

# Maria Caracausi

## List of Publications by Year in descending order

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Version: 2024-02-01

31  
papers

1,061  
citations

471371

17  
h-index

454834

30  
g-index

33  
all docs

33  
docs citations

33  
times ranked

1152  
citing authors

#	ARTICLE	IF	CITATIONS
1	Cognitive profiles in children and adolescents with Down syndrome. <i>Scientific Reports</i> , 2022, 12, 1936.	1.6	21
2	A reassessment of Jackson's checklist and identification of two Down syndrome sub-phenotypes. <i>Scientific Reports</i> , 2022, 12, 3104.	1.6	3
3	One-carbon pathway and cognitive skills in children with Down syndrome. <i>Scientific Reports</i> , 2021, 11, 4225.	1.6	15
4	Is the Age of Developmental Milestones a Predictor for Future Development in Down Syndrome?. <i>Brain Sciences</i> , 2021, 11, 655.	1.1	14
5	The transcriptome profile of human trisomy 21 blood cells. <i>Human Genomics</i> , 2021, 15, 25.	1.4	13
6	Structural Characterization of the Highly Restricted Down Syndrome Critical Region on 21q22.13: New KCNJ6 and DSCR4 Transcript Isoforms. <i>Frontiers in Genetics</i> , 2021, 12, 770359.	1.1	8
7	Plasma metabolome and cognitive skills in Down syndrome. <i>Scientific Reports</i> , 2020, 10, 10491.	1.6	23
8	Genetics and genomics of Down syndrome. <i>International Review of Research in Developmental Disabilities</i> , 2019, , 1-39.	0.6	6
9	Reference quantitative transcriptome dataset for adult <i>Caenorhabditis elegans</i> . <i>Data in Brief</i> , 2019, 25, 104152.	0.5	1
10	Human trisomy 21 fibroblasts rescue methotrexate toxic effect after treatment with 5-methyltetrahydrofolate and 5-formyltetrahydrofolate. <i>Journal of Cellular Physiology</i> , 2019, 234, 15010-15024.	2.0	12
11	Partial trisomy 21 map: Ten cases further supporting the highly restricted Down syndrome critical region (HR-DSCR) on human chromosome 21. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e797.	0.6	28
12	Human protein-coding genes and gene feature statistics in 2019. <i>BMC Research Notes</i> , 2019, 12, 315.	0.6	106
13	Dataset of differential gene expression between total normal human thyroid and histologically normal thyroid adjacent to papillary thyroid carcinoma. <i>Data in Brief</i> , 2019, 24, 103835.	0.5	2
14	Analysis of a nanoparticle-enriched fraction of plasma reveals miRNA candidates for Down syndrome pathogenesis. <i>International Journal of Molecular Medicine</i> , 2019, 43, 2303-2318.	1.8	16
15	On the length, weight and GC content of the human genome. <i>BMC Research Notes</i> , 2019, 12, 106.	0.6	125
16	MTHFR C677T polymorphism analysis: A simple, effective restriction enzyme-based method improving previous protocols. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2019, 7, e628.	0.6	14
17	Plasma and urinary metabolomic profiles of Down syndrome correlate with alteration of mitochondrial metabolism. <i>Scientific Reports</i> , 2018, 8, 2977.	1.6	80
18	Integrated Quantitative Transcriptome Maps of Human Trisomy 21 Tissues and Cells. <i>Frontiers in Genetics</i> , 2018, 9, 125.	1.1	38

#	ARTICLE	IF	CITATIONS
19	Systematic identification of human housekeeping genes possibly useful as references in gene expression studies. <i>Molecular Medicine Reports</i> , 2017, 16, 2397-2410.	1.1	71
20	Genotype-phenotype correlation for congenital heart disease in Down syndrome through analysis of partial trisomy 21 cases. <i>Genomics</i> , 2017, 109, 391-400.	1.3	27
21	Integrated Transcriptome Map Highlights Structural and Functional Aspects of the Normal Human Heart. <i>Journal of Cellular Physiology</i> , 2017, 232, 759-770.	2.0	28
22	A molecular view of the normal human thyroid structure and function reconstructed from its reference transcriptome map. <i>BMC Genomics</i> , 2017, 18, 739.	1.2	27
23	Difficulty in obtaining the complete mRNA coding sequence at 5' end region (5' end mRNA artifact): Causes, consequences in biology and medicine and possible solutions for obtaining the actual amino acid sequence of proteins (Review). <i>International Journal of Molecular Medicine</i> , 2017, 39, 1063-1071.	1.8	18
24	GeneBase 1.1: a tool to summarize data from NCBI gene datasets and its application to an update of human gene statistics. <i>Database: the Journal of Biological Databases and Curation</i> , 2016, 2016, baw153.	1.4	105
25	Systematic reanalysis of partial trisomy 21 cases with or without Down syndrome suggests a small region on 21q22.13 as critical to the phenotype. <i>Human Molecular Genetics</i> , 2016, 25, ddw116.	1.4	74
26	A quantitative transcriptome reference map of the normal human hippocampus. <i>Hippocampus</i> , 2016, 26, 13-26.	0.9	28
27	Identification of minimal eukaryotic introns through GeneBase, a user-friendly tool for parsing the NCBI Gene databank. <i>DNA Research</i> , 2015, 22, 495-503.	1.5	60
28	Integrated differential transcriptome maps of Acute Megakaryoblastic Leukemia (AMKL) in children with or without Down Syndrome (DS). <i>BMC Medical Genomics</i> , 2014, 7, 63.	0.7	37
29	Improving mRNA 5' coding sequence determination in the mouse genome. <i>Mammalian Genome</i> , 2014, 25, 149-159.	1.0	4
30	A quantitative transcriptome reference map of the normal human brain. <i>Neurogenetics</i> , 2014, 15, 267-287.	0.7	33
31	An integrated route to identifying new pathogenesis-based therapeutic approaches for trisomy 21 (Down Syndrome) following the thought of Jérôme Lejeune. <i>Science Postprint</i> , 2013, 1, .	0.3	20