Marta Lionetti

List of Publications by Year in descending order

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567281 501196 34 806 15 28 citations h-index g-index papers 34 34 34 1460 docs citations times ranked citing authors all docs

#	Article	IF	CITATIONS
1	The Dynamics of Nucleotide Variants in the Progression from Low–Intermediate Myeloma Precursor Conditions to Multiple Myeloma: Studying Serial Samples with a Targeted Sequencing Approach. Cancers, 2022, 14, 1035.	3.7	O
2	MGUS and clonal hematopoiesis show unrelated clinical and biological trajectories in an older population cohort. Blood Advances, 2022, 6, 5702-5706.	5.2	3
3	Clinical, Morphological and Clonal Progression of VEXAS Syndrome in the Context of Myelodysplasia Treated with Azacytidine. Clinical Hematology International, 2022, 4, 52-55.	1.7	7
4	Genomics of Smoldering Multiple Myeloma: Time for Clinical Translation of Findings?. Cancers, 2021, 13, 3319.	3.7	2
5	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. Clinical Cancer Research, 2021, 27, 6479-6490.	7.0	9
6	Transcriptomic Analysis in Multiple Myeloma and Primary Plasma Cell Leukemia with $t(11;14)$ Reveals Different Expression Patterns with Biological Implications in Venetoclax Sensitivity. Cancers, 2021, 13, 4898.	3.7	8
7	Time to first treatment and P53 dysfunction in chronic lymphocytic leukaemia: results of the O-CLL1 study in early stage patients. Scientific Reports, 2020, 10, 18427.	3.3	13
8	Limits and Applications of Genomic Analysis of Circulating Tumor DNA as a Liquid Biopsy in Asymptomatic Forms of Multiple Myeloma. HemaSphere, 2020, 4, e402.	2.7	15
9	Application of Next-Generation Sequencing for the Genomic Characterization of Patients with Smoldering Myeloma. Cancers, 2020, 12, 1332.	3.7	7
10	Frequency and clinical relevance of coding and noncoding <i>NOTCH1</i> mutations in early stage Binet A chronic lymphocytic leukemia patients. Hematological Oncology, 2020, 38, 406-408.	1.7	5
11	Revealing Transcriptome Deregulation upon Genomic Complexity in Multiple Myeloma. Blood, 2020, 136, 3-4.	1.4	O
12	Circulating tumor DNA as a liquid biopsy in plasma cell dyscrasias. Haematologica, 2018, 103, e245-e248.	3.5	29
13	Global methylation patterns in primary plasma cell leukemia. Leukemia Research, 2018, 73, 95-102.	0.8	13
14	Utilizing next-generation sequencing in the management of multiple myeloma. Expert Review of Molecular Diagnostics, 2017, 17, 653-663.	3.1	28
15	Compendium of <i><scp>FAM</scp>46C</i> gene mutations in plasma cell dyscrasias. British Journal of Haematology, 2016, 174, 642-645.	2.5	34
16	Prospective validation of predictive value of abdominal computed tomography scan on time to first treatment in Rai O chronic lymphocytic leukemia patients: results of the multicenter Oâ€ <scp>CLL</scp> 1â€ <scp>GISL</scp> study. European Journal of Haematology, 2016, 96, 36-45.	2.2	7
17	Primary plasma cell leukemia 2.0: advances in biology and clinical management. Expert Review of Hematology, 2016, 9, 1063-1073.	2.2	15
18	Molecular spectrum of <i>TP53</i> mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. Oncotarget, 2016, 7, 21353-21361.	1.8	40

#	Article	IF	Citations
19	Long non-coding RNAs in normal and malignant hematopoiesis. Oncotarget, 2016, 7, 50666-50681.	1.8	50
20	Molecular Classification and Pharmacogenetics of Primary Plasma Cell Leukemia: An Initial Approach toward Precision Medicine. International Journal of Molecular Sciences, 2015, 16, 17514-17534.	4.1	23
21	Whole-exome sequencing of primary plasma cell leukemia discloses heterogeneous mutational patterns. Oncotarget, 2015, 6, 17543-17558.	1.8	55
22	Association between gene and miRNA expression profiles and stereotyped subset #4 B-cell receptor in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2015, 56, 3150-3158.	1.3	23
23	Insulin Growth Factor 1 Receptor Expression Is Associated with NOTCH1 Mutation, Trisomy 12 and Aggressive Clinical Course in Chronic Lymphocytic Leukaemia. PLoS ONE, 2015, 10, e0118801.	2.5	15
24	Molecular spectrum of <i>BRAF, NRAS</i> and <i>KRAS</i> gene mutations in plasma cell dyscrasias: implication for MEK-ERK pathway activation. Oncotarget, 2015, 6, 24205-24217.	1.8	65
25	A compendium of <i>DIS3</i> mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	1.8	40
26	Genomeâ€wide analysis of primary plasma cell leukemia identifies recurrent imbalances associated with changes in transcriptional profiles. American Journal of Hematology, 2013, 88, 16-23.	4.1	60
27	Transcriptional Characterization of a Prospective Series of Primary Plasma Cell Leukemia Revealed Signatures Associated with Tumor Progression and Poorer Outcome. Clinical Cancer Research, 2013, 19, 3247-3258.	7.0	50
28	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. Clinical Cancer Research, 2013, 19, 3130-3142.	7.0	86
29	MicroRNAs in the Pathobiology of Multiple Myeloma. Current Cancer Drug Targets, 2012, 12, 823-837.	1.6	44
30	B-Cell Receptor Configuration and Adverse Cytogenetics Are Associated with Autoimmune Hemolytic Anemia in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 1780-1780.	1.4	0
31	The Expression Pattern of Small Nucleolar and Small Cajal Body-Specific RNAs Characterizes Distinct Molecular Subtypes of Multiple Myeloma. Blood, 2012, 120, 3955-3955.	1.4	0
32	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. Blood, 2011, 118, 2847-2847.	1.4	0
33	Integrative highâ€resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. Genes Chromosomes and Cancer, 2009, 48, 521-531.	2.8	60
34	Biological and Clinical Relevance of Surrogate Markers of IgVH Mutational Status in B-Cell Chronic Lymphocytic Leukemia Blood, 2008, 112, 1062-1062.	1.4	0