

# Eleonora Porcu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8559514/publications.pdf>

Version: 2024-02-01

17  
papers

4,671  
citations

687363

13  
h-index

888059

17  
g-index

25  
all docs

25  
docs citations

25  
times ranked

12476  
citing authors

#	ARTICLE	IF	CITATIONS
1	The individual and global impact of copy-number variants on complex human traits. <i>American Journal of Human Genetics</i> , 2022, 109, 647-668.	6.2	31
2	Possible association of 16p11.2 copy number variation with altered lymphocyte and neutrophil counts. <i>Npj Genomic Medicine</i> , 2022, 7, .	3.8	3
3	Causal Inference Methods to Integrate Omics and Complex Traits. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2021, 11, a040493.	6.2	9
4	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. <i>Scientific Reports</i> , 2021, 11, 3100.	3.3	15
5	Triangulating evidence from longitudinal and Mendelian randomization studies of metabolomic biomarkers for type 2 diabetes. <i>Scientific Reports</i> , 2021, 11, 6197.	3.3	18
6	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. <i>Nature Genetics</i> , 2021, 53, 1300-1310.	21.4	590
7	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , 2021, 12, 5647.	12.8	61
8	Mendelian randomization integrating GWAS and eQTL data reveals genetic determinants of complex and clinical traits. <i>Nature Communications</i> , 2019, 10, 3300.	12.8	193
9	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. <i>Nature Communications</i> , 2017, 8, 744.	12.8	64
10	Bayesian association scan reveals loci associated with human lifespan and linked biomarkers. <i>Nature Communications</i> , 2017, 8, 15842.	12.8	64
11	Whole-genome sequence-based analysis of thyroid function. <i>Nature Communications</i> , 2015, 6, 5681.	12.8	75
12	Rare coding variants and X-linked loci associated with age at menarche. <i>Nature Communications</i> , 2015, 6, 7756.	12.8	32
13	Rare variant genotype imputation with thousands of study-specific whole-genome sequences: implications for cost-effective study designs. <i>European Journal of Human Genetics</i> , 2015, 23, 975-983.	2.8	92
14	Parent-of-origin-specific allelic associations among 106 genomic loci for age at menarche. <i>Nature</i> , 2014, 514, 92-97.	27.8	548
15	Defining the role of common variation in the genomic and biological architecture of adult human height. <i>Nature Genetics</i> , 2014, 46, 1173-1186.	21.4	1,818
16	Seventy-five genetic loci influencing the human red blood cell. <i>Nature</i> , 2012, 492, 369-375.	27.8	320
17	New gene functions in megakaryopoiesis and platelet formation. <i>Nature</i> , 2011, 480, 201-208.	27.8	401