

# Andrea Ganna

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6294168/publications.pdf>

Version: 2024-02-01

64  
papers

13,342  
citations

109321

35  
h-index

106344

65  
g-index

85  
all docs

85  
docs citations

85  
times ranked

29750  
citing authors

#	ARTICLE	IF	CITATIONS
1	Effect of General Adiposity and Central Body Fat Distribution on the Circulating Metabolome: A Multicohort Nontargeted Metabolomics Observational and Mendelian Randomization Study. <i>Diabetes</i> , 2022, 71, 329-339.	0.6	14
2	Fast estimation of genetic correlation for biobank-scale data. <i>American Journal of Human Genetics</i> , 2022, 109, 24-32.	6.2	11
3	Mendelian randomization of genetically independent aging phenotypes identifies LPA and VCAM1 as biological targets for human aging. <i>Nature Aging</i> , 2022, 2, 19-30.	11.6	17
4	Multi-ancestry fine mapping implicates OAS1 splicing in risk of severe COVID-19. <i>Nature Genetics</i> , 2022, 54, 125-127.	21.4	75
5	Rare coding variants in ten genes confer substantial risk for schizophrenia. <i>Nature</i> , 2022, 604, 509-516.	27.8	326
6	Genome-wide risk prediction of common diseases across ancestries in one million people. <i>Cell Genomics</i> , 2022, 2, 100118.	6.5	34
7	The human genetic epidemiology of COVID-19. <i>Nature Reviews Genetics</i> , 2022, 23, 533-546.	16.3	64
8	Novel genes and sex differences in COVID-19 severity. <i>Human Molecular Genetics</i> , 2022, 31, 3789-3806.	2.9	38
9	The 22q11.2 region regulates presynaptic gene-products linked to schizophrenia. <i>Nature Communications</i> , 2022, 13, .	12.8	22
10	Detailed stratified GWAS analysis for severe COVID-19 in four European populations. <i>Human Molecular Genetics</i> , 2022, 31, 3945-3966.	2.9	46
11	Sex-dimorphic genetic effects and novel loci for fasting glucose and insulin variability. <i>Nature Communications</i> , 2021, 12, 24.	12.8	87
12	Response to Comment on "Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior". <i>Science</i> , 2021, 371, .	12.6	5
13	Genetic analyses identify widespread sex-differential participation bias. <i>Nature Genetics</i> , 2021, 53, 663-671.	21.4	124
14	COVID-19 tissue atlases reveal SARS-CoV-2 pathology and cellular targets. <i>Nature</i> , 2021, 595, 107-113.	27.8	537
15	Hematopoietic mosaic chromosomal alterations increase the risk for diverse types of infection. <i>Nature Medicine</i> , 2021, 27, 1012-1024.	30.7	109
16	Mapping the human genetic architecture of COVID-19. <i>Nature</i> , 2021, 600, 472-477.	27.8	640
17	Clinical Conditions and Their Impact on Utility of Genetic Scores for Prediction of Acute Coronary Syndrome. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003283.	3.6	4
18	Using symptom-based case predictions to identify host genetic factors that contribute to COVID-19 susceptibility. <i>PLoS ONE</i> , 2021, 16, e0255402.	2.5	6

#	ARTICLE	IF	CITATIONS
19	Addendum: The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2021, 597, E3-E4.	27.8	45
20	Age-dependent impact of the major common genetic risk factor for COVID-19 on severity and mortality. <i>Journal of Clinical Investigation</i> , 2021, 131, .	8.2	72
21	Polygenic risk score for general cognitive function is associated with measures of cognition in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e053977.	0.8	0
22	Common and rare variants in topologically associated domains for cognitive function in South Asians from the LASI-DAD Study.. <i>Alzheimer's and Dementia</i> , 2021, 17 Suppl 3, e054029.	0.8	0
23	A Multi-Cohort Metabolomics Analysis Discloses Sphingomyelin (32:1) Levels to be Inversely Related to Incident Ischemic Stroke. <i>Journal of Stroke and Cerebrovascular Diseases</i> , 2020, 29, 104476.	1.6	14
24	Non-targeted urine metabolomics and associations with prevalent and incident type 2 diabetes. <i>Scientific Reports</i> , 2020, 10, 16474.	3.3	11
25	Development and validation of risk prediction models for multiple cardiovascular diseases and Type 2 diabetes. <i>PLoS ONE</i> , 2020, 15, e0235758.	2.5	13
26	Association Between Episodic Memory and Genetic Risk Factors for Alzheimer's Disease in South Asians from the Longitudinal Aging Study in Indiaâ€œDiagnostic Assessment of Dementia (LASIâ€œDAD). <i>Journal of the American Geriatrics Society</i> , 2020, 68, S45-S53.	2.6	10
27	Common and rare variants in Alzheimerâ€™s disease genes are associated with episodic memory in South Asians from the LASIâ€œDAD study. <i>Alzheimer's and Dementia</i> , 2020, 16, e045189.	0.8	0
28	Proteomic profiles before and during weight loss: Results from randomized trial of dietary intervention. <i>Scientific Reports</i> , 2020, 10, 7913.	3.3	22
29	The mutational constraint spectrum quantified from variation in 141,456 humans. <i>Nature</i> , 2020, 581, 434-443.	27.8	6,140
30	Discriminating bipolar depression from major depressive disorder with polygenic risk scores. <i>Psychological Medicine</i> , 2020, 51, 1-8.	4.5	12
31	The plasma protein profile and cardiovascular risk differ between intima-media thickness of the common carotid artery and the bulb: A meta-analysis and a longitudinal evaluation. <i>Atherosclerosis</i> , 2020, 295, 25-30.	0.8	18
32	Large-scale GWAS reveals insights into the genetic architecture of same-sex sexual behavior. <i>Science</i> , 2019, 365, .	12.6	245
33	The metabolites urobilin and sphingomyelin (30:1) are associated with incident heart failure in the general population. <i>ESC Heart Failure</i> , 2019, 6, 764-773.	3.1	23
34	Polygenic adaptation on height is overestimated due to uncorrected stratification in genome-wide association studies. <i>ELife</i> , 2019, 8, .	6.0	276
35	Genome studies must account for historyâ€™Response. <i>Science</i> , 2019, 366, 1461-1462.	12.6	4
36	Identification of metabolic profiles associated with human exposure to perfluoroalkyl substances. <i>Journal of Exposure Science and Environmental Epidemiology</i> , 2019, 29, 196-205.	3.9	55

#	ARTICLE	IF	CITATIONS
37	Exploring Comorbidity Within Mental Disorders Among a Danish National Population. <i>JAMA Psychiatry</i> , 2019, 76, 259.	11.0	374
38	Functional architecture of low-frequency variants highlights strength of negative selection across coding and non-coding annotations. <i>Nature Genetics</i> , 2018, 50, 1600-1607.	21.4	132
39	Genetic predictors of testosterone and their associations with cardiovascular disease and risk factors: A Mendelian randomization investigation. <i>International Journal of Cardiology</i> , 2018, 267, 171-176.	1.7	49
40	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.	6.2	102
41	Deep coverage whole genome sequences and plasma lipoprotein(a) in individuals of European and African ancestries. <i>Nature Communications</i> , 2018, 9, 2606.	12.8	79
42	Glucose challenge metabolomics implicates medium-chain acylcarnitines in insulin resistance. <i>Scientific Reports</i> , 2018, 8, 8691.	3.3	47
43	Insights into the genetic epidemiology of Crohn's and rare diseases in the Ashkenazi Jewish population. <i>PLoS Genetics</i> , 2018, 14, e1007329.	3.5	66
44	Loss of Cardioprotective Effects at the <i>ADAMTS7</i> Locus as a Result of Gene-Smoking Interactions. <i>Circulation</i> , 2017, 135, 2336-2353.	1.6	51
45	The impact of rare variation on gene expression across tissues. <i>Nature</i> , 2017, 550, 239-243.	27.8	229
46	Heterogeneous contribution of microdeletions in the development of common generalised and focal epilepsies. <i>Journal of Medical Genetics</i> , 2017, 54, 598-606.	3.2	22
47	Nonparametric estimation of the rediscovery rate. <i>Statistics in Medicine</i> , 2016, 35, 3203-3212.	1.6	2
48	Effects of cigarette smoking on cardiovascular-related protein profiles in two community-based cohort studies. <i>Atherosclerosis</i> , 2016, 254, 52-58.	0.8	18
49	Ultra-rare disruptive and damaging mutations influence educational attainment in the general population. <i>Nature Neuroscience</i> , 2016, 19, 1563-1565.	14.8	90
50	Prediction impact curve is a new measure integrating intervention effects in the evaluation of risk models. <i>Journal of Clinical Epidemiology</i> , 2016, 69, 89-95.	5.0	8
51	The metabolic fingerprint of p,p'-DDE and HCB exposure in humans. <i>Environment International</i> , 2016, 88, 60-66.	10.0	61
52	Large-scale non-targeted metabolomic profiling in three human population-based studies. <i>Metabolomics</i> , 2016, 12, 1.	3.0	29
53	Effect of Insulin Resistance on Monounsaturated Fatty Acid Levels: A Multi-cohort Non-targeted Metabolomics and Mendelian Randomization Study. <i>PLoS Genetics</i> , 2016, 12, e1006379.	3.5	20
54	5 year mortality predictors in 498,103 UK Biobank participants: a prospective population-based study. <i>Lancet</i> , The, 2015, 386, 533-540.	13.7	319

#	ARTICLE	IF	CITATIONS
55	Gene Å— dietary pattern interactions in obesity: analysis of up to 68 317 adults of European ancestry. <i>Human Molecular Genetics</i> , 2015, 24, 4728-4738.	2.9	84
56	Gene-based meta-analysis of genome-wide association studies implicates new loci involved in obesity. <i>Human Molecular Genetics</i> , 2015, 24, 6849-6860.	2.9	55
57	Genome-wide meta-analysis identifies six novel loci associated with habitual coffee consumption. <i>Molecular Psychiatry</i> , 2015, 20, 647-656.	7.9	235
58	Large-scale Metabolomic Profiling Identifies Novel Biomarkers for Incident Coronary Heart Disease. <i>PLoS Genetics</i> , 2014, 10, e1004801.	3.5	225
59	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
60	Genetic determinants of mortality. Can findings from genome-wide association studies explain variation in human mortality?. <i>Human Genetics</i> , 2013, 132, 553-561.	3.8	29
61	Sex-stratified Genome-wide Association Studies Including 270,000 Individuals Show Sexual Dimorphism in Genetic Loci for Anthropometric Traits. <i>PLoS Genetics</i> , 2013, 9, e1003500.	3.5	371
62	Multilocus Genetic Risk Scores for Coronary Heart Disease Prediction. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2013, 33, 2267-2272.	2.4	138
63	Utilizing Twins as Controls for Non-Twin Case-Materials in Genome Wide Association Studies. <i>PLoS ONE</i> , 2013, 8, e83101.	2.5	6
64	Risk Prediction Measures for Case-Cohort and Nested Case-Control Designs: An Application to Cardiovascular Disease. <i>American Journal of Epidemiology</i> , 2012, 175, 715-724.	3.4	75