Ayush Giri

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/6121619/publications.pdf

Version: 2024-02-01

40 papers	4,818 citations	331670 21 h-index	254184 43 g-index
50 all docs	50 docs citations	50 times ranked	10144 citing authors

#	Article	IF	Citations
1	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
2	A catalog of genetic loci associated with kidney function from analyses of a million individuals. Nature Genetics, 2019, 51, 957-972.	21.4	549
3	Rare and low-frequency coding variants alter human adult height. Nature, 2017, 542, 186-190.	27.8	544
4	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. Nature Genetics, 2017, 49, 834-841.	21.4	426
5	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. Nature Genetics, 2019, 51, 51-62.	21.4	328
6	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. Nature Genetics, 2018, 50, 26-41.	21.4	286
7	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. Nature Genetics, 2019, 51, 1459-1474.	21.4	251
8	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. Nature Genetics, 2016, 48, 1162-1170.	21.4	223
9	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. Nature Communications, 2019, 10, 4130.	12.8	133
10	Population Stratification in Genetic Association Studies. Current Protocols in Human Genetics, 2017, 95, 1.22.1-1.22.23.	3.5	108
11	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
12	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. Nature Communications, 2019, 10, 3842.	12.8	90
13	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. Nature Genetics, 2019, 51, 452-469.	21.4	89
14	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. American Journal of Human Genetics, 2016, 99, 40-55.	6.2	82
15	Obesity and pelvic organ prolapse: a systematic review and meta-analysis of observational studies. American Journal of Obstetrics and Gynecology, 2017, 217, 11-26.e3.	1.3	81
16	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. Nature Genetics, 2022, 54, 761-771.	21.4	68
17	Genetic epidemiology of pelvic organ prolapse: a systematic review. American Journal of Obstetrics and Gynecology, 2014, 211, 326-335.	1.3	62
18	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. American Journal of Human Genetics, 2016, 99, 8-21.	6.2	60

#	Article	IF	Citations
19	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. American Journal of Human Genetics, 2016, 99, 22-39.	6.2	50
20	New Blood Pressureâ€“Associated Loci Identified in Meta-Analyses of 475â€‰000 Individuals. Circulation: Cardiovascular Genetics, 2017, 10, .	5.1	48
21	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. Frontiers in Genetics, 2019, 10, 511.	2.3	32
22	African genetic ancestry interacts with body mass index to modify risk for uterine fibroids. PLoS Genetics, 2017, 13, e1006871.	3.5	25
23	A genome-wide association study meta-analysis of clinical fracture in 10,012 African American women. Bone Reports, 2016, 5, 233-242.	0.4	20
24	Calcium: magnesium intake ratio and colorectal carcinogenesis, results from the prostate, lung, colorectal, and ovarian cancer screening trial. British Journal of Cancer, 2019, 121, 796-804.	6.4	19
25	Rare variants in fox-1 homolog A (RBFOX1) are associated with lower blood pressure. PLoS Genetics, 2017, 13, e1006678.	3.5	18
26	Genetic Determinants of Pelvic Organ Prolapse among African American and Hispanic Women in the Womenâ€™s Health Initiative. PLoS ONE, 2015, 10, e0141647.	2.5	17
27	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. American Journal of Hypertension, 2019, 32, 1146-1153.	2.0	17
28	Family history and pelvic organ prolapse: a systematic review and meta-analysis. International Urogynecology Journal, 2021, 32, 759-774.	1.4	16
29	Subclinical Hypothyroidism and Risk for Incident Ischemic Stroke Among Postmenopausal Women. Thyroid, 2014, 24, 1210-1217.	4.5	14
30	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. Scientific Reports, 2020, 10, 7561.	3.3	13
31	Genetic Determinants of Metabolism and Benign Prostate Enlargement: Associations with Prostate Volume. PLoS ONE, 2015, 10, e0132028.	2.5	13
32	Risk factors for degenerative, symptomatic rotator cuff tears: a case-control study. Journal of Shoulder and Elbow Surgery, 2022, 31, 806-812.	2.6	13
33	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
34	Risk factors for rotator cuff disease: A systematic review and meta-analysis of diabetes, hypertension, and hyperlipidemia. Annals of Physical and Rehabilitation Medicine, 2023, 66, 101631.	2.3	10
35	Obesity and sex influence fatty infiltration of the rotator cuff: the Rotator Cuff Outcomes Workgroup (ROW) and Multicenter Orthopaedic Outcomes Network (MOON) cohorts. Journal of Shoulder and Elbow Surgery, 2022, 31, 726-735.	2.6	7
36	Admixture mapping of pelvic organ prolapse in African Americans from the Womenâ€™s Health Initiative Hormone Therapy trial. PLoS ONE, 2017, 12, e0178839.	2.5	4

#	Article	IF	Citations
37	Association of Apparent Treatment-Resistant Hypertension With Differential Risk of End-Stage Kidney Disease Across Racial Groups in the Million Veteran Program. Hypertension, 2021, 78, 376-386.	2.7	2
38	Development and Validation of an Electronic Medical Record Algorithm to Identify Phenotypes of Rotator Cuff Tear. PM and R, 2020, 12, 1099-1105.	1.6	1
39	Associations of biogeographic ancestry with hypertension traits. Journal of Hypertension, 2021, 39, 633-642.	0.5	1
40	Phenome-Wide Association Study of UMOD Gene Variants and Differential Associations With Clinical Outcomes Across Populations in the Million Veteran Program a Multiethnic Biobank. Kidney International Reports, 2022, 7, 1802-1818.	0.8	1