Allison Piovesan

List of Publications by Year
in descending order

36 papers	1,963 citations	448610 19 h-index	355658 38 g-index
39 all docs	39 docs citations	39 times ranked	3116 citing authors

#	Article	IF	Citations
1	A reassessment of Jacksonâ€™s checklist and identification of two Down syndrome sub-phenotypes. Scientific Reports, 2022, 12, 3104.	1.6	3
2	One-carbon pathway and cognitive skills in children with Down syndrome. Scientific Reports, 2021, 11, 4225.	1.6	15
3	Is the Age of Developmental Milestones a Predictor for Future Development in Down Syndrome?. Brain Sciences, 2021, 11, 655.	1.1	14
4	The transcriptome profile of human trisomy 21 blood cells. Human Genomics, 2021, 15, 25.	1.4	13
5	Structural Characterization of the Highly Restricted Down Syndrome Critical Region on 21q22.13: New KCNJ6 and DSCR4 Transcript Isoforms. Frontiers in Genetics, 2021, 12, 770359.	1.1	8
6	Plasma metabolome and cognitive skills in Down syndrome. Scientific Reports, 2020, 10, 10491.	1.6	23
7	Genetics and genomics of Down syndrome. International Review of Research in Developmental Disabilities, 2019, , 1-39.	0.6	6
8	Reference quantitative transcriptome dataset for adult Caenorhabditis elegans. Data in Brief, 2019, 25, 104152.	0.5	1
9	Human trisomy 21 fibroblasts rescue methotrexate toxic effect after treatment with 5â€methylâ€tetrahydrofolate and 5â€formylâ€tetrahydrofolate. Journal of Cellular Physiology, 2019, 234, 15010-15024.	2.0	12
10	Partial trisomy 21 map: Ten cases further supporting the highly restricted Down syndrome critical region (HRâ€ÐSCR) on human chromosome 21. Molecular Genetics & Genomic Medicine, 2019, 7, e797.	0.6	28
11	Human protein-coding genes and gene feature statistics in 2019. BMC Research Notes, 2019, 12, 315.	0.6	106
12	Dataset of differential gene expression between total normal human thyroid and histologically normal thyroid adjacent to papillary thyroid carcinoma. Data in Brief, 2019, 24, 103835.	0.5	2
13	Analysis of a nanoparticleâ€enriched fraction of plasma reveals miRNA candidates for Down syndrome pathogenesis. International Journal of Molecular Medicine, 2019, 43, 2303-2318.	1.8	16
14	On the length, weight and GC content of the human genome. BMC Research Notes, 2019, 12, 106.	0.6	125
15	MTHFR C677T polymorphism analysis: A simple, effective restriction enzymeâ€based method improving previous protocols. Molecular Genetics & Genomic Medicine, 2019, 7, e628.	0.6	14
16	Plasma and urinary metabolomic profiles of Down syndrome correlate with alteration of mitochondrial metabolism. Scientific Reports, 2018, 8, 2977.	1.6	80
17	Integrated Quantitative Transcriptome Maps of Human Trisomy 21 Tissues and Cells. Frontiers in Genetics, 2018, 9, 125.	1.1	38
18	Systematic identification of human housekeeping genes possibly useful as references in gene expression studies. Molecular Medicine Reports, 2017, 16, 2397-2410.	1.1	71

#	Article	IF	Citations
19	Genotype-phenotype correlation for congenital heart disease in Down syndrome through analysis of partial trisomy 21 cases. Genomics, 2017, 109, 391-400.	1.3	27
20	Integrated Transcriptome Map Highlights Structural and Functional Aspects of the Normal Human Heart. Journal of Cellular Physiology, 2017, 232, 759-770.	2.0	28
21	A molecular view of the normal human thyroid structure and function reconstructed from its reference transcriptome map. BMC Genomics, 2017, 18, 739.	1.2	27
22	Difficulty in obtaining the complete mRNA coding sequence at 5â€² region (5â€² end mRNA artifact): Causes, consequences in biology and medicine and possible solutions for obtaining the actual amino acid sequence of proteins (Review). International Journal of Molecular Medicine, 2017, 39, 1063-1071.	1.8	18
23	GeneBase 1.1: a tool to summarize data from NCBI gene datasets and its application to an update of human gene statistics. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw153.	1.4	105
24	Systematic reanalysis of partial trisomy 21 cases with or without Down syndrome suggests a small region on 21q22.13 as critical to the phenotype. Human Molecular Genetics, 2016, 25, ddw116.	1.4	74
25	A quantitative transcriptome reference map of the normal human hippocampus. Hippocampus, 2016, 26, 13-26.	0.9	28
26	Identification of minimal eukaryotic introns through GeneBase, a user-friendly tool for parsing the NCBI Gene databank. DNA Research, 2015, 22, 495-503.	1.5	60
27	Extensive microRNA-mediated crosstalk between lncRNAs and mRNAs in mouse embryonic stem cells. Genome Research, 2015, 25, 655-666.	2.4	95
28	Integrated differential transcriptome maps of Acute Megakaryoblastic Leukemia (AMKL) in children with or without Down Syndrome (DS). BMC Medical Genomics, 2014, 7, 63.	0.7	37
29	Improving mRNA 5â€² coding sequence determination in the mouse genome. Mammalian Genome, 2014, 25, 149-159.	1.0	4
30	A quantitative transcriptome reference map of the normal human brain. Neurogenetics, 2014, 15, 267-287.	0.7	33
31	Characterization of human gene locus CYYR1: a complex multi-transcript system. Molecular Biology Reports, 2014, 41, 6025-6038.	1.0	7
32	An estimation of the number of cells in the human body. Annals of Human Biology, 2013, 40, 463-471.	0.4	757
33	Universal tight correlation of codon bias and pool of RNA codons (codonome): The genome is optimized to allow any distribution of gene expression values in the transcriptome from bacteria to humans. Genomics, 2013, 101, 282-289.	1.3	34
34	An integrated route to identifying new pathogenesis-based therapeutic approaches for trisomy 21 (Down Syndrome) following the thought of JÃ©rÃ´me Lejeune. Science Postprint, 2013, 1, .	0.3	20
35	Genome-scale analysis of human mRNA 5â€² coding sequences based on expressed sequence tag (EST) database. Genomics, 2012, 100, 125-130.	1.3	11
36	Complexity of Bidirectional Transcription and Alternative Splicing at Human RCAN3 Locus. PLoS ONE, 2011, 6, e24508.	1.1	12