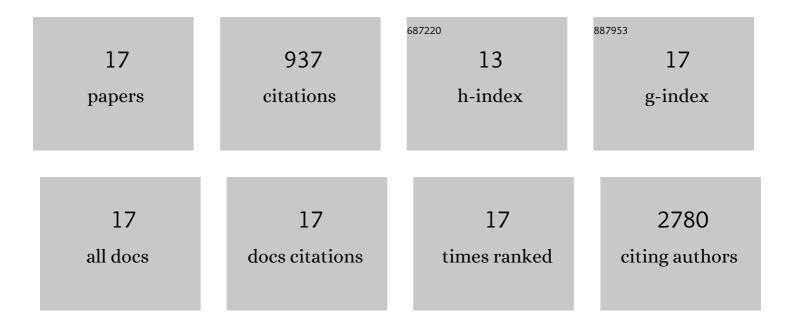
Daniele Braga

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/8219306/publications.pdf Version: 2024-02-01



DANIELE REACA

#	Article	IF	CITATIONS
1	Gut vascular barrier impairment leads to intestinal bacteria dissemination and colorectal cancer metastasis to liver. Cancer Cell, 2021, 39, 708-724.e11.	7.7	175
2	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	5.8	169
3	Genomewide Association Study Using a High-Density Single Nucleotide Polymorphism Array and Case-Control Design Identifies a Novel Essential Hypertension Susceptibility Locus in the Promoter Region of Endothelial NO Synthase. Hypertension, 2012, 59, 248-255.	1.3	144
4	Identification of a choroid plexus vascular barrier closing during intestinal inflammation. Science, 2021, 374, 439-448.	6.0	115
5	Self-renewal and phenotypic conversion are the main physiological responses of macrophages to the endogenous estrogen surge. Scientific Reports, 2017, 7, 44270.	1.6	58
6	Target Sequencing, Cell Experiments, and a Population Study Establish Endothelial Nitric Oxide Synthase (<i>eNOS</i>) Gene as Hypertension Susceptibility Gene. Hypertension, 2013, 62, 844-852.	1.3	48
7	Analysis of immune, microbiota and metabolome maturation in infants in a clinical trial of Lactobacillus paracasei CBAÂL74-fermented formula. Nature Communications, 2020, 11, 2703.	5.8	45
8	Interaction between polyphenols intake and PON1 gene variants on markers of cardiovascular disease: a nutrigenetic observational study. Journal of Translational Medicine, 2016, 14, 186.	1.8	38
9	TET2 and CSMD1 genes affect SBP response to hydrochlorothiazide in never-treated essential hypertensives. Journal of Hypertension, 2015, 33, 1301-1309.	0.3	29
10	Genome-wide association study identifies CAMKID variants involved in blood pressure response to losartan: the SOPHIA study. Pharmacogenomics, 2014, 15, 1643-1652.	0.6	27
11	Exome sequencing identifies variants in two genes encoding the LIM-proteins NRAP and FHL1 in an Italian patient with BAG3 myofibrillar myopathy. Journal of Muscle Research and Cell Motility, 2016, 37, 101-115.	0.9	23
12	A longitudinal study highlights shared aspects of the transcriptomic response to cardiogenic and septic shock. Critical Care, 2019, 23, 414.	2.5	20
13	Transcriptome Analysis of iPSC-Derived Neurons from Rubinstein-Taybi Patients Reveals Deficits in Neuronal Differentiation. Molecular Neurobiology, 2020, 57, 3685-3701.	1.9	15
14	Identification of a transcriptome profile associated with improvement of organ function in septic shock patients after early supportive therapy. Critical Care, 2018, 22, 312.	2.5	14
15	The burden of multiple sclerosis variants in continental Italians and Sardinians. Multiple Sclerosis Journal, 2015, 21, 1385-1395.	1.4	10
16	Left ventricular diastolic function associated with common genetic variation in ATP12Ain a general population. BMC Medical Genetics, 2014, 15, 121.	2.1	4
17	Application of an Exploratory Knowledge-Discovery Pipeline Based on Machine Learning to Multi-Scale OMICS Data to Characterise Myocardial Injury in a Cohort of Patients with Septic Shock: An Observational Study. Journal of Clinical Medicine, 2021, 10, 4354.	1.0	3