

Gert Van Peer

List of Publications by Year in descending order

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Version: 2024-02-01

15
papers

1,060
citations

759233

12
h-index

1058476

14
g-index

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all docs

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docs citations

15
times ranked

2558
citing authors

#	ARTICLE	IF	CITATIONS
1	Localization and Expression of Nuclear Factor of Activated T-Cells 5 in Myoblasts Exposed to Pro-inflammatory Cytokines or Hyperosmolar Stress and in Biopsies from Myositis Patients. <i>Frontiers in Physiology</i> , 2018, 9, 126.	2.8	14
2	A high-throughput 3â€™ UTR reporter screening identifies microRNA interactomes of cancer genes. <i>PLoS ONE</i> , 2018, 13, e0194017.	2.5	15
3	miSTAR: miRNA target prediction through modeling quantitative and qualitative miRNA binding site information in a stacked model structure. <i>Nucleic Acids Research</i> , 2016, 45, gkw1260.	14.5	18
4	MYCN-driven regulatory mechanisms controlling LIN28B in neuroblastoma. <i>Cancer Letters</i> , 2015, 366, 123-132.	7.2	51
5	MYCN-targeting miRNAs are predominantly downregulated during MYCN-driven neuroblastoma tumor formation. <i>Oncotarget</i> , 2015, 6, 5204-5216.	1.8	38
6	Expressed Repeat Elements Improve RT-qPCR Normalization across a Wide Range of Zebrafish Gene Expression Studies. <i>PLoS ONE</i> , 2014, 9, e109091.	2.5	38
7	miRBase Tracker: keeping track of microRNA annotation changes. <i>Database: the Journal of Biological Databases and Curation</i> , 2014, 2014, .	3.0	73
8	MicroRNA-128-3p is a novel oncomiR targeting PHF6 in T-cell acute lymphoblastic leukemia. <i>Haematologica</i> , 2014, 99, 1326-1333.	3.5	55
9	The need for transparency and good practices in the qPCR literature. <i>Nature Methods</i> , 2013, 10, 1063-1067.	19.0	251
10	Identification of miR-145 as a Key Regulator of the Pigmentary Process. <i>Journal of Investigative Dermatology</i> , 2013, 133, 201-209.	0.7	99
11	Effective Alu Repeat Based RT-Qpcr Normalization in Cancer Cell Perturbation Experiments. <i>PLoS ONE</i> , 2013, 8, e71776.	2.5	13
12	Accurate RT-qPCR gene expression analysis on cell culture lysates. <i>Scientific Reports</i> , 2012, 2, 222.	3.3	52
13	Genome-wide promoter methylation analysis in neuroblastoma identifies prognostic methylation biomarkers. <i>Genome Biology</i> , 2012, 13, R95.	9.6	64
14	Regulatory Networks Governed by MicroRNAs in T-ALL Oncogenesis and Normal T-Cell Development. <i>Blood</i> , 2011, 118, 1366-1366.	1.4	0
15	The miR-17-92 MicroRNA Cluster Regulates Multiple Components of the TGF-Î² Pathway in Neuroblastoma. <i>Molecular Cell</i> , 2010, 40, 762-773.	9.7	279