

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 | 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 |
| 2 | 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 |
| 3 | Differential repetitive DNA methylation in multiple myeloma molecular subgroups. <i>Carcinogenesis</i> , 2009, 30, 1330-1335. | 2.8 | 99 |
| 4 | 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 |
| 5 | 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 |
| 6 | 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 |
| 7 | Molecular Analysis of 11q13 Breakpoints in Multiple Myeloma. <i>Blood</i> , 1999, 93, 1330-1337. | 1.4 | 80 |
| 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 | Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. <i>Oncotarget</i> , 2016, 7, 14814-14830. | 1.8 | 79 |
| 10 | Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. <i>BMC Medical Genomics</i> , 2013, 6, 27. | 1.5 | 73 |
| 11 | 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 |
| 12 | 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 |
| 13 | 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 |
| 14 | Inhibition of EZH2 triggers the tumor suppressive miR-29b network in multiple myeloma. <i>Oncotarget</i> , 2017, 8, 106527-106537. | 1.8 | 60 |
| 15 | 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 |
| 16 | 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 |
| 17 | Clinical relevance of p53 and bcl-2 protein over-expression in laryngeal squamous-cell carcinoma. , 1998, 79, 263-268. | | 46 |
| 18 | Transcriptional features of multiple myeloma patients with chromosome 1q gain. <i>Leukemia</i> , 2007, 21, 1113-1116. | 7.2 | 45 |

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|----|--|-----|-----------|
| 19 | 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 |
| 20 | <i>IL21R</i> expressing CD14 ⁺ CD16 ⁺ monocytes expand in multiple myeloma patients leading to increased osteoclasts. <i>Haematologica</i> , 2017, 102, 773-784. | 3.5 | 36 |
| 21 | Replacement of miR-155 Elicits Tumor Suppressive Activity and Antagonizes Bortezomib Resistance in Multiple Myeloma. <i>Cancers</i> , 2019, 11, 236. | 3.7 | 35 |
| 22 | A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. <i>Scientific Reports</i> , 2018, 8, 6557. | 3.3 | 34 |
| 23 | 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 |
| 24 | 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 |
| 25 | LncRNA NEAT1 in Paraspeckles: A Structural Scaffold for Cellular DNA Damage Response Systems?. <i>Non-coding RNA</i> , 2020, 6, 26. | 2.6 | 27 |
| 26 | Long non-coding RNAs in B-cell malignancies: a comprehensive overview. <i>Oncotarget</i> , 2017, 8, 60605-60623. | 1.8 | 25 |
| 27 | 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 |
| 28 | 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 |
| 29 | Long Non-Coding RNAs in Multiple Myeloma. <i>Genes</i> , 2018, 9, 69. | 2.4 | 22 |
| 30 | In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. <i>Genes</i> , 2016, 7, 107. | 2.4 | 17 |
| 31 | Mechanisms of Immune Evasion in Multiple Myeloma: Open Questions and Therapeutic Opportunities. <i>Cancers</i> , 2021, 13, 3213. | 3.7 | 16 |
| 32 | Repetitive DNA Hypomethylation in Multiple Myeloma. <i>Blood</i> , 2008, 112, 2703-2703. | 1.4 | 16 |
| 33 | 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 |
| 34 | DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. <i>Haematologica</i> , 2022, 107, 921-932. | 3.5 | 14 |
| 35 | 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 |
| 36 | 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 |

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|----|---|-----|-----------|
| 37 | 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 |
| 38 | 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 |
| 39 | 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 |
| 40 | Expression Pattern and Biological Significance of the lncRNA ST3GAL6-AS1 in Multiple Myeloma. <i>Cancers</i> , 2020, 12, 782. | 3.7 | 6 |
| 41 | In Vitro Silencing of lncRNAs Using LNA GapmeRs. <i>Methods in Molecular Biology</i> , 2021, 2348, 157-166. | 0.9 | 5 |
| 42 | 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 |
| 43 | Clinical relevance of p53 and bcl-2 protein overexpression in laryngeal squamous cell carcinoma. <i>International Journal of Cancer</i> , 1998, 79, 263-268. | 5.1 | 2 |
| 44 | Lack of Bcl10 gene mutations in laryngeal squamous cell carcinoma. <i>Journal of Laryngology and Otology</i> , 2002, 116, 610-612. | 0.8 | 1 |
| 45 | Bioinformatics Pipeline to Analyze lncRNA Arrays. <i>Methods in Molecular Biology</i> , 2021, 2348, 45-53. | 0.9 | 1 |
| 46 | 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 |
| 47 | 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 |
| 48 | Dissecting the Biological Relevance and Clinical Impact of lncRNA MIAT in Multiple Myeloma. <i>Cancers</i> , 2021, 13, 5518. | 3.7 | 0 |