Brunilda Balliu

List of Publications by Year
in descending order

26 papers	1,777 citations	687363 13 h-index	610901 24 g-index
32 all docs	32 docs citations	32 times ranked	4021 citing authors

#	Article	IF	Citations
1	Evaluating supervised and unsupervised background noise correction in human gut microbiome data. PLoS Computational Biology, 2022, 18, e1009838.	3.2	6
2	Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes. Genome Medicine, 2022, 14, 31.	8.2	7
3	Single-cell RNA-seq reveals cell typeâ€“specific molecular and genetic associations to lupus. Science, 2022, 376, eabf1970.	12.6	156
4	Association of imageâ€defined risk factors with clinical features, histopathology, and outcomes in neuroblastoma. Cancer Medicine, 2021, 10, 2232-2241.	2.8	24
5	Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors. IScience, 2021, 24, 102188.	4.1	13
6	Technology dictates algorithms: recent developments in read alignment. Genome Biology, 2021, 22, 249.	8.8	51
7	An integrated approach to identify environmental modulators of genetic risk factors for complex traits. American Journal of Human Genetics, 2021, 108, 1866-1879.	6.2	9
8	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. PLoS ONE, 2020, 15, e0239474.	2.5	53
9	The impact of sex on gene expression across human tissues. Science, 2020, 369, .	12.6	329
10	A vast resource of allelic expression data spanning human tissues. Genome Biology, 2020, 21, 234.	8.8	68
11	Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. Cell, 2020, 181, 1464-1474.	28.9	147
12	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
13	A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.		0
14	Genetic regulation of gene expression and splicing during a 10-year period of human aging. Genome Biology, 2019, 20, 230.	8.8	57
15	Powerful testing via hierarchical linkage disequilibrium in haplotype association studies. Biometrical Journal, 2019, 61, 747-768.	1.0	7
16	Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. Communications Biology, 2019, 2, 186.	4.4	20
17	Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. Nature Medicine, 2019, 25, 911-919.	30.7	221
18	Distinctive facial features in idiopathic Moyamoya disease in Caucasians: a first systematic analysis. PeerJ, 2018, 6, e4740.	2.0	8

#	Article	IF	Citations
19	Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. Nature Genetics, 2017, 49, 1752-1757.	21.4	432
20	Impact of the X Chromosome and sex on regulatory variation. Genome Research, 2016, 26, 768-777.	5.5	88
21	Gene coexpression network analysis for family studies based on a meta-analytic approach. BMC Proceedings, 2016, 10, 119-123.	1.6	1
22	A Novel Test for Detecting SNPâ€“SNP Interactions in Case-Only Trio Studies. Genetics, 2016, 202, 1289-1297.	2.9	10
23	A Retrospective Likelihood Approach for Efficient Integration of Multiple Omics Factors in Caseâ€Control Association Studies. Genetic Epidemiology, 2015, 39, 156-165.	1.3	9
24	Classification and Visualization Based on Derived Image Features: Application to Genetic Syndromes. PLoS ONE, 2014, 9, e109033.	2.5	9
25	CHEK2*1100delC homozygosity in the Netherlandsâ€”prevalence and risk of breast and lung cancer. European Journal of Human Genetics, 2014, 22, 46-51.	2.8	29
26	Combining Family and Twin Data in Association Studies to Estimate the Noninherited Maternal Antigens Effect. Genetic Epidemiology, 2012, 36, 811-819.	1.3	2