

Martina Manzoni

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7593791/publications.pdf>

Version: 2024-02-01

29
papers

1,087
citations

567281

15
h-index

501196

28
g-index

29
all docs

29
docs citations

29
times ranked

1921
citing authors

#	ARTICLE	IF	CITATIONS
1	Circulating tumor DNA reveals genetics, clonal evolution, and residual disease in classical Hodgkin lymphoma. <i>Blood</i> , 2018, 131, 2413-2425.	1.4	223
2	Drugging the lncRNA MALAT1 via LNA gapmer ASO inhibits gene expression of proteasome subunits and triggers anti-multiple myeloma activity. <i>Leukemia</i> , 2018, 32, 1948-1957.	7.2	179
3	Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. <i>Leukemia</i> , 2020, 34, 234-244.	7.2	80
4	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. <i>Oncotarget</i> , 2016, 7, 14814-14830.	1.8	79
5	Molecular spectrum of <i>BRAF</i> , <i>NRAS</i> and <i>KRAS</i> gene mutations in plasma cell dyscrasias: implication for MEK-ERK pathway activation. <i>Oncotarget</i> , 2015, 6, 24205-24217.	1.8	65
6	Therapeutic vulnerability of multiple myeloma to MIR17PTi, a first-in-class inhibitor of pri-miR-17-92. <i>Blood</i> , 2018, 132, 1050-1063.	1.4	52
7	Disentangling the microRNA regulatory milieu in multiple myeloma: integrative genomics analysis outlines mixed miRNA-TF circuits and pathway-derived networks modulated in t(4;14) patients. <i>Oncotarget</i> , 2016, 7, 2367-2378.	1.8	41
8	Molecular spectrum of <i>TP53</i> mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. <i>Oncotarget</i> , 2016, 7, 21353-21361.	1.8	40
9	Compendium of <i>FAM46C</i> gene mutations in plasma cell dyscrasias. <i>British Journal of Haematology</i> , 2016, 174, 642-645.	2.5	34
10	A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. <i>Scientific Reports</i> , 2018, 8, 6557.	3.3	34
11	Inactivation of CK1 $\hat{\pm}$ in multiple myeloma empowers drug cytotoxicity by affecting AKT and $\hat{\beta}$ -catenin survival signaling pathways. <i>Oncotarget</i> , 2017, 8, 14604-14619.	1.8	30
12	Circulating tumor DNA as a liquid biopsy in plasma cell dyscrasias. <i>Haematologica</i> , 2018, 103, e245-e248.	3.5	29
13	Long non-coding RNA NEAT1 shows high expression unrelated to molecular features and clinical outcome in multiple myeloma. <i>Haematologica</i> , 2019, 104, e72-e76.	3.5	27
14	Reduction of Cardiac Fibrosis by Interference With YAP-Dependent Transactivation. <i>Circulation Research</i> , 2022, 131, 239-257.	4.5	26
15	The small GTPase RhoU lays downstream of JAK/STAT signaling and mediates cell migration in multiple myeloma. <i>Blood Cancer Journal</i> , 2018, 8, 20.	6.2	19
16	In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. <i>Genes</i> , 2016, 7, 107.	2.4	17
17	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. <i>HemaSphere</i> , 2020, 4, e402.	2.7	15
18	Insulin Growth Factor 1 Receptor Expression Is Associated with NOTCH1 Mutation, Trisomy 12 and Aggressive Clinical Course in Chronic Lymphocytic Leukaemia. <i>PLoS ONE</i> , 2015, 10, e0118801.	2.5	15

#	ARTICLE	IF	CITATIONS
19	Microenvironmental regulation of the IL-23R/IL-23 axis overrides chronic lymphocytic leukemia indolence. <i>Science Translational Medicine</i> , 2018, 10, .	12.4	13
20	Global methylation patterns in primary plasma cell leukemia. <i>Leukemia Research</i> , 2018, 73, 95-102.	0.8	13
21	Surrogate molecular markers for IGHV mutational status in chronic lymphocytic leukemia for predicting time to first treatment. <i>Leukemia Research</i> , 2015, 39, 840-845.	0.8	12
22	Expanding the repertoire of miRNAs and miRNA-offset RNAs expressed in multiple myeloma by small RNA deep sequencing. <i>Blood Cancer Journal</i> , 2019, 9, 21.	6.2	10
23	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 6479-6490.	7.0	9
24	Evaluation of damaging effects of splicing mutations: Validation of an in vitro method for diagnostic laboratories. <i>Clinica Chimica Acta</i> , 2014, 436, 276-282.	1.1	7
25	Application of Next-Generation Sequencing for the Genomic Characterization of Patients with Smoldering Myeloma. <i>Cancers</i> , 2020, 12, 1332.	3.7	7
26	Expression Pattern and Biological Significance of the lncRNA ST3GAL6-AS1 in Multiple Myeloma. <i>Cancers</i> , 2020, 12, 782.	3.7	6
27	Whole-Blood Transcriptional Profiles Enable Early Prediction of the Presence of Coronary Atherosclerosis and High-Risk Plaque Features at Coronary CT Angiography. <i>Biomedicines</i> , 2022, 10, 1309.	3.2	4
28	Bioinformatics Pipeline to Analyze lncRNA Arrays. <i>Methods in Molecular Biology</i> , 2021, 2348, 45-53.	0.9	1
29	The Atypical Gtpase Rho Lies Downstream IL6/STAT3 and Regulates Myeloma Plasma Cells Adhesion/Motility. <i>Blood</i> , 2016, 128, 5661-5661.	1.4	0