Stefano Cagnin

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	SPP1 genotype is a determinant of disease severity in Duchenne muscular dystrophy. Neurology, 2011, 76, 219-226.	1.5	194
2	The Mitochondrial Calcium Uniporter Controls Skeletal Muscle Trophism InÂVivo. Cell Reports, 2015, 10, 1269-1279.	2.9	170
3	Involvement of MicroRNAs in the Regulation of Muscle Wasting during Catabolic Conditions. Journal of Biological Chemistry, 2014, 289, 21909-21925.	1.6	129
4	Overview of Electrochemical DNA Biosensors: New Approaches to Detect the Expression of Life. Sensors, 2009, 9, 3122-3148.	2.1	119
5	Parallel protein and transcript profiles of FSHD patient muscles correlate to the D4Z4 arrangement and reveal a common impairment of slow to fast fibre differentiation and a general deregulation of MyoD-dependent genes. Proteomics, 2006, 6, 5303-5321.	1.3	105
6	Reconstruction and functional analysis of altered molecular pathways in human atherosclerotic arteries. BMC Genomics, 2009, 10, 13.	1.2	80
7	Decellularized Allogeneic Heart Valves Demonstrate Self-Regeneration Potential after a Long-Term Preclinical Evaluation. PLoS ONE, 2014, 9, e99593.	1.1	71
8	Single cell analysis reveals the involvement of the long non-coding RNA Pvt1 in the modulation of muscle atrophy and mitochondrial network. Nucleic Acids Research, 2019, 47, 1653-1670.	6.5	63
9	lncRNAs as Novel Indicators of Patients' Prognosis in Stage I Epithelial Ovarian Cancer: A Retrospective and Multicentric Study. Clinical Cancer Research, 2017, 23, 2356-2366.	3.2	57
10	Meta-analysis of expression signatures of muscle atrophy: gene interaction networks in early and late stages. BMC Genomics, 2008, 9, 630.	1.2	55
11	Transcriptomic Analysis of Single Isolated Myofibers Identifies miR-27a-3p and miR-142-3p as Regulators of Metabolism in Skeletal Muscle. Cell Reports, 2019, 26, 3784-3797.e8.	2.9	55
12	Helicobacter pylori Affects the Antigen Presentation Activity of Macrophages Modulating the Expression of the Immune Receptor CD300E through miR-4270. Frontiers in Immunology, 2017, 8, 1288.	2.2	45
13	A Single Cell but Many Different Transcripts: A Journey into the World of Long Non-Coding RNAs. International Journal of Molecular Sciences, 2020, 21, 302.	1.8	45
14	New miRNA labeling method for bead-based quantification. BMC Molecular Biology, 2010, 11, 44.	3.0	28
15	A fully electronic sensor for the measurement of cDNA hybridization kinetics. Biosensors and Bioelectronics, 2007, 22, 2108-2114.	5.3	25
16	Tissue-Specific Expression and Regulatory Networks of Pig MicroRNAome. PLoS ONE, 2014, 9, e89755.	1.1	22
17	Helicobacter pylori Dampens HLA-II Expression on Macrophages via the Up-Regulation of miRNAs Targeting CIITA. Frontiers in Immunology, 2019, 10, 2923.	2.2	22
18	Overview of Micro- and Nano-Technology Tools for Stem Cell Applications: Micropatterned and Microelectronic Devices. Sensors, 2012, 12, 15947-15982.	2.1	21

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19	Partial <i>F8</i> gene duplication (factor VIII Padua) associated with high factor VIII levels and familial thrombophilia. Blood, 2021, 137, 2383-2393.	0.6	20
20	The immune receptor CD300e negatively regulates T cell activation by impairing the STAT1-dependent antigen presentation. Scientific Reports, 2020, 10, 16501.	1.6	16
21	SPP1 genotype is a determinant of disease severity in Duchenne muscular dystrophy. Neurology, 2011, 77, 1858-1859.	1.5	15
22	timeClip: pathway analysis for time course data without replicates. BMC Bioinformatics, 2014, 15, S3.	1.2	15
23	Gene expression changes of single skeletal muscle fibers in response to modulation of the mitochondrial calcium uniporter (MCU). Genomics Data, 2015, 5, 64-67.	1.3	15
24	Altered Gene Transcription in Human Cells Treated with Ludox® Silica Nanoparticles. International Journal of Environmental Research and Public Health, 2014, 11, 8867-8890.	1.2	12
25	SAMHD1â€deficient fibroblasts from Aicardiâ€Goutières Syndrome patients can escape senescence and accumulate mutations. FASEB Journal, 2020, 34, 631-647.	0.2	12
26	The Prion Protein Regulates Synaptic Transmission by Controlling the Expression of Proteins Key to Synaptic Vesicle Recycling and Exocytosis. Molecular Neurobiology, 2019, 56, 3420-3436.	1.9	9
27	Perturbations of the Proteome and of Secreted Metabolites in Primary Astrocytes from the hSOD1(G93A) ALS Mouse Model. International Journal of Molecular Sciences, 2021, 22, 7028.	1.8	9
28	Insights into how environment shapes post-mortem RNA transcription in mouse brain. Scientific Reports, 2021, 11, 13008.	1.6	9
29	Regulation of Endoplasmic Reticulum–Mitochondria Tethering and Ca2+ Fluxes by TDP-43 via GSK3β. International Journal of Molecular Sciences, 2021, 22, 11853.	1.8	9
30	Systems Biology Approach to the Dissection of the Complexity of Regulatory Networks in the S. scrofa Cardiocirculatory System. International Journal of Molecular Sciences, 2013, 14, 23160-23187.	1.8	7
31	Dynamic culture of dropletâ€confined cell arrays. Biotechnology Progress, 2010, 26, 220-231.	1.3	6
32	RNA-sequencing reveals that STRN, ZNF484 and WNK1 add to the value of mitochondrial MT-COI and COX10 as markers of unstable coronary artery disease. PLoS ONE, 2019, 14, e0225621.	1.1	5
33	Neurocognitive assessment and DNA sequencing expand the phenotype and genotype spectrum of Alström syndrome. American Journal of Medical Genetics, Part A, 2021, 185, 732-742.	0.7	5
34	Expression and Functional Analyses of Nymphaea caerulea MADS-Box Genes Contribute to Clarify the Complex Flower Patterning of Water Lilies. Frontiers in Plant Science, 2021, 12, 730270.	1.7	5
35	The Interplay of Microtubules with Mitochondria–ER Contact Sites (MERCs) in Glioblastoma. Biomolecules, 2022, 12, 567.	1.8	5
36	Statistical Test of Expression Pattern (STEPath): a new strategy to integrate gene expression data with genomic information in individual and meta-analysis studies. BMC Bioinformatics, 2011, 12, 92.	1.2	4

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37	MyoData: An expression knowledgebase at single cell/nucleus level for the discovery of coding-noncoding RNA functional interactions in skeletal muscle. Computational and Structural Biotechnology Journal, 2021, 19, 4142-4155.	1.9	4
38	Isolation and Transcriptomic Profiling of Single Myofibers from Mice. Bio-protocol, 2019, 9, e3378.	0.2	3
39	Genes and response to aerobic training. , 2019, , 169-188.		2
40	Single-Cell RNAseq Analysis of IncRNAs. Methods in Molecular Biology, 2021, 2348, 71-90.	0.4	1
41	P2.01-021 miRNA Deep Sequencing of Early-Stage Lung Cancer Patients to Evaluate the Dynamic Change of Circulating Biomarkers in Response to Surgery. Journal of Thoracic Oncology, 2017, 12, S796-S797.	0.5	0
42	Single-Cell Transcriptomics and Proteomics of Skeletal Muscle: Technology and Applications. , 2019, , 253-281.		0