

Marina Martello

List of Publications by Year in descending order

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73
papers

589
citations

840119

11
h-index

610482

24
g-index

74
all docs

74
docs citations

74
times ranked

1252
citing authors

#	ARTICLE	IF	CITATIONS
1	PET/CT Improves the Definition of Complete Response and Allows to Detect Otherwise Unidentifiable Skeletal Progression in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2015, 21, 4384-4390.	3.2	140
2	Integrative analysis of the genomic and transcriptomic landscape of double-refractory multiple myeloma. <i>Blood Advances</i> , 2020, 4, 830-844.	2.5	54
3	Hypoxia inducible factor-1 alpha as a therapeutic target in multiple myeloma. <i>Oncotarget</i> , 2014, 5, 1779-1792.	0.8	53
4	Therapeutic targeting of hypoxia and hypoxia-inducible factor 1 alpha in multiple myeloma. <i>Translational Research</i> , 2015, 165, 641-650.	2.2	47
5	Bortezomib and thalidomide induced peripheral neuropathy in multiple myeloma: clinical and molecular analyses of a phase 3 study. <i>American Journal of Hematology</i> , 2014, 89, 1085-1091.	2.0	45
6	Minimal Residual Disease Assessment Within the Bone Marrow of Multiple Myeloma: A Review of Caveats, Clinical Significance and Future Perspectives. <i>Frontiers in Oncology</i> , 2019, 9, 699.	1.3	43
7	The genetic and genomic background of multiple myeloma patients achieving complete response after induction therapy with bortezomib, thalidomide and dexamethasone (VTD). <i>Oncotarget</i> , 2016, 7, 9666-9679.	0.8	33
8	Next-Generation Sequencing for Clinical Management of Multiple Myeloma: Ready for Prime Time?. <i>Frontiers in Oncology</i> , 2020, 10, 189.	1.3	33
9	HIF-1 α inhibition blocks the cross talk between multiple myeloma plasma cells and tumor microenvironment. <i>Experimental Cell Research</i> , 2014, 328, 444-455.	1.2	27
10	A real world efficacy and safety analysis of combined carfilzomib, lenalidomide, and dexamethasone (KRd) in relapsed/refractory multiple myeloma. <i>Hematological Oncology</i> , 2021, 39, 41-50.	0.8	22
11	Clonal and subclonal TP53 molecular impairment is associated with prognosis and progression in multiple myeloma. <i>Blood Cancer Journal</i> , 2022, 12, 15.	2.8	14
12	Prognostic impact of serial measurements of serum-free light chain assay throughout the course of newly diagnosed multiple myeloma treated with bortezomib-based regimens. <i>Leukemia and Lymphoma</i> , 2016, 57, 2058-2064.	0.6	12
13	Molecular Remission After Bortezomib-Thalidomide-Dexamethasone Compared with Thalidomide-Dexamethasone as Consolidation Therapy Following Double Autologous Transplantation for Multiple Myeloma: Results of a Qualitative and Quantitative Analysis. <i>Blood</i> , 2010, 116, 861-861.	0.6	11
14	Correlation between eight-gene expression profiling and response to therapy of newly diagnosed multiple myeloma patients treated with thalidomide and dexamethasone incorporated into double autologous transplantation. <i>Annals of Hematology</i> , 2013, 92, 1271-1280.	0.8	10
15	Opposite activation of the Hedgehog pathway in CD138+ plasma cells and CD138 ⁺ CD19+ B cells identifies two subgroups of patients with multiple myeloma and different prognosis. <i>Leukemia</i> , 2016, 30, 1869-1876.	3.3	9
16	Droplet digital polymerase chain reaction for the assessment of disease burden in hairy cell leukemia. <i>Hematological Oncology</i> , 2022, 40, 58-63.	0.8	8
17	Current and emerging triplet combination therapies for relapsed and refractory multiple myeloma. <i>Expert Review of Hematology</i> , 2016, 9, 315-323.	1.0	5
18	Novel agent-based salvage autologous stem cell transplantation for relapsed multiple myeloma. <i>Annals of Hematology</i> , 2017, 96, 2071-2078.	0.8	4

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19	Disease-Specific Derangement of Circulating Endocannabinoids and N-Acylethanolamines in Myeloproliferative Neoplasms. <i>International Journal of Molecular Sciences</i> , 2020, 21, 3399.	1.8	4
20	Maintenance therapy with bortezomib and dexamethasone after autotransplantation for high-risk multiple myeloma. <i>Bone Marrow Transplantation</i> , 2020, 55, 1865-1867.	1.3	4
21	Treatment optimization for multiple myeloma: schedule-dependent synergistic cytotoxicity of pomalidomide and carfilzomib in <i>in vitro</i> and <i>ex vivo</i> models. <i>Haematologica</i> , 2018, 103, e602-e606.	1.7	2
22	HIF 1 Alpha: A Suitable Target for Multiple Myeloma. <i>Blood</i> , 2011, 118, 2901-2901.	0.6	2
23	The Poor Outcome of Multiple Myeloma (MM) Patients Carrying At Diagnosis Deleted TP53 and or Amplified MDM4 Might Be Related to the Deregulation of Genes Involved in Cell Cycle Control and DNA Damage Repair. <i>Blood</i> , 2012, 120, 1810-1810.	0.6	2
24	The Genomic and Transcriptomic Landscape of Double-Refractory Multiple Myeloma. <i>Blood</i> , 2019, 134, 3056-3056.	0.6	1
25	Negative Selective Pressure Exerted By Maintenance Therapy Promotes the Extinction of Sub-Clones Carrying High-Risk Lesions in Multiple Myeloma. <i>Blood</i> , 2019, 134, 1778-1778.	0.6	1
26	High Number of Copy Number Alterations and Over-Expression of Genes Involved in the Response Mechanisms to Genotoxic Stress Both Characterize Newly Diagnosed Multiple Myeloma (MM) Patients Carrying Amplified MDM4 and/or Deleted p53. <i>Blood</i> , 2011, 118, 3935-3935.	0.6	1
27	A Branching Evolution Model at Relapse Characterizes Multiple Myeloma Patients Who Responded to up-Front Combination Therapy Including New Drugs. <i>Blood</i> , 2016, 128, 2080-2080.	0.6	1
28	OAB-059: Towards a comprehensive multimodal minimal residual disease assessment in multiple myeloma: the role of circulating cell-free DNA to define the extent of disease spreading. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, S37.	0.2	1
29	Hedgehog Pathway Over Expression Identifies Myeloma Patients With Worse Prognosis. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2015, 15, e38.	0.2	0
30	Evolutionary Fitness of Relapsed Multiple Myeloma Patients Who Responded to Upfront Combination Therapy Including New Drugs. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2017, 17, e12.	0.2	0
31	A More Mature Immunophenotypic Make-up of Multiple Myeloma Clone(s) at Diagnosis Correlates With a Higher Genomic Instability. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2017, 17, e11-e12.	0.2	0
32	Rare, but complex chromosomal rearrangements, defined "Chromoanagenesis", caused by single-step or stepwise catastrophic genomic events, significantly impact on Multiple Myeloma patients. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e78-e79.	0.2	0
33	Analysis of the genomic and transcriptomic landscape of chemoresistant multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e58-e59.	0.2	0
34	VarianThinker: a classification method to confidently approach the mutation heterogeneity in Multiple Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e72-e73.	0.2	0
35	PF560 A MATURATION INDEX DEFINES NEWLY DIAGNOSED MULTIPLE MYELOMA PATIENTS WITH ADVANCED IMMUNOPHENOTYPIC AND MOLECULAR DIFFERENTIATION PROFILES ASSOCIATED WITH POOR PROGNOSIS. <i>HemaSphere</i> , 2019, 3, 232.	1.2	0
36	A Maturation Index defines Newly Diagnosed Multiple Myeloma Patients with advanced immunophenotypic and Molecular Differentiation profiles associated with poor prognosis. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e69-e70.	0.2	0

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37	Abstract B53: Evaluation of HIF-1 α mRNA inhibitor as antimultiple myeloma agent. , 2011, , .		0
38	A 41-Gene Signature Predicts Complete Response (CR) to Bortezomib-Thalidomide-Dexamethasone (VTD) As Induction Therapy Prior to Autologous Stem-Cell Transplantation (ASCT) in Multiple Myeloma (MM). Blood, 2011, 118, 805-805.	0.6	0
39	Abstract 1873: Gene expression analysis of newly diagnosed Multiple Myeloma (MM) patients carrying amplifiedMDM4and/or deletedp53. , 2012, , .		0
40	SIRT Regulates the Molecular Interaction Between c-MYC and HIF-1 α in Multiple Myeloma. Blood, 2012, 120, 574-574.	0.6	0
41	Abstract 3749: Genomic characterization of the putative myeloma stem cells clone reveals alterations possibly correlated with the origin of disease.. , 2013, , .		0
42	Abstract 2207: A 41-gene signature predicts complete response (CR) to Bortezomib-Thalidomide-Dexamethasone (VTD) as induction therapy prior to autologous stem-cell transplantation (ASCT) in multiple myeloma (MM).. , 2013, , .		0
43	Abstract 3415: SIRT regulates the molecular interaction between c-MYC and HIF-1 α in multiple myeloma.. , 2013, , .		0
44	Impact Of p53 Impaired Function On Outcomes Of Multiple Myeloma Patients Carrying Deleted TP53 and/Or Amplified MDM4. Blood, 2013, 122, 1855-1855.	0.6	0
45	Abstract 3608: HIF-1 α inhibition blocks the cross talk between multiple myeloma plasmacells and tumour microenvironment. , 2014, , .		0
46	Abstract 3884: Gene expression profiling and copy number alterations of circulating clonotypic B cells of multiple myeloma newly diagnosed patients reveals pathways potentially involved in the development and in the disease persistence. , 2014, , .		0
47	Abstract 5595: Impact of p53 impaired function on outcomes of multiple myeloma patients carrying deleted TP53 and/or amplified MDM4. , 2014, , .		0
48	High-Throughput Molecular Profiling of Multiple Myeloma (MM) Clonotypic CD19+ B Cells Highlights Pathways Potentially Involved in the Disease Endurance. Blood, 2014, 124, 2054-2054.	0.6	0
49	Virtual Karyotype Reconstruction By SNPs Array of Newly Diagnosed Multiple Myeloma (MM) Patients Enrolled in the EMN02 Clinical Trial. Blood, 2014, 124, 2033-2033.	0.6	0
50	A Long Tail of Sub-Clonal TP53 Mutations Emerged By Ultra-Deep Sequencing of Newly Diagnosed Multiple Myeloma (MM). Blood, 2014, 124, 3400-3400.	0.6	0
51	Abstract 4248: A long tail of sub-clonal TP53 mutations emerged by ultra-deep sequencing of newly diagnosed multiple myeloma (MM). , 2015, , .		0
52	Abstract 1521: High-throughput molecular profiling of Multiple Myeloma clonotypic CD19+ B cells highlights pathways potentially involved in the disease endurance. , 2015, , .		0
53	The Alternate Activation of Hedgehog Pathway, Either in CD138+ or in CD138-CD19+ Multiple Myeloma Primary Cells, Impacts on Disease Outcome. Blood, 2015, 126, 2961-2961.	0.6	0
54	An Amplicon-Targeted Ultra-Deep Sequencing Approach Reveals the Presence at the Onset of Multiple Myeloma and the Selection over Time of TP53 Sub-Clonal Variants, Which Adversely Influence Patients' Overall Survival. Blood, 2015, 126, 24-24.	0.6	0

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55	Abstract 3189: The alternate activation of hedgehog pathway, either in CD138+ or in CD138-CD19+ multiple myeloma primary cells, impacts on disease outcome. , 2016, , .		0
56	Abstract 5022: The selection of TP53 sub-clonal variants over time identifies MM patients with adverse clinical outcome. , 2016, , .		0
57	Abstract 3936: A branching evolution model at relapse characterizes multiple myeloma patients who responded to upfront combination therapy including new drugs. , 2017, , .		0
58	Abstract 1758: A more mature immunophenotypic makeup of multiple myeloma clone(s) at diagnosis correlates with a higher genomic instability. , 2017, , .		0
59	Abstract 2176: Whole-genome analysis of CNAs identifies four main evolution trajectories in multiple myeloma (MM) patients front-line treated with PI-based regimens. , 2018, , .		0
60	Abstract 3387: The pliancy of plasma cell differentiation status conceals a gradient of chromosomal instability in newly diagnosed multiple myeloma patients. , 2018, , .		0
61	PS1346 CLONAL EVOLUTION IN MULTIPLE MYELOMA PATIENTS RECEIVING MAINTENANCE THERAPY. HemaSphere, 2019, 3, 615.	1.2	0
62	Abstract 473: Higher levels of genomic complexity correlates with an advanced plasma cell differentiation status in newly diagnosed multiple myeloma patients. , 2019, , .		0
63	Abstract 470: Chromosomal instability and bad prognosis both connote a multiple myeloma (MM) sub-type carrying 13qCN loss and 1qCN gain. , 2019, , .		0
64	A Maturation Index Defines Newly Diagnosed Multiple Myeloma Patients with Advanced Immunophenotypic and Molecular Differentiation Profiles Associated with Poor Prognosis. Blood, 2019, 134, 1797-1797.	0.6	0
65	Inter-Cell Networking Profiling Enables Comprehensive Characterization of Immune-Mediated Activity of Anti-CD38 Therapy through Ex-Vivo Analysis of Multiple Myeloma Patients. Blood, 2019, 134, 3372-3372.	0.6	0
66	Abstract 2700: Negative selective pressure exerted by maintenance therapy promotes the extinction of sub-clones carrying high-risk lesions in multiple myeloma. , 2020, , .		0
67	P-036: Implementation of IgH/k Next Generation Sequencing for Multiple Myeloma Minimal Residual Disease monitoring: advantages in patientsâ€™ management during daily clinical practice.. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S58.	0.2	0
68	P-053: BoBafit: a Copy Number-clustering tool to refit and recalibrate the diploid region of Multiple Myeloma genomic profiles. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S67.	0.2	0
69	OAB-006: A novel algorithm to identify, characterize and define the prognostic impact of complex catastrophic events in Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S4-S5.	0.2	0
70	OAB-057: Temporal-weight estimation of the copy number alterations of of 1384 Multiple Myeloma patients defines an ancestry index impacting patients survival. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, S35-S36.	0.2	0
71	Abstract 470: Chromosomal instability and bad prognosis both connote a multiple myeloma (MM) sub-type carrying 13qCN loss and 1qCN gain. , 2019, , .		0
72	Abstract 473: Higher levels of genomic complexity correlates with an advanced plasma cell differentiation status in newly diagnosed multiple myeloma patients. , 2019, , .		0

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73	: A copy number clustering tool designed to refit and recalibrate the baseline region of tumorsâ€™ profiles. Computational and Structural Biotechnology Journal, 2022, 20, 3718-3728.	1.9	0