

Francesco Russo

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

572
citations

14
h-index

23
g-index

35
ext. papers

686
ext. citations

5.8
avg. IF

3.42
L-index

#	Paper	IF	Citations
31	AMBRA1 regulates cyclin D to guard S-phase entry and genomic integrity. <i>Nature</i> , 2021 , 592, 799-803	50.4	24
30	Exploring Noninvasive Biomarkers with the miRandola Database: A Tool for Translational Medicine. <i>Methods in Molecular Biology</i> , 2021 , 2284, 445-455	1.4	1
29	MiREDiBase, a manually curated database of validated and putative editing events in microRNAs. <i>Scientific Data</i> , 2021 , 8, 199	8.2	4
28	Secreted breast tumor interstitial fluid microRNAs and their target genes are associated with triple-negative breast cancer, tumor grade, and immune infiltration. <i>Breast Cancer Research</i> , 2020 , 22, 73	8.3	8
27	The miR-28-5p Targetome Discovery Identified SREBF2 as One of the Mediators of the miR-28-5p Tumor Suppressor Activity in Prostate Cancer Cells. <i>Cells</i> , 2020 , 9,	7.9	11
26	Comorbidity landscape of the Danish patient population affected by chromosome abnormalities. <i>Genetics in Medicine</i> , 2019 , 21, 2485-2495	8.1	7
25	Combing the Hairball: Improving Visualization of miRNA-Target Interaction Networks. <i>Methods in Molecular Biology</i> , 2019 , 1970, 279-289	1.4	
24	Identification of Disease-miRNA Networks Across Different Cancer Types Using SWIM. <i>Methods in Molecular Biology</i> , 2019 , 1970, 169-181	1.4	5
23	Identification of hyper-rewired genomic stress non-oncogene addiction genes across 15 cancer types. <i>Npj Systems Biology and Applications</i> , 2019 , 5, 27	5	8
22	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018 , 46, D354-D359	20.1	44
21	Interplay Between Long Noncoding RNAs and MicroRNAs in Cancer. <i>Methods in Molecular Biology</i> , 2018 , 1819, 75-92	1.4	28
20	The Interplay of Non-coding RNAs and X Chromosome Inactivation in Human Disease. <i>RNA Technologies</i> , 2018 , 229-238	0.2	
19	MicroRNAs, Regulatory Networks, and Comorbidities: Decoding Complex Systems. <i>Methods in Molecular Biology</i> , 2017 , 1580, 281-295	1.4	1
18	Klinefelter syndrome comorbidities linked to increased X chromosome gene dosage and altered protein interactome activity. <i>Human Molecular Genetics</i> , 2017 , 26, 1219-1229	5.6	51
17	The miRNA Pull Out Assay as a Method to Validate the miR-28-5p Targets Identified in Other Tumor Contexts in Prostate Cancer. <i>International Journal of Genomics</i> , 2017 , 2017, 5214806	2.5	7
16	Discovering the miR-26a-5p Targetome in Prostate Cancer Cells. <i>Journal of Cancer</i> , 2017 , 8, 2729-2739	4.5	17
15	Methods for the Identification of PTEN-Targeting MicroRNAs. <i>Methods in Molecular Biology</i> , 2016 , 1388, 111-38	1.4	3

14	Circulating Noncoding RNAs as Clinical Biomarkers 2016 , 239-258		3
13	Discovering miRNA Regulatory Networks in Holt-Oram Syndrome Using a Zebrafish Model. <i>Frontiers in Bioengineering and Biotechnology</i> , 2016 , 4, 60	5.8	11
12	Identification of BRAF 3'UTR Isoforms in Melanoma. <i>Journal of Investigative Dermatology</i> , 2015 , 135, 1694-1697	4.3	11
11	MicroRNA 19a replacement partially rescues fin and cardiac defects in zebrafish model of Holt Oram syndrome. <i>Scientific Reports</i> , 2015 , 5, 18240	4.9	15
10	A new method for discovering disease-specific MiRNA-target regulatory networks. <i>PLoS ONE</i> , 2015 , 10, e0122473	3.7	7
9	Computational design of artificial RNA molecules for gene regulation. <i>Methods in Molecular Biology</i> , 2015 , 1269, 393-412	1.4	16
8	A knowledge base for the discovery of function, diagnostic potential and drug effects on cellular and extracellular miRNAs. <i>BMC Genomics</i> , 2014 , 15 Suppl 3, S4	4.5	21
7	Comprehensive reconstruction and visualization of non-coding regulatory networks in human. <i>Frontiers in Bioengineering and Biotechnology</i> , 2014 , 2, 69	5.8	20
6	Extracellular circulating viral microRNAs: current knowledge and perspectives. <i>Frontiers in Genetics</i> , 2013 , 4, 120	4.5	32
5	miR-EdiTar: a database of predicted A-to-I edited miRNA target sites. <i>Bioinformatics</i> , 2012 , 28, 3166-8	7.2	23
4	miRandola: extracellular circulating microRNAs database. <i>PLoS ONE</i> , 2012 , 7, e47786	3.7	129
3	Variability in the incidence of miRNAs and genes in fragile sites and the role of repeats and CpG islands in the distribution of genetic material. <i>PLoS ONE</i> , 2010 , 5, e11166	3.7	43
2	Prediction of human targets for viral-encoded microRNAs by thermodynamics and empirical constraints. <i>Journal of Rnai and Gene Silencing</i> , 2010 , 6, 379-85		18
1	MiREDiBase: a manually curated database of validated and putative editing events in microRNAs		4