

# Domenica Ronchetti

## List of Publications by Year in descending order

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Version: 2024-02-01

48  
papers

1,895  
citations

257450

24  
h-index

265206

42  
g-index

48  
all docs

48  
docs citations

48  
times ranked

2795  
citing authors

#	ARTICLE	IF	CITATIONS
1	DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. <i>Haematologica</i> , 2022, 107, 921-932.	3.5	14
2	In Vitro Silencing of lncRNAs Using LNA GapmeRs. <i>Methods in Molecular Biology</i> , 2021, 2348, 157-166.	0.9	5
3	Epigenetic Regulation of Mitochondrial Quality Control Genes in Multiple Myeloma: A Sequenom MassARRAY Pilot Investigation on HMCLs. <i>Journal of Clinical Medicine</i> , 2021, 10, 1295.	2.4	5
4	Mechanisms of Immune Evasion in Multiple Myeloma: Open Questions and Therapeutic Opportunities. <i>Cancers</i> , 2021, 13, 3213.	3.7	16
5	Transcriptomic Analysis in Multiple Myeloma and Primary Plasma Cell Leukemia with t(11;14) Reveals Different Expression Patterns with Biological Implications in Venetoclax Sensitivity. <i>Cancers</i> , 2021, 13, 4898.	3.7	8
6	Bioinformatics Pipeline to Analyze lncRNA Arrays. <i>Methods in Molecular Biology</i> , 2021, 2348, 45-53.	0.9	1
7	Dissecting the Biological Relevance and Clinical Impact of lncRNA MIAT in Multiple Myeloma. <i>Cancers</i> , 2021, 13, 5518.	3.7	0
8	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
9	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespective of Cytogenetic Groups or Clinical Outcome. <i>Non-coding RNA</i> , 2020, 6, 11.	2.6	11
10	lncRNA NEAT1 in Paraspeckles: A Structural Scaffold for Cellular DNA Damage Response Systems?. <i>Non-coding RNA</i> , 2020, 6, 26.	2.6	27
11	Expression Pattern and Biological Significance of the lncRNA ST3GAL6-AS1 in Multiple Myeloma. <i>Cancers</i> , 2020, 12, 782.	3.7	6
12	Replacement of miR-155 Elicits Tumor Suppressive Activity and Antagonizes Bortezomib Resistance in Multiple Myeloma. <i>Cancers</i> , 2019, 11, 236.	3.7	35
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	Long Non-Coding RNAs in Multiple Myeloma. <i>Genes</i> , 2018, 9, 69.	2.4	22
15	A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. <i>Scientific Reports</i> , 2018, 8, 6557.	3.3	34
16	IL21R expressing CD14 <sup>+</sup> CD16 <sup>+</sup> monocytes expand in multiple myeloma patients leading to increased osteoclasts. <i>Haematologica</i> , 2017, 102, 773-784.	3.5	36
17	Long non-coding RNAs in B-cell malignancies: a comprehensive overview. <i>Oncotarget</i> , 2017, 8, 60605-60623.	1.8	25
18	Inhibition of EZH2 triggers the tumor suppressive miR-29b network in multiple myeloma. <i>Oncotarget</i> , 2017, 8, 106527-106537.	1.8	60

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19	In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. <i>Genes</i> , 2016, 7, 107.	2.4	17
20	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. <i>Oncotarget</i> , 2016, 7, 14814-14830.	1.8	79
21	lncRNA profiling in early-stage chronic lymphocytic leukemia identifies transcriptional fingerprints with relevance in clinical outcome. <i>Blood Cancer Journal</i> , 2016, 6, e468-e468.	6.2	47
22	A p53-Dependent Tumor Suppressor Network Is Induced by Selective miR-125a Inhibition in Multiple Myeloma Cells. <i>Journal of Cellular Physiology</i> , 2014, 229, 2106-2116.	4.1	86
23	Distinct patterns of global promoter methylation in early stage chronic lymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 264-273.	2.8	10
24	Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. <i>BMC Medical Genomics</i> , 2013, 6, 27.	1.5	73
25	The expression pattern of small nucleolar and small Cajal body-specific RNAs characterizes distinct molecular subtypes of multiple myeloma. <i>Blood Cancer Journal</i> , 2012, 2, e96-e96.	6.2	70
26	Gene Expression Profiling of Bone Marrow Endothelial Cells in Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , 2009, 15, 5369-5378.	7.0	91
27	Differential repetitive DNA methylation in multiple myeloma molecular subgroups. <i>Carcinogenesis</i> , 2009, 30, 1330-1335.	2.8	99
28	Concomitant downregulation of proliferation/survival pathways dependent on FGF-R3, JAK2 and BCMA in human multiple myeloma cells by multi-kinase targeting. <i>Biochemical Pharmacology</i> , 2009, 78, 1139-1147.	4.4	9
29	Integrative high-resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 521-531.	2.8	60
30	An integrative genomic approach reveals coordinated expression of intronic miR-335, miR-342, and miR-561 with deregulated host genes in multiple myeloma. <i>BMC Medical Genomics</i> , 2008, 1, 37.	1.5	104
31	Repetitive DNA Hypomethylation in Multiple Myeloma. <i>Blood</i> , 2008, 112, 2703-2703.	1.4	16
32	Relevance of Ras gene mutations in the context of the molecular heterogeneity of multiple myeloma. <i>Hematological Oncology</i> , 2007, 25, 6-10.	1.7	8
33	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 226-238.	2.8	62
34	Transcriptional features of multiple myeloma patients with chromosome 1q gain. <i>Leukemia</i> , 2007, 21, 1113-1116.	7.2	45
35	Molecular and Transcriptional Characterization of the Novel 17p11.2-p12 Chromosome Amplification in Multiple Myeloma. <i>Blood</i> , 2007, 110, 2486-2486.	1.4	0
36	Genome-Wide Analysis of DNA Copy Number in Multiple Myeloma Using High-Density SNP Arrays Reveals Clustering Patterns with Distinct Transcriptional Profiles. <i>Blood</i> , 2007, 110, 2482-2482.	1.4	0

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37	Transcription repression activity is associated with the type I isoform of the MMSET gene involved in t(4;14) in multiple myeloma. <i>British Journal of Haematology</i> , 2005, 131, 214-218.	2.5	24
38	Characterization of oncogene dysregulation in multiple myeloma by combined FISH and DNA microarray analyses. <i>Genes Chromosomes and Cancer</i> , 2005, 42, 117-127.	2.8	49
39	Association Between p53 Gene Mutations and Tobacco and Alcohol Exposure in Laryngeal Squamous Cell Carcinoma. <i>JAMA Otolaryngology</i> , 2004, 130, 303.	1.2	15
40	Lack of Bcl10 gene mutations in laryngeal squamous cell carcinoma. <i>Journal of Laryngology and Otology</i> , 2002, 116, 610-612.	0.8	1
41	p63 in Laryngeal Squamous Cell Carcinoma: Evidence for a Role of TA-p63 Down-Regulation in Tumorigenesis and Lack of Prognostic Implications of p63 Immunoreactivity. <i>Laboratory Investigation</i> , 2002, 82, 1327-1334.	3.7	40
42	Deregulated FGFR3 mutants in multiple myeloma cell lines with t(4;14): comparative analysis of Y373C, K650E and the novel G384D mutations. <i>Oncogene</i> , 2001, 20, 3553-3562.	5.9	98
43	Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. <i>Blood</i> , 1999, 93, 1330-1337.	1.4	80
44	Clinical relevance of p53 and bcl-2 protein over-expression in laryngeal squamous-cell carcinoma. , 1998, 79, 263-268.		46
45	Clinical relevance of p53 and bcl-2 protein over-expression in laryngeal squamous-cell carcinoma. <i>International Journal of Cancer</i> , 1998, 79, 263-268.	5.1	2
46	Identification of a Novel Gene, PSD, Adjacent to NFKB2/lyt-10, Which Contains Sec7 and Pleckstrin-Homology Domains. <i>Genomics</i> , 1997, 46, 251-259.	2.9	27
47	A Novel Chromosomal Translocation t(4; 14)(p16.3; q32) in Multiple Myeloma Involves the Fibroblast Growth-Factor Receptor 3 Gene. <i>Blood</i> , 1997, 90, 4062-4070.	1.4	201
48	Reverse transcriptase/polymerase chain reaction follow-up and minimal residual disease detection in t(1;19)-positive acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 1996, 92, 653-658.	2.5	24