

# Brunilda Balliu

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1894380/publications.pdf>

Version: 2024-02-01

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  | Shared genetic origin of asthma, hay fever and eczema elucidates allergic disease biology. <i>Nature Genetics</i> , 2017, 49, 1752-1757.                                      | 21.4 | 432       |
| 2  | The impact of sex on gene expression across human tissues. <i>Science</i> , 2020, 369, .  | 12.6 | 329       |
| 3  | Identification of rare-disease genes using blood transcriptome sequencing and large control cohorts. <i>Nature Medicine</i> , 2019, 25, 911-919.                              | 30.7 | 221       |
| 4  | Single-cell RNA-seq reveals cell type-specific molecular and genetic associations to lupus. <i>Science</i> , 2022, 376, eabf1970.   | 12.6 | 156       |
| 5  | Molecular Transducers of Physical Activity Consortium (MoTrPAC): Mapping the Dynamic Responses to Exercise. <i>Cell</i> , 2020, 181, 1464-1474.                               | 28.9 | 147       |
| 6  | Impact of the X Chromosome and sex on regulatory variation. <i>Genome Research</i> , 2016, 26, 768-777.   | 5.5  | 88        |
| 7  | A vast resource of allelic expression data spanning human tissues. <i>Genome Biology</i> , 2020, 21, 234.   | 8.8  | 68        |
| 8  | Genetic regulation of gene expression and splicing during a 10-year period of human aging. <i>Genome Biology</i> , 2019, 20, 230.   | 8.8  | 57        |
| 9  | A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. <i>PLoS ONE</i> , 2020, 15, e0239474.  | 2.5  | 53        |
| 10 | Technology dictates algorithms: recent developments in read alignment. <i>Genome Biology</i> , 2021, 22, 249.   | 8.8  | 51        |
| 11 | CHEK2*1100delC homozygosity in the Netherlands prevalence and risk of breast and lung cancer. <i>European Journal of Human Genetics</i> , 2014, 22, 46-51.                    | 2.8  | 29        |
| 12 | Association of image-defined risk factors with clinical features, histopathology, and outcomes in neuroblastoma. <i>Cancer Medicine</i> , 2021, 10, 2232-2241.                | 2.8  | 24        |
| 13 | Genetic analyses of human fetal retinal pigment epithelium gene expression suggest ocular disease mechanisms. <i>Communications Biology</i> , 2019, 2, 186.                   | 4.4  | 20        |
| 14 | Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors. <i>IScience</i> , 2021, 24, 102188.  | 4.1  | 13        |
| 15 | A Novel Test for Detecting SNP-SNP Interactions in Case-Only Trio Studies. <i>Genetics</i> , 2016, 202, 1289-1297.  | 2.9  | 10        |
| 16 | Classification and Visualization Based on Derived Image Features: Application to Genetic Syndromes. <i>PLoS ONE</i> , 2014, 9, e109033.                                       | 2.5  | 9         |
| 17 | A Retrospective Likelihood Approach for Efficient Integration of Multiple Omics Factors in Case-Control Association Studies. <i>Genetic Epidemiology</i> , 2015, 39, 156-165. | 1.3  | 9         |
| 18 | An integrated approach to identify environmental modulators of genetic risk factors for complex traits. <i>American Journal of Human Genetics</i> , 2021, 108, 1866-1879.     | 6.2  | 9         |

| #  | ARTICLE  | IF  | CITATIONS |
|----|--|-----|-----------|
| 19 | Distinctive facial features in idiopathic Moyamoya disease in Caucasians: a first systematic analysis. PeerJ, 2018, 6, e4740.  | 2.0 | 8         |
| 20 | Powerful testing via hierarchical linkage disequilibrium in haplotype association studies. Biometrical Journal, 2019, 61, 747-768.                                   | 1.0 | 7         |
| 21 | Integration of genetic colocalizations with physiological and pharmacological perturbations identifies cardiometabolic disease genes. Genome Medicine, 2022, 14, 31. | 8.2 | 7         |
| 22 | Evaluating supervised and unsupervised background noise correction in human gut microbiome data. PLoS Computational Biology, 2022, 18, e1009838.                     | 3.2 | 6         |
| 23 | Combining Family and Twin Data in Association Studies to Estimate the Noninherited Maternal Antigens Effect. Genetic Epidemiology, 2012, 36, 811-819.                | 1.3 | 2         |
| 24 | Gene coexpression network analysis for family studies based on a meta-analytic approach. BMC Proceedings, 2016, 10, 119-123.   | 1.6 | 1         |
| 25 | A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.   |     | 0         |
| 26 | A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity. , 2020, 15, e0239474.   |     | 0         |