Gerolamo Lanfranchi

List of Publications by Year
in descending order

22	859	623734 14	713466 21
papers	citations	h-index	g-index

23	23	23	1623
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	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.	4.1	4
2	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.	6.4	55
3	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.	14.5	63
4	Isolation and Transcriptomic Profiling of Single Myofibers from Mice. Bio-protocol, 2019, 9, e3378.	0.4	3
5	Gene and MicroRNA Expression Are Predictive of Tumor Response in Rectal Adenocarcinoma Patients Treated With Preoperative Chemoradiotherapy. Journal of Cellular Physiology, 2017, 232, 426-435.	4.1	54
6	NELL1, whose high expression correlates with negative outcomes, has different methylation patterns in alveolar and embryonal rhabdomyosarcoma. Oncotarget, 2017, 8, 33086-33099.	1.8	14
7	MicroRNA-27a Contributes to Rhabdomyosarcoma Cell Proliferation by Suppressing RARA and RXRA. PLoS ONE, 2015, 10, e0125171.	2.5	26
8	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
9	The Mitochondrial Calcium Uniporter Controls Skeletal Muscle Trophism InÂVivo. Cell Reports, 2015, 10, 1269-1279.	6.4	170
10	Altered Gene Transcription in Human Cells Treated with LudoxÂ® Silica Nanoparticles. International Journal of Environmental Research and Public Health, 2014, 11, 8867-8890.	2.6	12
11	Involvement of MicroRNAs in the Regulation of Muscle Wasting during Catabolic Conditions. Journal of Biological Chemistry, 2014, 289, 21909-21925.	3.4	129
12	Tissue-Specific Expression and Regulatory Networks of Pig MicroRNAome. PLoS ONE, 2014, 9, e89755.	2.5	22
13	Decellularized Allogeneic Heart Valves Demonstrate Self-Regeneration Potential after a Long-Term Preclinical Evaluation. PLoS ONE, 2014, 9, e99593.	2.5	71
14	Microgenomic Analysis in Skeletal Muscle: Expression Signatures of Individual Fast and Slow Myofibers. PLoS ONE, 2011, 6, e16807.	2.5	91
15	New miRNA labeling method for bead-based quantification. BMC Molecular Biology, 2010, 11, 44.	3.0	28
16	The effects of Ankrd2 alteration indicate its involvement in cell cycle regulation during muscle differentiation. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 1023-1035.	4.1	34
17	Characterization of 16 novel human genes showing high similarity to yeast sequences. Yeast, 2001, 18, 69-80.	1.7	25
18	Characterization of 16 novel human genes showing high similarity to yeast sequences. Yeast, 2001, 18, 69-80.	1.7	1

#	Article	IF	Citations
19	The preliminary transcript map of a human skeletal muscle. Human Molecular Genetics, 1997, 6, 1445-1450.	2.9	14
20	The DNA Sequence of Cosmid 14â€“13b from Chromosome XIV ofSaccharomyces cerevisiae Reveals an Unusually High Number of Overlapping Open Reading Frames. , 1997, 13, 261-266.		6
21	The DNA sequence of cosmid 14-5 from chromosome XIV reveals 21 open reading frames including a novel gene encoding a globin-like domain. Yeast, 1996, 12, 1071-1076.	1.7	12
22	A putative serine/threonine protein kinase gene on chromosome III ofSaccharomyces cerevisiae. Yeast, 1992, 8, 71-77.	1.7	10