Luiz O F Penalva

List of Publications by Year
in descending order

72 papers	7,837 citations	101384 36 h-index	98622 67 g-index
76 all docs	76 docs citations	76 times ranked	16812 citing authors

#	Article	IF	Citations
1	The RNA-Binding Protein Musashi1 Regulates a Network of Cell Cycle Genes in Group 4 Medulloblastoma. Cells, 2022, 11, 56.	1.8	3
2	Synergism of Proneurogenic miRNAs Provides a More Effective Strategy to Target Glioma Stem Cells. Cancers, 2021, 13, 289.	1.7	7
3	Deciphering the Role of Intestinal Crypt Cell Populations in Resistance to Chemotherapy. Cancer Research, 2021, 81, 2730-2744.	0.4	4
4	Musashi1 Contribution to Glioblastoma Development via Regulation of a Network of DNA Replication, Cell Cycle and Division Genes. Cancers, 2021, 13, 1494.	1.7	9
5	Murine intestinal stem cells are highly sensitive to modulation of the T3/TRÎ±1-dependent pathway. Development (Cambridge), 2021, 148, .	1.2	10
6	Altered lipid metabolism marks glioblastoma stem and non-stem cells in separate tumor niches. Acta Neuropathologica Communications, 2021, 9, 101.	2.4	60
7	Structural Characterization of the RNA-Binding Protein SERBP1 Reveals Intrinsic Disorder and Atypical RNA Binding Modes. Frontiers in Molecular Biosciences, 2021, 8, 744707.	1.6	12
8	<i>ELF4</i> Is a Target of miR-124 and Promotes Neuroblastoma Proliferation and Undifferentiated State. Molecular Cancer Research, 2020, 18, 68-78.	1.5	14
9	The RNA-binding protein SERBP1 functions as a novel oncogenic factor in glioblastoma by bridging cancer metabolism and epigenetic regulation. Genome Biology, 2020, 21, 195.	3.8	55
10	MSI1 Promotes the Expression of the GBM Stem Cell Marker CD44 by Impairing miRNA-Dependent Degradation. Cancers, 2020, 12, 3654.	1.7	7
11	Genomic analyses of early responses to radiation in glioblastoma reveal new alterations at transcription, splicing, and translation levels. Scientific Reports, 2020, 10, 8979.	1.6	11
12	Zika Virus Targets Glioblastoma Stem Cells through a SOX2-Integrin Î±vÎ²5 Axis. Cell Stem Cell, 2020, 26, 187-204.e10.	5.2	126
13	Proneural and mesenchymal glioma stem cells display major differences in splicing and lncRNA profiles. Npj Genomic Medicine, 2020, 5, 2.	1.7	29
14	The Diverse Roles of RNA-Binding Proteins in Glioma Development. Advances in Experimental Medicine and Biology, 2019, 1157, 29-39.	0.8	26
15	Antagonism between the RNA-binding protein Musashi1 and miR-137 and its potential impact on neurogenesis and glioblastoma development. Rna, 2019, 25, 768-782.	1.6	25
16	Patient-derived conditionally reprogrammed cells maintain intra-tumor genetic heterogeneity. Scientific Reports, 2018, 8, 4097.	1.6	34
17	Luteolin inhibits Musashi1 binding to RNA and disrupts cancer phenotypes in glioblastoma cells. RNA Biology, 2018, 15, 1420-1432.	1.5	39
18	Increased expression of the thyroid hormone nuclear receptor TRÎ±1 characterizes intestinal tumors with high Wnt activity. Oncotarget, 2018, 9, 30979-30996.	0.8	12

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19	Riborex: fast and flexible identification of differential translation from Ribo-seq data. Bioinformatics, 2017, 33, 1735-1737.	1.8	78
20	RNA processing as an alternative route to attack glioblastoma. Human Genetics, 2017, 136, 1129-1141.	1.8	42
21	MicroRNA-195 acts as an anti-proliferative miRNA in human melanoma cells by targeting Prohibitin 1. BMC Cancer, 2017, 17, 750.	1.1	23
22	The 3â€² end of the story: deciphering combinatorial interactions that control mRNA fate. Genome Biology, 2017, 18, 227.	3.8	0
23	From mechanisms to therapy: RNA processingâ€™s impact on human genetics. Human Genetics, 2017, 136, 1013-1014.	1.8	0
24	Functional genomics analyses of RNA-binding proteins reveal the splicing regulator SNRPB as an oncogenic candidate in glioblastoma. Genome Biology, 2016, 17, 125.	3.8	83
25	Musashi1 Impacts Radio-Resistance in Glioblastoma by Controlling DNA-Protein Kinase Catalytic Subunit. American Journal of Pathology, 2016, 186, 2271-2278.	1.9	38
26	miR-124, -128, and -137 Orchestrate Neural Differentiation by Acting on Overlapping Gene Sets Containing a Highly Connected Transcription Factor Network. Stem Cells, 2016, 34, 220-232.	1.4	53
27	IGF2BP3 Modulates the Interaction of Invasion-Associated Transcripts with RISC. Cell Reports, 2016, 15, 1876-1883.	2.9	67
28	High-throughput analyses of hnRNP H1 dissects its multi-functional aspect. RNA Biology, 2016, 13, 400-411.	1.5	50
29	A Mouse Model of Targeted Musashi1 Expression in Whole Intestinal Epithelium Suggests Regulatory Roles in Cell Cycle and Stemness. Stem Cells, 2015, 33, 3621-3634.	1.4	25
30	RNA-Binding Protein Musashi1 Is a Central Regulator of Adhesion Pathways in Glioblastoma. Molecular and Cellular Biology, 2015, 35, 2965-2978.	1.1	51
31	Leveraging cross-link modification events in CLIP-seq for motif discovery. Nucleic Acids Research, 2015, 43, 95-103.	6.5	40
32	Computational challenges, tools, and resources for analyzing coâ€•and postâ€transcriptional events in high throughput. Wiley Interdisciplinary Reviews RNA, 2015, 6, 291-310.	3.2	16
33	WTAP is a novel oncogenic protein in acute myeloid leukemia. Leukemia, 2014, 28, 1171-1174.	3.3	208
34	RNA binding protein HuR regulates the expression of ABCA1. Journal of Lipid Research, 2014, 55, 1066-1076.	2.0	33
35	Genomic Analyses Reveal Broad Impact of miR-137 on Genes Associated with Malignant Transformation and Neuronal Differentiation in Glioblastoma Cells. PLoS ONE, 2014, 9, e85591.	1.1	38
36	A compendium of RNA-binding motifs for decoding gene regulation. Nature, 2013, 499, 172-177.	13.7	1,281

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37	Translation regulation gets its â€˜omicsâ€™ moment. Wiley Interdisciplinary Reviews RNA, 2013, 4, 617-630.	3.2	44
38	Musashi1 as a potential therapeutic target and diagnostic marker for lung cancer. Oncotarget, 2013, 4, 739-750.	0.8	43
39	Post-Transcriptional Gene Networks. , 2013, , 1725-1728.		0
40	The Oncogenic RNA-Binding Protein Musashi1 Is Regulated by HuR via mRNA Translation and Stability in Glioblastoma Cells. Molecular Cancer Research, 2012, 10, 143-155.	1.5	65
41	Before It Gets Started: Regulating Translation at the 5â€² UTR. Comparative and Functional Genomics, 2012, 2012, 1-8.	2.0	193
42	Site identification in high-throughput RNAâ€"protein interaction data. Bioinformatics, 2012, 28, 3013-3020.	1.8	272
43	The RNA-Binding Protein Musashi1 Affects Medulloblastoma Growth via a Network of Cancer-Related Genes and Is an Indicator of Poor Prognosis. American Journal of Pathology, 2012, 181, 1762-1772.	1.9	73
44	The RNA-Binding Protein Musashi1: A Major Player in Intestinal Epithelium Renewal and Colon Cancer Development. Current Colorectal Cancer Reports, 2012, 8, 290-297.	1.0	7
45	Musashi1: an RBP with versatile functions in normal and cancer stem cells. Frontiers in Bioscience - Landmark, 2012, 17, 54.	3.0	50
46	RIP-Chip Analysis: RNA-Binding Protein Immunoprecipitation-Microarray (Chip) Profiling. Methods in Molecular Biology, 2011, 703, 247-263.	0.4	75
47	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	2.6	1,257
48	Latent rank change detection for analysis of splice-junction microarrays with nonlinear effects. Annals of Applied Statistics, 2011, 5, .	0.5	0
49	Genomic Analyses of the RNA-binding Protein Hu Antigen R (HuR) Identify a Complex Network of Target Genes and Novel Characteristics of Its Binding Sites. Journal of Biological Chemistry, 2011, 286, 37063-37066.	1.6	68
50	Two-tiered Approach Identifies a Network of Cancer and Liver Disease-related Genes Regulated by miR-122. Journal of Biological Chemistry, 2011, 286, 18066-18078.	1.6	54
51	MicroRNA-16 and MicroRNA-424 Regulate Cell-Autonomous Angiogenic Functions in Endothelial Cells via Targeting Vascular Endothelial Growth Factor Receptor-2 and Fibroblast Growth Factor Receptor-1. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2595-2606.	1.1	227
52	miR-33a/b contribute to the regulation of fatty acid metabolism and insulin signaling. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 9232-9237.	3.3	615
53	The oncogenic RNA-binding protein Musashi1 is regulated by tumor suppressor miRNAs. RNA Biology, 2011, 8, 817-828.	1.5	64
54	Sequence signatures and mRNA concentration can explain twoâ€thirds of protein abundance variation in a human cell line. Molecular Systems Biology, 2010, 6, 400.	3.2	526

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55	Genomic Analyses of Musashi1 Downstream Targets Show a Strong Association with Cancer-related Processes. Journal of Biological Chemistry, 2009, 284, 12125-12135.	1.6	79
56	A comprehensive in silico expression analysis of RNA binding proteins in normal and tumor tissue; identification of potential players in tumor formation. RNA Biology, 2009, 6, 426-433.	1.5	51
57	Integrating shotgun proteomics and mRNA expression data to improve protein identification. Bioinformatics, 2009, 25, 1397-1403.	1.8	59
58	Global signatures of protein and mRNA expression levels. Molecular BioSystems, 2009, 5, 1512-26.	2.9	841
59	Mining gene functional networks to improve mass-spectrometry-based protein identification. Bioinformatics, 2009, 25, 2955-2961.	1.8	34
60	Musashi1 modulates cell proliferation genes in the medulloblastoma cell line Daoy. BMC Cancer, 2008, 8, 280.	1.1	59
61	Over-represented sequences located on 3' UTRs are potentially involved in regulatory functions. RNA Biology, 2008, 5, 255-262.	1.5	14
62	A Two-Phase Innate Host Response to Alphavirus Infection Identified by mRNP-Tagging In Vivo. PLoS Pathogens, 2007, 3, e199.	2.1	19
63	Vascular Biology and the Sex of Flies: Regulation of Vascular Smooth Muscle Cell Proliferation by Wilmsâ€™ Tumor 1â€“Associating Protein. Trends in Cardiovascular Medicine, 2007, 17, 230-234.	2.3	20
64	Post-Transcription Meets Post-Genomic: The Saga of RNA Binding Proteins in a New Era. RNA Biology, 2006, 3, 101-109.	1.5	58
65	Biotinylated tags for recovery and characterization of ribonucleoprotein complexes. BioTechniques, 2004, 37, 604-610.	0.8	27
66	RNA-binding proteins to assess gene expression states of co-cultivated cells in response to tumor cells. Molecular Cancer, 2004, 3, 24.	7.9	34
67	Gene Expression Analysis of Messenger RNP Complexes. , 2004, 257, 125-134.		42
68	RNA Binding Protein Sex-Lethal (Sxl) and Control of Drosophila Sex Determination and Dosage Compensation. Microbiology and Molecular Biology Reviews, 2003, 67, 343-359.	2.9	149
69	Switch in 3â€² Splice Site Recognition between Exon Definition and Splicing Catalysis Is Important for Sex-lethal Autoregulation. Molecular and Cellular Biology, 2001, 21, 1986-1996.	1.1	27
70	The Drosophila <i>fl(2)d</i> Gene, Required for Female-Specific Splicing of <i>Sxl</i> and <i>tra</i> Pre-mRNAs, Encodes a Novel Nuclear Protein With a HQ-Rich Domain. Genetics, 2000, 155, 129-139.	1.2	44
71	Indirect evidence of alteration in the expression of the rDNA genes in interspecific hybrids between. Molecular Genetics and Genomics, 1996, 250, 89.	2.4	3
72	Regulation of the Gene <i>Sex-lethal</i>: A Comparative Analysis of <i>Drosophila melanogaster</i> and <i>Drosophila subobscura</i>. Genetics, 1996, 144, 1653-1664.	1.2	34