

Raffaella Casadei

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

31
papers

918
citations

12
h-index

30
g-index

33
ext. papers

1,183
ext. citations

3.9
avg, IF

3.21
L-index

#	Paper	IF	Citations
31	Cytochalasin B Modulates Nanomechanical Patterning and Fate in Human Adipose-Derived Stem Cells. <i>Cells</i> , 2022 , 11, 1629	7.9	3
30	The crucial role of non-enzymatic NO-production in plants. An EPR study. <i>Phytochemistry</i> , 2021 , 188, 112794	4	0
29	Nitric Oxide: The Key Molecule for Polyphenols Antimicrobial Action. <i>Journal of Biosciences and Medicines</i> , 2020 , 08, 153-165	0.2	
28	Herb-Derived Products: Natural Tools to Delay and Counteract Stem Cell Senescence. <i>Stem Cells International</i> , 2020 , 2020, 8827038	5	5
27	Sex-Specific Transcriptome Differences in Human Adipose Mesenchymal Stem Cells. <i>Genes</i> , 2020 , 11,	4.2	8
26	Discovery of the First-in-Class GSK-3 β /HDAC Dual Inhibitor as Disease-Modifying Agent To Combat Alzheimer's Disease. <i>ACS Medicinal Chemistry Letters</i> , 2019 , 10, 469-474	4.3	20
25	Sex-Specific Transcriptome Differences in Substantia Nigra Tissue: A Meta-Analysis of Parkinson's Disease Data. <i>Genes</i> , 2018 , 9,	4.2	10
24	Difficulty in obtaining the complete mRNA coding sequence at 5'UTR region (5'UTR 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	4.4	2
23	Meta-Analysis of Parkinson's Disease Transcriptome Data Using TRAM Software: Whole Substantia Nigra Tissue and Single Dopamine Neuron Differential Gene Expression. <i>PLoS ONE</i> , 2016 , 11, e0161567	3.7	32
22	Improving mRNA 5'UTR coding sequence determination in the mouse genome. <i>Mammalian Genome</i> , 2014 , 25, 149-59	3.2	4
21	Characterization of human gene locus CYR1: a complex multi-transcript system. <i>Molecular Biology Reports</i> , 2014 , 41, 6025-38	2.8	4
20	An estimation of the number of cells in the human body. <i>Annals of Human Biology</i> , 2013 , 40, 463-71	1.7	552
19	Genome-scale analysis of human mRNA 5'UTR coding sequences based on expressed sequence tag (EST) database. <i>Genomics</i> , 2012 , 100, 125-30	4.3	10
18	Complexity of bidirectional transcription and alternative splicing at human RCAN3 locus. <i>PLoS ONE</i> , 2011 , 6, e24508	3.7	8
17	Identification of housekeeping genes suitable for gene expression analysis in the zebrafish. <i>Gene Expression Patterns</i> , 2011 , 11, 271-6	1.5	54
16	TRAM (Transcriptome Mapper): database-driven creation and analysis of transcriptome maps from multiple sources. <i>BMC Genomics</i> , 2011 , 12, 121	4.5	30
15	Identification and analysis of human RCAN3 (DSCR1L2) mRNA and protein isoforms. <i>Gene</i> , 2008 , 407, 159-68	3.8	11

14	Systematic analysis of mRNA 5'coding sequence incompleteness in Danio rerio: an automated EST-based approach. <i>Biology Direct</i> , 2007 , 2, 34	7.2	4
13	Sequence, "subtle" alternative splicing and expression of the CYR1 (cysteine/tyrosine-rich 1) mRNA in human neuroendocrine tumors. <i>BMC Cancer</i> , 2007 , 7, 66	4.8	13
12	UniGene Tabulator: a full parser for the UniGene format. <i>Bioinformatics</i> , 2006 , 22, 2570-1	7.2	21
11	Proteins encoded by human Down syndrome critical region gene 1-like 2 (DSCR1L2) mRNA and by a novel DSCR1L2 mRNA isoform interact with cardiac troponin I (TNNI3). <i>Gene</i> , 2006 , 372, 128-36	3.8	12
10	Differential expression of alternatively spliced mRNA forms of the insulin-like growth factor 1 receptor in human neuroendocrine tumors. <i>Oncology Reports</i> , 2006 , 15, 1249	3.5	1
9	Differential expression of alternatively spliced mRNA forms of the insulin-like growth factor 1 receptor in human neuroendocrine tumors. <i>Oncology Reports</i> , 2006 , 15, 1249-56	3.5	12
8	Uncertainty principle of genetic information in a living cell. <i>Theoretical Biology and Medical Modelling</i> , 2005 , 2, 40	2.3	8
7	Sequence analysis of ADARB1 gene in patients with familial bipolar disorder. <i>Journal of Affective Disorders</i> , 2004 , 81, 79-85	6.6	6
6	Gene expression profile analysis in human T lymphocytes from patients with Down Syndrome. <i>Annals of Human Genetics</i> , 2004 , 68, 546-54	2.2	40
5	mRNA 5'region sequence incompleteness: a potential source of systematic errors in translation initiation codon assignment in human mRNAs. <i>Gene</i> , 2003 , 321, 185-93	3.8	16
4	Segmental paralogy in the human genome: a large-scale triplication on 1p, 6p, and 21q. <i>Mammalian Genome</i> , 2002 , 13, 456-62	3.2	13
3	Seven BMPs and all their receptors are simultaneously expressed in osteosarcoma cells 2002 , 20, 143		3
2	Sequence and expression analysis of the beta-2-microglobulin gene in dialysis patients. <i>Amyloid: the International Journal of Experimental and Clinical Investigation: the Official Journal of the International Society of Amyloidosis</i> , 2002 , 9, 212-5	2.7	
1	Cysteine and tyrosine-rich 1 (CYR1), a novel unpredicted gene on human chromosome 21 (21q21.2), encodes a cysteine and tyrosine-rich protein and defines a new family of highly conserved vertebrate-specific genes. <i>Gene</i> , 2002 , 290, 141-51	3.8	14