

Fabio Mirabella

List of Publications by Year in descending order

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Version: 2024-02-01

22
papers

1,241
citations

687363
13
h-index

794594
19
g-index

22
all docs

22
docs citations

22
times ranked

2672
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. <i>Journal of Clinical Oncology</i> , 2015, 33, 3911-3920.	1.6	463
2	Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. <i>Leukemia</i> , 2014, 28, 384-390.	7.2	252
3	Selective FLT3 inhibition of FLT3-ITD+ acute myeloid leukaemia resulting in secondary D835Y mutation: a model for emerging clinical resistance patterns. <i>Leukemia</i> , 2012, 26, 1462-1470.	7.2	105
4	Overexpression of EZH2 in multiple myeloma is associated with poor prognosis and dysregulation of cell cycle control. <i>Blood Cancer Journal</i> , 2017, 7, e549-e549.	6.2	81
5	Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , 2013, 162, 348-359.	2.5	53
6	HSF1 Is Essential for Myeloma Cell Survival and A Promising Therapeutic Target. <i>Clinical Cancer Research</i> , 2018, 24, 2395-2407.	7.0	46
7	MMSET is the key molecular target in t(4;14) myeloma. <i>Blood Cancer Journal</i> , 2013, 3, e114-e114.	6.2	40
8	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , 2019, 9, 1.	6.2	40
9	Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. <i>Nature Communications</i> , 2016, 7, 13656.	12.8	32
10	Hsp70 inhibition induces myeloma cell death via the intracellular accumulation of immunoglobulin and the generation of proteotoxic stress. <i>Cancer Letters</i> , 2013, 339, 49-59.	7.2	31
11	A Conserved Insulator That Recruits CTCF and Cohesin Exists between the Closely Related but Divergently Regulated Interleukin-3 and Granulocyte-Macrophage Colony-Stimulating Factor Genes. <i>Molecular and Cellular Biology</i> , 2009, 29, 1682-1693.	2.3	28
12	The Human IL-3/Granulocyte-Macrophage Colony-Stimulating Factor Locus Is Epigenetically Silent in Immature Thymocytes and Is Progressively Activated during T Cell Development. <i>Journal of Immunology</i> , 2010, 184, 3043-3054.	0.8	28
13	Understanding the interplay between the proteasome pathway and autophagy in response to dual PI3K/mTOR inhibition in myeloma cells is essential for their effective clinical application. <i>Leukemia</i> , 2013, 27, 2397-2403.	7.2	22
14	The Inducible Tissue-Specific Expression of the Human IL-3/GM-CSF Locus Is Controlled by a Complex Array of Developmentally Regulated Enhancers. <i>Journal of Immunology</i> , 2012, 189, 4459-4469.	0.8	9
15	A Novel Functional Role for MMSET in RNA Processing Based on the Link Between the REIIBP Isoform and Its Interaction with the SMN Complex. <i>PLoS ONE</i> , 2014, 9, e99493.	2.5	5
16	Inhibition of the Epigenetic Modifier EZH2 Upregulates Cell Cycle Control Genes to Inhibit Myeloma Cell Growth and Overcome High-Risk Disease Features. <i>Blood</i> , 2016, 128, 3289-3289.	1.4	2
17	Identifying Ultra-High Risk Myeloma By Integrated Molecular Genetic and Gene Expression Profiling. <i>Blood</i> , 2016, 128, 4407-4407.	1.4	2
18	Mutational Patterns and Copy Number Changes at Diagnosis Are a Powerful Tool to Predict Outcome: Result of the Sequencing Study of 463 Newly Diagnosed Myeloma Trial Patients. <i>Blood</i> , 2014, 124, 637-637.	1.4	1

#	ARTICLE	IF	CITATIONS
19	DNA Methylation Profiling of Myeloma Trial Patients Reveals Specific Epigenetic Changes Associated with Outcome. Blood, 2016, 128, 804-804.	1.4	1
20	Prior epigenetic priming of cytokine genes in naive T cells is required for their subsequent activation by inducible enhancers. Epigenetics and Chromatin, 2013, 6, .	3.9	0
21	High-Resolution, Genome Wide Analysis of DNA Methylation Provides Insights Into the Epigenetic Architecture of t(4;14) Myeloma.. Blood, 2012, 120, 2385-2385.	1.4	0
22	Discovery Of Genome Wide Epigenetic Programming In t(4;14) Multiple Myeloma and In The Progression From Myeloma To Plasma Cell Leukemia Via Methyl Binding Domain Protein Capture and Sequencing. Blood, 2013, 122, 599-599.	1.4	0