, 79, 1656-1667.	2.7	12
92	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.	0.8	11
93	Family-based analyses reveal novel genetic overlap between cytokine interleukin-8 and risk for suicide attempt. Brain, Behavior, and Immunity, 2019, 80, 292-299.	4.1	11
94	Further evidence supporting a potential role for ADH1B in obesity. Scientific Reports, 2021, 11, 1932.	3.3	11
95	Highly efficient induced pluripotent stem cell reprogramming of cryopreserved lymphoblastoid cell lines. Journal of Biological Methods, 2020, 7, e124.	0.6	11
96	Gene Expression Differences Between Offspring of Long-Lived Individuals and Controls in Candidate Longevity Regions: Evidence forPAPSS2as a Longevity Gene. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2016, 71, 1295-1299.	3.6	10
97	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
98	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.	3.8	10
99	Transcriptomic Profiling of Fibropapillomatosis in Green Sea Turtles (Chelonia mydas) From South Texas. Frontiers in Immunology, 2021, 12, 630988.	4.8	10
100	Genomeâ€wide significant linkage of schizophreniaâ€related neuroanatomical trait to 12q24. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2015, 168, 678-686.	1.7	9
101	Common polygenic variation contributes to risk of migraine in the Norfolk Island population. Human Genetics, 2015, 134, 1079-1087.	3.8	9
102	ADAM19: A Novel Target for Metabolic Syndrome in Humans and Mice. Mediators of Inflammation, 2017, 2017, 1-9.	3.0	9
103	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.	3.3	9
104	Whole genome sequence analysis of platelet traits in the NHLBI Trans-Omics for Precision Medicine (TOPMed) initiative. Human Molecular Genetics, 2022, 31, 347-361.	2.9	9
105	Associations of cannabis use disorder with cognition, brain structure, and brain function in African Americans. Human Brain Mapping, 2021, 42, 1727-1741.	3.6	9
106	Whole-genome sequencing to understand the genetic architecture of common gene expression and biomarker phenotypes. Human Molecular Genetics, 2015, 24, 1504-1512.	2.9	8
107	Exome sequences of multiplex, multigenerational families reveal schizophrenia risk loci with potential implications for neurocognitive performance. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2017, 174, 817-827.	1.7	8
108	Transition from pre-diabetes to diabetes and predictors of risk in Mexican-Americans. Diabetes, Metabolic Syndrome and Obesity: Targets and Therapy, 2017, Volume 10, 491-503.	2.4	8

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109	Neurocognitive impairment in type 2 diabetes: evidence for shared genetic aetiology. Diabetologia, 2020, 63, 977-986.	6.3	8
110	Effects of copy number variable regions on local gene expression in white blood cells of Mexican Americans. European Journal of Human Genetics, 2015, 23, 1229-1235.	2.8	7
111	Lack of Association betweenSLC30A8Variants and Type 2 Diabetes in Mexican American Families. Journal of Diabetes Research, 2016, 2016, 1-9.	2.3	7
112	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.	1.3	7
113	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.	0.8	6
114	Role of miRNA-mRNA Interaction in Neural Stem Cell Differentiation of Induced Pluripotent Stem Cells. International Journal of Molecular Sciences, 2020, 21, 6980.	4.1	6
115	Minimal Relationship between Local Gyrification and General Cognitive Ability in Humans. Cerebral Cortex, 2020, 30, 3439-3450.	2.9	6
116	Soluble Forms of Intercellular and Vascular Cell Adhesion Molecules Independently Predict Progression to Type 2 Diabetes in Mexican American Families. PLoS ONE, 2016, 11, e0151177.	2.5	6
117	Gestational Age and the Cord Blood Lipidomic Profile in Late Preterm and Term Infants. Neonatology, 2018, 114, 215-222.	2.0	5
118	Whole Genome Sequencing Identifies CRISPLD2 as a Lung Function Gene in Children With Asthma. Chest, 2019, 156, 1068-1079.	0.8	5
119	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.	4.1	5
120	Genetic Overlap Profiles of Cognitive Ability in Psychotic and Affective Illnesses: A Multisite Study of Multiplex Pedigrees. Biological Psychiatry, 2021, 90, 373-384.	1.3	5
121	New approaches for the discovery of lipid-related genes. Clinical Lipidology, 2011, 6, 495-500.	0.4	3
122	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.	3.8	3
123	Identifying the Lipidomic Effects of a Rare Loss-of-Function Deletion in ANGPTL3. Circulation Genomic and Precision Medicine, 2021, 14, e003232.	3.6	3
124	A Phenomic Scan of the Norfolk Island Genetic Isolate Identifies a Major Pleiotropic Effect Locus Associated with Metabolic and Renal Disorder Markers. PLoS Genetics, 2015, 11, e1005593.	3.5	3
125	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.	1.7	3
126	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.	2.3	2

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127	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.	0.9	2
128	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.	2.6	2
129	Rare coding variants in RCN3 are associated with blood pressure. BMC Genomics, 2022, 23, 148.	2.8	2
130	Data on genetic associations of carotid atherosclerosis markers in Mexican American and European American rheumatoid arthritis subjects. Data in Brief, 2018, 17, 820-829.	1.0	1
131	UTILITY OF PERIPHERAL miRNA EXPRESSION PROFILES AS BIOMARKERS AND PATHOLOGICAL INDICATORS OF NEUROPSYCHIATRIC DISEASE. European Neuropsychopharmacology, 2019, 29, S915-S916.	0.7	1
132	Genetic Architecture of Human Obesity Traits in the Rhesus Macaque. Obesity, 2019, 27, 479-488.	3.0	1
133	A QTL on chromosome 3q23 influences processing speed in humans. Genes, Brain and Behavior, 2019, 18, e12530.	2.2	1
134	Multi-phenotype genome-wide association studies of the Norfolk Island isolate implicate pleiotropic loci involved in chronic kidney disease. Scientific Reports, 2021, 11, 19425.	3.3	1
135	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.	1.4	1
136	The Entire Primary Sequence of Factor VIII Is Synthesized As Two Polypeptide Chains in Hemophilia A Patients with the Intron-22-Inversion. Blood, 2011, 118, 1176-1176.	1.4	1
137	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.	1.4	1
138	Combining meta- and mega- analytic approaches for multi-site diffusion imaging based genetic studies: From the ENIGMA-DTI working group. , 2014, , .		0
139	106. Genome-Wide Significant Locus on Chromosome 5 Influences Psychosis Risk and General Intellectual Ability. Biological Psychiatry, 2018, 83, S43-S44.	1.3	0
140	F49. Genetic Basis of Changes in Neurocognition and Psychopathology Between Childhood and Adulthood. Biological Psychiatry, 2018, 83, S256-S257.	1.3	0
141	SU74THE POTENTIAL OF LOCAL GYRIFICATION INDEX AS A NEUROPHENOTYPE. European Neuropsychopharmacology, 2019, 29, S1306.	0.7	0
142	SA80INTERLEUKIN-8 (BUT NOT INTERLEUKIN-6) SHARES GENETIC OVERLAP WITH RISK FOR SUICIDE ATTEMPTS IN WOMEN (BUT NOT IN MEN). European Neuropsychopharmacology, 2019, 29, S1231.	0.7	0
143	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.	1.3	0
144	F145. Extremely Weak Relationship Between Gyrification and Intelligence. Biological Psychiatry, 2019, 85, S269.	1.3	0

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145	Genetic determinants of metabolic biomarkers and their associations with cardiometabolic traits in Hispanic/Latino adolescents. Pediatric Research, 2021, , .	2.3	0
146	F8 and HLA-II Haplotypes in the Hispanic Population: Implications for Inhibitor Risk Development in Hispanic Hemophilia A Patients. Blood, 2012, 120, 3365-3365.	1.4	0
147	Common SNPs within or near Three Immune Response Genes Implicated in the Risk of FVIII Immunogenicity in Hemophilia A Do Not Influence Steady-State Levels of Their Encoded mRNAs. Blood, 2012, 120, 3366-3366.	1.4	0
148	Abstract 180: Missense Mutations in ABCA1 and CETP Associate with Changes in the HDL Proteome in Primate Half-Sibs Discordant for HDL Cholesterol Levels. Arteriosclerosis, Thrombosis, and Vascular Biology, 2018, 38, .	2.4	0
149	1653-P: Association between Genetic Admixture Estimates for Five Ancestral Populations and Diabetes-Related Traits in Pacific Islanders. Diabetes, 2020, 69, 1653-P.	0.6	0
150	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
151	New approaches for the discovery of lipidâ€'related genes. Clinical Lipidology, 2011, 6, 495-500.	0.4	0
152	The Factor II (FII) Expression Quantitative Trait Locus (eQTL) Prothrombin G20210A Is Pleiotropically Associated with Plasma Fibrinogen Levels and Has a Profound Effect on Obesity in Mexican Americans of South Texas. Blood, 2021, 138, 1059-1059.	1.4	0
153	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.	1.4	0
154	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.	1.4	0
155	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.	1.4	0