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UK Biobank

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Analysis of 200,000 Exome-Sequenced UK Biobank Subjects Implicates Genes Involved in Increased and Decreased Risk of Hypertension. <i>Pulse</i> , 2021, 9, 17-29.	0.9	10
2	Whole-exome sequencing reveals a role of HTRA1 and EGFL8 in brain white matter hyperintensities. <i>Brain</i> , 2021, 144, 2670-2682.	3.7	21
3	Investigation of Association of Rare, Functional Genetic Variants With Heavy Drinking and Problem Drinking in Exome Sequenced UK Biobank Participants. <i>Alcohol and Alcoholism</i> , 2021, , .	0.9	1
5	Rare Missense Functional Variants at <i>COL4A1</i> and <i>COL4A2</i> in Sporadic Intracerebral Hemorrhage. <i>Neurology</i> , 2021, 97, .	1.5	6
6	Genetic pleiotropy of <i>ERCC6</i> loss-of-function and deleterious missense variants links retinal dystrophy, arrhythmia, and immunodeficiency in diverse ancestries. <i>Human Mutation</i> , 2021, 42, 969-977.	1.1	3
7	Fast numerical optimization for genome sequencing data in population biobanks. <i>Bioinformatics</i> , 2021, 37, 4148-4155.	1.8	9
9	The power of large-scale exome sequencing. <i>Nature Reviews Genetics</i> , 2021, 22, 549-549.	7.7	6
11	Clonal myelopoiesis promotes adverse outcomes in chronic kidney disease. <i>Leukemia</i> , 2022, 36, 507-515.	3.3	49
12	Genetic insights into biological mechanisms governing human ovarian ageing. <i>Nature</i> , 2021, 596, 393-397.	13.7	183
14	Rare variant contribution to human disease in 281,104 UK Biobank exomes. <i>Nature</i> , 2021, 597, 527-532.	13.7	224
16	Phenotypic Expression and Outcomes in Individuals With Rare Genetic Variants of Hypertrophic Cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2021, 78, 1097-1110.	1.2	55
18	Coding and Noncoding Variation in <i>LRRK2</i> and Parkinson's Disease Risk. <i>Movement Disorders</i> , 2022, 37, 95-105.	2.2	14
20	Clinical translation of hidradenitis suppurativa genetic studies requires global collaboration. <i>British Journal of Dermatology</i> , 2022, 186, 183-185.	1.4	7
21	Rare, Damaging DNA Variants in <i>CORIN</i> and Risk of Coronary Artery Disease: Insights From Functional Genomics and Large-Scale Sequencing Analyses. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003399.	1.6	10
28	Exome sequencing and analysis of 454,787 UK Biobank participants. <i>Nature</i> , 2021, 599, 628-634.	13.7	377
29	Polygenic basis and biomedical consequences of telomere length variation. <i>Nature Genetics</i> , 2021, 53, 1425-1433.	9.4	145
31	Gene-level analysis of rare variants in 379,066 whole exome sequences identifies an association of <i>GIGYF1</i> loss of function with type 2 diabetes. <i>Scientific Reports</i> , 2021, 11, 21565.	1.6	25
32	Mutation saturation for fitness effects at human CpG sites. <i>ELife</i> , 2021, 10, .	2.8	23

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34	Effect of Loss-of-Function Genetic Variants in <i>PCSK9</i> on Glycemic Traits, Neurocognitive Impairment, and Hepatobiliary Function. <i>Diabetes Care</i> , 2022, 45, 251-254.	4.3	1
35	Rare coding variants in DNA damage repair genes associated with timing of natural menopause. <i>Human Genetics and Genomics Advances</i> , 2022, 3, 100079.	1.0	4
40	Rare coding variants in 35 genes associate with circulating lipid levels—A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
41	Genetic data sharing and artificial intelligence in the era of personalized medicine based on a cross-sectional analysis of the Saudi human genome program. <i>Scientific Reports</i> , 2022, 12, 1405.	1.6	18
42	Evaluation of Evidence for Pathogenicity Demonstrates That <i>BLK</i> , <i>KLF11</i> , and <i>PAX4</i> Should Not Be Included in Diagnostic Testing for MODY. <i>Diabetes</i> , 2022, 71, 1128-1136.	0.3	27
43	Clinical pharmacogenetic analysis in 5,001 individuals with diagnostic Exome Sequencing data. <i>Npj Genomic Medicine</i> , 2022, 7, 12.	1.7	10
44	Genetic associations of protein-coding variants in human disease. <i>Nature</i> , 2022, 603, 95-102.	13.7	67
45	Analysis of rare genetic variation underlying cardiometabolic diseases and traits among 200,000 individuals in the UK Biobank. <i>Nature Genetics</i> , 2022, 54, 240-250.	9.4	68
47	Human lifespan is linked to truncating variants in single genes. <i>Nature Aging</i> , 0, , .	5.3	0
48	Reduced reproductive success is associated with selective constraint on human genes. <i>Nature</i> , 2022, 603, 858-863.	13.7	29
49	The burden of rare protein-truncating genetic variants on human lifespan. <i>Nature Aging</i> , 2022, 2, 289-294.	5.3	6
50	Exome-wide screening identifies novel rare risk variants for major depression disorder. <i>Molecular Psychiatry</i> , 2022, 27, 3069-3074.	4.1	15
51	Identification of Rare Loss-of-Function Genetic Variation Regulating Body Fat Distribution. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2022, 107, 1065-1077.	1.8	12
52	Ribosomal protein S6 kinase beta-1 gene variants cause hypertrophic cardiomyopathy. <i>Journal of Medical Genetics</i> , 2021, , jmedgenet-2021-107866.	1.5	1
54	Gene-SCOUT: identifying genes with similar continuous trait fingerprints from phenome-wide association analyses. <i>Nucleic Acids Research</i> , 2022, 50, 4289-4301.	6.5	3
55	Genetic and environmental determinants of diastolic heart function. , 2022, 1, 361-371.		12
56	The Value of Rare Genetic Variation in the Prediction of Common Obesity in European Ancestry Populations. <i>Frontiers in Endocrinology</i> , 2022, 13, 863893.	1.5	7
57	Gene-based whole genome sequencing meta-analysis of 250 circulating proteins in three isolated European populations. <i>Molecular Metabolism</i> , 2022, 61, 101509.	3.0	3

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59	Rare and Common Genetic Variation Underlying the Risk of Hypertrophic Cardiomyopathy in a National Biobank. <i>JAMA Cardiology</i> , 2022, 7, 715.	3.0	22
60	Genome-wide association of polygenic risk extremes for Alzheimer's disease in the UK Biobank. <i>Scientific Reports</i> , 2022, 12, 8404.	1.6	27
63	A spectrum of recessiveness among Mendelian disease variants in UK Biobank. <i>American Journal of Human Genetics</i> , 2022, 109, 1298-1307.	2.6	26
64	Exome-wide analysis of copy number variation shows association of the human leukocyte antigen region with asthma in UK Biobank. <i>BMC Medical Genomics</i> , 2022, 15, .	0.7	6
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70	Association of Common and Rare Genetic Variation in the 3-â€Hydroxy-â€Methylglutaryl Coenzyme A Reductase Gene and Cataract Risk. <i>Journal of the American Heart Association</i> , 2022, 11, .	1.6	4
72	Clinical features of UK Biobank subjects carrying protein-truncating variants in genes implicated in schizophrenia pathogenesis. <i>Psychiatric Genetics</i> , 2022, 32, 156-161.	0.6	3
77	Preface to theme issue on pragmatic and virtual trials: Progress and challenges. <i>Contemporary Clinical Trials</i> , 2022, 119, 106816.	0.8	2
78	Small dataset solves big problem: An outlier-insensitive binary classifier for inhibitory potency prediction. <i>Knowledge-Based Systems</i> , 2022, 251, 109242.	4.0	10
80	Inherited basis of visceral, abdominal subcutaneous and gluteofemoral fat depots. <i>Nature Communications</i> , 2022, 13, .	5.8	43
81	Investigating the characteristics of genes and variants associated with self-reported hearing difficulty in older adults in the UK Biobank. <i>BMC Biology</i> , 2022, 20, .	1.7	7
82	Genome-wide analyses of 200,453 individuals yield new insights into the causes and consequences of clonal hematopoiesis. <i>Nature Genetics</i> , 2022, 54, 1155-1166.	9.4	109
83	Frequency, Penetrance, and Variable Expressivity of Dilated Cardiomyopathy-Associated Putative Pathogenic Gene Variants in UK Biobank Participants. <i>Circulation</i> , 2022, 146, 110-124.	1.6	25
85	New Horizons: the value of UK Biobank to research on endocrine and metabolic disorders. <i>Journal of Clinical Endocrinology and Metabolism</i> , 0, , .	1.8	3
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91	Standard operating procedures for biobank in oncology. <i>Frontiers in Molecular Biosciences</i> , 0, 9, .	1.6	13
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94	A genome sequencing system for universal newborn screening, diagnosis, and precision medicine for severe genetic diseases. <i>American Journal of Human Genetics</i> , 2022, 109, 1605-1619.	2.6	58
95	Rare coding variation provides insight into the genetic architecture and phenotypic context of autism. <i>Nature Genetics</i> , 2022, 54, 1320-1331.	9.4	155
97	Human genotype-to-phenotype predictions: Boosting accuracy with nonlinear models. <i>PLoS ONE</i> , 2022, 17, e0273293.	1.1	6
98	Study of variants in genes implicated in rare familial migraine syndromes and their association with migraine in 200,000 exome-sequenced UK Biobank participants. <i>Annals of Human Genetics</i> , 0, , .	0.3	4
101	Multimodal biomedical AI. <i>Nature Medicine</i> , 2022, 28, 1773-1784.	15.2	191
102	The impact of Mendelian sleep and circadian genetic variants in a population setting. <i>PLoS Genetics</i> , 2022, 18, e1010356.	1.5	2
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107	Whole Exome Sequencing Study Identifies Novel Rare Risk Variants for Habitual Coffee Consumption Involved in Olfactory Receptor and Hyperphagia. <i>Nutrients</i> , 2022, 14, 4330.	1.7	0
109	The contribution of functional HNF1A variants and polygenic susceptibility to risk of type 2 diabetes in ancestrally diverse populations. <i>Diabetologia</i> , 0, , .	2.9	1

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110	Prevalence and Disease Expression of Pathogenic and Likely Pathogenic Variants Associated With Inherited Cardiomyopathies in the General Population. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	1.6	18
111	Genetic map of regional sulcal morphology in the human brain from UK biobank data. <i>Nature Communications</i> , 2022, 13, .	5.8	9
112	Mapping the genetic architecture of cortical morphology through neuroimaging: progress and perspectives. <i>Translational Psychiatry</i> , 2022, 12, .	2.4	10
113	Gene Sequencing Identifies Perturbation in Nitric Oxide Signaling as a Nonlipid Molecular Subtype of Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2022, 15, .	1.6	4
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121	Identifying shared genetic factors underlying epilepsy and congenital heart disease in Europeans. <i>Human Genetics</i> , 0, , .	1.8	0
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129	Common and rare variant associations with clonal haematopoiesis phenotypes. <i>Nature</i> , 2022, 612, 301-309.	13.7	74

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131	Clonal Hematopoiesis and Risk of Incident Lung Cancer. <i>Journal of Clinical Oncology</i> , 2023, 41, 1423-1433.	0.8	10
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168	Systematic elucidation of genetic mechanisms underlying cholesterol uptake. <i>Cell Genomics</i> , 2023, , 100304.	3.0	2
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