

# 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	Risk factors for rotator cuff disease: A systematic review and meta-analysis of diabetes, hypertension, and hyperlipidemia. <i>Annals of Physical and Rehabilitation Medicine</i> , 2023, 66, 101631.	2.3	10
2	Risk factors for degenerative, symptomatic rotator cuff tears: a case-control study. <i>Journal of Shoulder and Elbow Surgery</i> , 2022, 31, 806-812.	2.6	13
3	Obesity and sex influence fatty infiltration of the rotator cuff: the Rotator Cuff Outcomes Workgroup (ROW) and Multicenter Orthopaedic Outcomes Network (MOON) cohorts. <i>Journal of Shoulder and Elbow Surgery</i> , 2022, 31, 726-735.	2.6	7
4	Phenome-Wide Association Study of UMOD Gene Variants and Differential Associations With Clinical Outcomes Across Populations in the Million Veteran Program a Multiethnic Biobank. <i>Kidney International Reports</i> , 2022, 7, 1802-1818.	0.8	1
5	A multiancestry genome-wide association study of unexplained chronic ALT elevation as a proxy for nonalcoholic fatty liver disease with histological and radiological validation. <i>Nature Genetics</i> , 2022, 54, 761-771.	21.4	68
6	Insights From a Large-Scale Whole-Genome Sequencing Study of Systolic Blood Pressure, Diastolic Blood Pressure, and Hypertension. <i>Hypertension</i> , 2022, 79, 1656-1667.	2.7	12
7	Family history and pelvic organ prolapse: a systematic review and meta-analysis. <i>International Urogynecology Journal</i> , 2021, 32, 759-774.	1.4	16
8	Association of Apparent Treatment-Resistant Hypertension With Differential Risk of End-Stage Kidney Disease Across Racial Groups in the Million Veteran Program. <i>Hypertension</i> , 2021, 78, 376-386.	2.7	2
9	Associations of biogeographic ancestry with hypertension traits. <i>Journal of Hypertension</i> , 2021, 39, 633-642.	0.5	1
10	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. <i>Nature Genetics</i> , 2020, 52, 1314-1332.	21.4	91
11	The polygenic architecture of left ventricular mass mirrors the clinical epidemiology. <i>Scientific Reports</i> , 2020, 10, 7561.	3.3	13
12	Development and Validation of an Electronic Medical Record Algorithm to Identify Phenotypes of Rotator Cuff Tear. <i>PM and R</i> , 2020, 12, 1099-1105.	1.6	1
13	Mapping eGFR loci to the renal transcriptome and phenome in the VA Million Veteran Program. <i>Nature Communications</i> , 2019, 10, 3842.	12.8	90
14	Genome-wide association meta-analyses and fine-mapping elucidate pathways influencing albuminuria. <i>Nature Communications</i> , 2019, 10, 4130.	12.8	133
15	Target genes, variants, tissues and transcriptional pathways influencing human serum urate levels. <i>Nature Genetics</i> , 2019, 51, 1459-1474.	21.4	251
16	Calcium: magnesium intake ratio and colorectal carcinogenesis, results from the prostate, lung, colorectal, and ovarian cancer screening trial. <i>British Journal of Cancer</i> , 2019, 121, 796-804.	6.4	19
17	Genome-Wide Association Study of Apparent Treatment-Resistant Hypertension in the CHARGE Consortium: The CHARGE Pharmacogenetics Working Group. <i>American Journal of Hypertension</i> , 2019, 32, 1146-1153.	2.0	17
18	A catalog of genetic loci associated with kidney function from analyses of a million individuals. <i>Nature Genetics</i> , 2019, 51, 957-972.	21.4	549

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19	A Trans-Ethnic Genome-Wide Association Study of Uterine Fibroids. <i>Frontiers in Genetics</i> , 2019, 10, 511.	2.3	32
20	Protein-coding variants implicate novel genes related to lipid homeostasis contributing to body-fat distribution. <i>Nature Genetics</i> , 2019, 51, 452-469.	21.4	89
21	Trans-ethnic association study of blood pressure determinants in over 750,000 individuals. <i>Nature Genetics</i> , 2019, 51, 51-62.	21.4	328
22	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. <i>Nature Genetics</i> , 2018, 50, 1412-1425.	21.4	924
23	Protein-altering variants associated with body mass index implicate pathways that control energy intake and expenditure in obesity. <i>Nature Genetics</i> , 2018, 50, 26-41.	21.4	286
24	Rare and low-frequency coding variants alter human adult height. <i>Nature</i> , 2017, 542, 186-190.	27.8	544
25	Obesity and pelvic organ prolapse: a systematic review and meta-analysis of observational studies. <i>American Journal of Obstetrics and Gynecology</i> , 2017, 217, 11-26.e3.	1.3	81
26	Genomic analyses identify hundreds of variants associated with age at menarche and support a role for puberty timing in cancer risk. <i>Nature Genetics</i> , 2017, 49, 834-841.	21.4	426
27	New Blood Pressure-Associated Loci Identified in Meta-Analyses of 475,000 Individuals. <i>Circulation: Cardiovascular Genetics</i> , 2017, 10, .	5.1	48
28	Population Stratification in Genetic Association Studies. <i>Current Protocols in Human Genetics</i> , 2017, 95, 1.22.1-1.22.23.	3.5	108
29	Admixture mapping of pelvic organ prolapse in African Americans from the Women's Health Initiative Hormone Therapy trial. <i>PLoS ONE</i> , 2017, 12, e0178839.	2.5	4
30	Rare variants in fox-1 homolog A (RBFox1) are associated with lower blood pressure. <i>PLoS Genetics</i> , 2017, 13, e1006678.	3.5	18
31	African genetic ancestry interacts with body mass index to modify risk for uterine fibroids. <i>PLoS Genetics</i> , 2017, 13, e1006871.	3.5	25
32	Exome Genotyping Identifies Pleiotropic Variants Associated with Red Blood Cell Traits. <i>American Journal of Human Genetics</i> , 2016, 99, 8-21.	6.2	60
33	A genome-wide association study meta-analysis of clinical fracture in 10,012 African American women. <i>Bone Reports</i> , 2016, 5, 233-242.	0.4	20
34	Meta-analysis identifies common and rare variants influencing blood pressure and overlapping with metabolic trait loci. <i>Nature Genetics</i> , 2016, 48, 1162-1170.	21.4	223
35	Platelet-Related Variants Identified by Exomechip Meta-analysis in 157,293 Individuals. <i>American Journal of Human Genetics</i> , 2016, 99, 40-55.	6.2	82
36	Large-Scale Exome-wide Association Analysis Identifies Loci for White Blood Cell Traits and Pleiotropy with Immune-Mediated Diseases. <i>American Journal of Human Genetics</i> , 2016, 99, 22-39.	6.2	50

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37	Genetic Determinants of Pelvic Organ Prolapse among African American and Hispanic Women in the Women's Health Initiative. PLoS ONE, 2015, 10, e0141647.	2.5	17
38	Genetic Determinants of Metabolism and Benign Prostate Enlargement: Associations with Prostate Volume. PLoS ONE, 2015, 10, e0132028.	2.5	13
39	Genetic epidemiology of pelvic organ prolapse: a systematic review. American Journal of Obstetrics and Gynecology, 2014, 211, 326-335.	1.3	62
40	Subclinical Hypothyroidism and Risk for Incident Ischemic Stroke Among Postmenopausal Women. Thyroid, 2014, 24, 1210-1217.	4.5	14