

Francesco Maura

List of Publications by Year in descending order

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Version: 2024-02-01

69
papers

2,815
citations

257450

24
h-index

197818

49
g-index

85
all docs

85
docs citations

85
times ranked

4642
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	Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , 2022, 123, 115-123.	5.0	22
3	Defining genomic events involved in the evolutionary trajectories of myeloma and its precursor conditions. <i>Seminars in Oncology</i> , 2022, , .	2.2	1
4	Bayesian networks elucidate complex genomic landscapes in cancer. <i>Communications Biology</i> , 2022, 5, 306.	4.4	5
5	Whole-genome sequencing reveals complex genomic features underlying anti-CD19 CAR T-cell treatment failures in lymphoma. <i>Blood</i> , 2022, 140, 491-503.	1.4	32
6	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. <i>Blood Cancer Journal</i> , 2022, 12, .	6.2	7
7	Designing Evolutionary-based Interception Strategies to Block the Transition from Precursor Phases to Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 15-23.	7.0	20
8	Initial Whole-Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. <i>Clinical Cancer Research</i> , 2021, 27, 2111-2118.	7.0	5
9	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. <i>Nature Communications</i> , 2021, 12, 293.	12.8	54
10	Positive selection as the unifying force for clonal evolution in multiple myeloma. <i>Leukemia</i> , 2021, 35, 1511-1515.	7.2	10
11	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. <i>Nature Communications</i> , 2021, 12, 1861.	12.8	68
12	mmsig: a fitting approach to accurately identify somatic mutational signatures in hematological malignancies. <i>Communications Biology</i> , 2021, 4, 424.	4.4	21
13	Familial patterns of hematologic precursors. <i>Blood</i> , 2021, 137, 1992-1993.	1.4	0
14	The mutagenic impact of melphalan in multiple myeloma. <i>Leukemia</i> , 2021, 35, 2145-2150.	7.2	32
15	Dynamics of minimal residual disease in patients with multiple myeloma on continuous lenalidomide maintenance: a single-arm, single-centre, phase 2 trial. <i>Lancet Haematology</i> , 2021, 8, e422-e432.	4.6	50
16	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , 2021, , .	7.2	8
17	Safety and Effectiveness of Weekly Carfilzomib, Lenalidomide, Dexamethasone, and Daratumumab Combination Therapy for Patients With Newly Diagnosed Multiple Myeloma. <i>JAMA Oncology</i> , 2021, 7, 862.	7.1	63
18	Copy number signatures predict chromothripsis and clinical outcomes in newly diagnosed multiple myeloma. <i>Nature Communications</i> , 2021, 12, 5172.	12.8	27

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19	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 6479-6490.	7.0	9
20	<i><i>CDKN2A</i></i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). <i>Haematologica</i> , 2021, 106, 2918-2926.	3.5	18
21	Chemotherapy-Related Mutational Signatures Reveal the Origins of Therapy-Related Myeloid Neoplasms. <i>Blood</i> , 2021, 138, 3271-3271.	1.4	1
22	675â€¦Genomic drivers of large B-cell lymphoma resistance to CD19 CAR-T therapy. , 2021, 9, A703-A703.		0
23	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Though Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. <i>Blood</i> , 2021, 138, 805-805.	1.4	1
24	Combination Venetoclax and Selinexor Effective in Relapsed/Refractory Multiple Myeloma with Translocation t(11;14). <i>Blood</i> , 2021, 138, 2270-2270.	1.4	1
25	Role of AID in the temporal pattern of acquisition of driver mutations in multiple myeloma. <i>Leukemia</i> , 2020, 34, 1476-1480.	7.2	39
26	Moving From Cancer Burden to Cancer Genomics for Smoldering Myeloma. <i>JAMA Oncology</i> , 2020, 6, 425.	7.1	41
27	Accelerated single cell seeding in relapsed multiple myeloma. <i>Nature Communications</i> , 2020, 11, 3617.	12.8	41
28	Targeted genomic analysis of cutaneous T cell lymphomas identifies a subset with aggressive clinicopathological features. <i>Blood Cancer Journal</i> , 2020, 10, 116.	6.2	6
29	COVID-19 Infections and Clinical Outcomes in Patients with Multiple Myeloma in New York City: A Cohort Study from Five Academic Centers. <i>Blood Cancer Discovery</i> , 2020, 1, 234-243.	5.0	46
30	Baseline VDJ clonotype detection using a targeted sequencing NGS assay: allowing for subsequent MRD assessment. <i>Blood Cancer Journal</i> , 2020, 10, 76.	6.2	9
31	Revealing the Impact of Structural Variants in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020, 1, 258-273.	5.0	81
32	Early Relapse Risk in Patients with Newly Diagnosed Multiple Myeloma Characterized by Next-generation Sequencing. <i>Clinical Cancer Research</i> , 2020, 26, 4832-4841.	7.0	33
33	IgCaller for reconstructing immunoglobulin gene rearrangements and oncogenic translocations from whole-genome sequencing in lymphoid neoplasms. <i>Nature Communications</i> , 2020, 11, 3390.	12.8	24
34	Second malignancies in multiple myeloma; emerging patterns and future directions. <i>Best Practice and Research in Clinical Haematology</i> , 2020, 33, 101144.	1.7	27
35	Reconstructing the evolutionary history of multiple myeloma. <i>Best Practice and Research in Clinical Haematology</i> , 2020, 33, 101145.	1.7	21
36	Minimal spatial heterogeneity in chronic lymphocytic leukemia at diagnosis. <i>Leukemia</i> , 2020, 34, 1929-1933.	7.2	2

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37	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	21.4	275
38	Timing the initiation of multiple myeloma. <i>Nature Communications</i> , 2020, 11, 1917.	12.8	99
39	The mutational landscape of normal human endometrial epithelium. <i>Nature</i> , 2020, 580, 640-646.	27.8	338
40	Integrative analysis of the genomic and transcriptomic landscape of double-refractory multiple myeloma. <i>Blood Advances</i> , 2020, 4, 830-844.	5.2	54
41	Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive <i>versus</i> Stable Myeloma Precursor Disease. <i>Blood</i> , 2020, 136, 47-48.	1.4	2
42	Long-Term Sustained Minimal Residual Disease (MRD) Negativity in Patients with Multiple Myeloma Treated with Continuous Lenalidomide Maintenance Therapy: A Clinical and Correlative Phase 2 Study. <i>Blood</i> , 2020, 136, 18-19.	1.4	0
43	A Pilot Study Evaluating Lenalidomide and CC-486 in Combination with Radiotherapy for Patients with Plasmacytoma (LENAZART study). <i>Blood</i> , 2020, 136, 8-10.	1.4	0
44	Revealing Transcriptome Deregulation upon Genomic Complexity in Multiple Myeloma. <i>Blood</i> , 2020, 136, 3-4.	1.4	0
45	Weekly Carfilzomib, Lenalidomide, Dexamethasone and Daratumumab (wKRd-D) Combination Therapy in Newly Diagnosed Multiple Myeloma: Final Results from a Clinical and Correlative Phase 2 Study. <i>Blood</i> , 2020, 136, 7-7.	1.4	1
46	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , 2020, 136, 8-9.	1.4	2
47	The Genomic Complexity of Multiple Myeloma Precursor Disease Can be Predicted Using Copy Number Signatures on Targeted Sequencing and SNP Array Data. <i>Blood</i> , 2020, 136, 10-10.	1.4	1
48	Initial Whole Genome Sequencing of Plasma Cell Neoplasms in First Responders and Recovery Workers Exposed to the World Trade Center Attack of September 11, 2001. <i>Blood</i> , 2020, 136, 50-51.	1.4	0
49	Copy Number Signatures Predict Chromothripsis and Poor Clinical Outcome in Newly Diagnosed Multiple Myeloma Patients. <i>Blood</i> , 2020, 136, 52-53.	1.4	2
50	Duration of Post-Autologous Hematopoietic Cell Transplant Anemia and Thrombocytopenia Are Associated with Prolonged Hospital Length-of-Stay for Multiple Myeloma Patients. <i>Blood</i> , 2020, 136, 5-6.	1.4	0
51	A practical guide for mutational signature analysis in hematological malignancies. <i>Nature Communications</i> , 2019, 10, 2969.	12.8	145
52	Stability and uniqueness of clonal immunoglobulin CDR3 sequences for MRD tracking in multiple myeloma. <i>American Journal of Hematology</i> , 2019, 94, 1364-1373.	4.1	22
53	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	12.8	183
54	Integration of transcriptional and mutational data simplifies the stratification of peripheral T cell lymphoma. <i>American Journal of Hematology</i> , 2019, 94, 628-634.	4.1	16

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55	Timing the initiation of multiple myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e6-e7.	0.4	1
56	Comprehensive detection of recurring genomic abnormalities: a targeted sequencing approach for multiple myeloma. <i>Blood Cancer Journal</i> , 2019, 9, 101.	6.2	40
57	The Genomic and Transcriptomic Landscape of Double-Refractory Multiple Myeloma. <i>Blood</i> , 2019, 134, 3056-3056.	1.4	1
58	Long-Term Sustained Minimal Residual Disease (MRD) Negativity in Multiple Myeloma Patients Treated with Lenalidomide Maintenance Therapy: A Clinical and Correlative Phase 2 Study. <i>Blood</i> , 2019, 134, 3127-3127.	1.4	2
59	Weekly Carfilzomib, Lenalidomide, Dexamethasone and Daratumumab (wKRd-D) Combination Therapy Provides Unprecedented MRD Negativity Rates in Newly Diagnosed Multiple Myeloma: A Clinical and Correlative Phase 2 Study. <i>Blood</i> , 2019, 134, 862-862.	1.4	34
60	Revealing the Impact of Recurrent and Rare Structural Variations in Multiple Myeloma. <i>Blood</i> , 2019, 134, 576-576.	1.4	5
61	Using Current Clinical Markers to Define High Risk Smoldering Multiple Myeloma: Agree to Disagree. <i>Blood</i> , 2019, 134, 1794-1794.	1.4	0
62	Timing the Initiation of Multiple Myeloma. <i>Blood</i> , 2019, 134, 573-573.	1.4	0
63	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018, 173, 611-623.e17.	28.9	398
64	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. <i>Leukemia</i> , 2018, 32, 2604-2616.	7.2	137
65	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018, 9, 3363.	12.8	163
66	Whole Genome Sequencing Reveals Recurrent Structural Driver Events in Peripheral T-Cell Lymphomas Not Otherwise Specified. <i>Blood</i> , 2018, 132, 4115-4115.	1.4	0
67	Next-generation sequencing of a family with a high penetrance of monoclonal gammopathies for the identification of candidate risk alleles. <i>Cancer</i> , 2017, 123, 3701-3708.	4.1	12
68	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. <i>Blood</i> , 2011, 118, 2847-2847.	1.4	0
69	Timing the Initiation of Multiple Myeloma. <i>SSRN Electronic Journal</i> , 0, , .	0.4	4