# Paola Benaglio

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/11922255/publications.pdf

Version: 2024-02-01

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|---|---|---|---|
| 20 papers | 1,848 citations | 516710 16 h-index | 713466 21 g-index |
| 27 all docs | 27 docs citations | 27 times ranked | 5794 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378. | 3.5 | 331 |
| 2 | Identification of heart rateâ€“associated loci and their effects on cardiac conduction and rhythm disorders. Nature Genetics, 2013, 45, 621-631. | 21.4 | 282 |
| 3 | Interpreting type 1 diabetes risk with genetics and single-cell epigenomics. Nature, 2021, 594, 398-402. | 27.8 | 170 |
| 4 | Large-Scale Profiling Reveals the Influence of Genetic Variation on Gene Expression in Human Induced Pluripotent Stem Cells. Cell Stem Cell, 2017, 20, 533-546.e7. | 11.1 | 157 |
| 5 | iPSCORE: A Resource of 222 iPSC Lines Enabling Functional Characterization of Genetic Variation across a Variety of Cell Types. Stem Cell Reports, 2017, 8, 1086-1100. | 4.8 | 147 |
| 6 | 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. | 2.7 | 144 |
| 7 | Subtle changes in chromatin loop contact propensity are associated with differential gene regulation and expression. Nature Communications, 2019, 10, 1054. | 12.8 | 100 |
| 8 | Systematic analysis of binding of transcription factors to noncoding variants. Nature, 2021, 591, 147-151. | 27.8 | 89 |
| 9 | Insights into the Mutational Burden of Human Induced Pluripotent Stem Cells from an Integrative Multi-Omics Approach. Cell Reports, 2018, 24, 883-894. | 6.4 | 85 |
| 10 | Comparative genome analysis of <scp>P</scp>seudomonas knackmussiiâ€...<scp>B</scp>13, the first bacterium known to degrade chloroaromatic compounds. Environmental Microbiology, 2015, 17, 91-104. | 3.8 | 52 |
| 11 | Target Sequencing, Cell Experiments, and a Population Study Establish Endothelial Nitric Oxide Synthase ( eNOS ) Gene as Hypertension Susceptibility Gene. Hypertension, 2013, 62, 844-852. | 2.7 | 48 |
| 12 | Next generation sequencing of pooled samples reveals new SNRNP200 mutations associated with retinitis pigmentosa. Human Mutation, 2011, 32, E2246-E2258. | 2.5 | 42 |
| 13 | Pgltools: a genomic arithmetic tool suite for manipulation of Hi-C peak and other chromatin interaction data. BMC Bioinformatics, 2017, 18, 207. | 2.6 | 35 |
| 14 | Allele-specific NKX2-5 binding underlies multiple genetic associations with human electrocardiographic traits. Nature Genetics, 2019, 51, 1506-1517. | 21.4 | 35 |
| 15 | Sequencing and characterizing the genome of Estrella lausannensis as an undergraduate project: training students and biological insights. Frontiers in Microbiology, 2015, 6, 101. | 3.5 | 32 |
| 16 | Human iPSC-Derived Retinal Pigment Epithelium: A Model System for Prioritizing and Functionally Characterizing Causal Variants at AMD Risk Loci. Stem Cell Reports, 2019, 12, 1342-1353. | 4.8 | 32 |
| 17 | Glucocorticoid signaling in pancreatic islets modulates gene regulatory programs and genetic risk of type 2 diabetes. PLoS Genetics, 2021, 17, e1009531. | 3.5 | 13 |
| 18 | Ultra High Throughput Sequencing in Human DNA Variation Detection: A Comparative Study on the NDUFA3-PRPF31 Region. PLoS ONE, 2010, 5, e13071. | 2.5 | 11 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | Mutational screening of splicing factor genes in cases with autosomal dominant retinitis pigmentosa. Molecular Vision, 2014, 20, 843-51. | 1.1 | 11 |
| 20 | FOXO1 mitigates the SMAD3/FOXL2C134W transcriptomic effect in a model of human adult granulosa cell tumor. Journal of Translational Medicine, 2021, 19, 90. | 4.4 | 5 |