

Namrata Gupta

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/854755/publications.pdf>

Version: 2024-02-01

26
papers

22,615
citations

304368

22
h-index

500791

28
g-index

28
all docs

28
docs citations

28
times ranked

47088
citing authors

#	ARTICLE	IF	CITATIONS
1	Rare coding variants in 35 genes associate with circulating lipid levelsâ€”A multi-ancestry analysis of 170,000 exomes. <i>American Journal of Human Genetics</i> , 2022, 109, 81-96.	2.6	24
2	Monogenic and Polygenic Contributions to QTc Prolongation in the Population. <i>Circulation</i> , 2022, 145, 1524-1533.	1.6	14
3	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2021, 597, E3-E4.	13.7	45
4	Pangenomics enables genotyping of known structural variants in 5202 diverse genomes. <i>Science</i> , 2021, 374, abg8871.	6.0	132
5	Heterozygous <i>ABCG5</i> Gene Deficiency and Risk of Coronary Artery Disease. <i>Circulation Genomic and Precision Medicine</i> , 2020, 13, 417-423.	1.6	45
6	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	13.7	6,140
7	A structural variation reference for medical and population genetics. <i>Nature</i> , 2020, 581, 444-451.	13.7	614
8	A missense variant in Mitochondrial Amidoxime Reducing Component 1 gene and protection against liver disease. <i>PLoS Genetics</i> , 2020, 16, e1008629.	1.5	101
9	Quality control and integration of genotypes from two calling pipelines for whole genome sequence data in the Alzheimer's disease sequencing project. <i>Genomics</i> , 2019, 111, 808-818.	1.3	26
10	DNA Sequence Variation in <i>ACVR1C</i> Encoding the Activin Receptor-Like Kinase 7 Influences Body Fat Distribution and Protects Against Type 2 Diabetes. <i>Diabetes</i> , 2019, 68, 226-234.	0.3	31
11	Analysis of predicted loss-of-function variants in UK Biobank identifies variants protective for disease. <i>Nature Communications</i> , 2018, 9, 1613.	5.8	78
12	The Genetic Landscape of Diamond-Blackfan Anemia. <i>American Journal of Human Genetics</i> , 2018, 103, 930-947.	2.6	184
13	Association Between Titin Loss-of-Function Variants and Early-Onset Atrial Fibrillation. <i>JAMA - Journal of the American Medical Association</i> , 2018, 320, 2354.	3.8	144
14	Quantifying the Impact of Rare and Ultra-rare Coding Variation across the Phenotypic Spectrum. <i>American Journal of Human Genetics</i> , 2018, 102, 1204-1211.	2.6	102
15	Multi-ethnic genome-wide association study for atrial fibrillation. <i>Nature Genetics</i> , 2018, 50, 1225-1233.	9.4	552
16	Association of Rare and Common Variation in the Lipoprotein Lipase Gene With Coronary Artery Disease. <i>JAMA - Journal of the American Medical Association</i> , 2017, 317, 937.	3.8	148
17	Clonal Hematopoiesis and Risk of Atherosclerotic Cardiovascular Disease. <i>New England Journal of Medicine</i> , 2017, 377, 111-121.	13.9	1,738
18	ANGPTL3 Deficiency and Protection Against Coronary Artery Disease. <i>Journal of the American College of Cardiology</i> , 2017, 69, 2054-2063.	1.2	348

#	ARTICLE	IF	CITATIONS
19	Analysis commons, a team approach to discovery in a big-data environment for genetic epidemiology. <i>Nature Genetics</i> , 2017, 49, 1560-1563.	9.4	93
20	Evaluating the Impact of Functional Genetic Variation on HIV-1 Control. <i>Journal of Infectious Diseases</i> , 2017, 216, 1063-1069.	1.9	20
21	Phenotypic Characterization of Genetically Lowered Human Lipoprotein(a) Levels. <i>Journal of the American College of Cardiology</i> , 2016, 68, 2761-2772.	1.2	186
22	Diagnostic Yield and Clinical Utility of Sequencing Familial Hypercholesterolemia Genes in Patients With Severe Hypercholesterolemia. <i>Journal of the American College of Cardiology</i> , 2016, 67, 2578-2589.	1.2	723
23	Targeted exonic sequencing of GWAS loci in the high extremes of the plasma lipids distribution. <i>Atherosclerosis</i> , 2016, 250, 63-68.	0.4	11
24	Analysis of protein-coding genetic variation in 60,706 humans. <i>Nature</i> , 2016, 536, 285-291.	13.7	9,051
25	Integration of Sequence Data from a Consanguineous Family with Genetic Data from an Outbred Population Identifies PLB1 as a Candidate Rheumatoid Arthritis Risk Gene. <i>PLoS ONE</i> , 2014, 9, e87645.	1.1	34
26	Genetics of rheumatoid arthritis contributes to biology and drug discovery. <i>Nature</i> , 2014, 506, 376-381.	13.7	1,974