

# Alessandro Lagana

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9894425/publications.pdf>

Version: 2024-02-01

43  
papers

1,118  
citations

516710

16  
h-index

414414

32  
g-index

47  
all docs

47  
docs citations

47  
times ranked

2113  
citing authors

#	ARTICLE	IF	CITATIONS
1	Discovery of a first-in-class EZH2 selective degrader. <i>Nature Chemical Biology</i> , 2020, 16, 214-222.	8.0	148
2	Neurocognitive and hypokinetic movement disorder with features of parkinsonism after BCMA-targeting CAR-T cell therapy. <i>Nature Medicine</i> , 2021, 27, 2099-2103.	30.7	92
3	A Critical Role for Fas-Mediated Off-Target Tumor Killing in T-cell Immunotherapy. <i>Cancer Discovery</i> , 2021, 11, 599-613.	9.4	90
4	A differentially expressed set of microRNAs in cerebro-spinal fluid (CSF) can diagnose CNS malignancies. <i>Oncotarget</i> , 2015, 6, 20829-20839.	1.8	89
5	MicroRNA-148a reduces tumorigenesis and increases TRAIL-induced apoptosis in NSCLC. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8650-8655.	7.1	86
6	Noncoding RNA: Current Deep Sequencing Data Analysis Approaches and Challenges. <i>Human Mutation</i> , 2016, 37, 1283-1298.	2.5	74
7	Mutation-derived Neoantigen-specific T-cell Responses in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2020, 26, 450-464.	7.0	62
8	miRandola 2017: a curated knowledge base of non-invasive biomarkers. <i>Nucleic Acids Research</i> , 2018, 46, D354-D359.	14.5	61
9	PDGFR-modulated miR-23b cluster and miR-125a-5p suppress lung tumorigenesis by targeting multiple components of KRAS and NF- $\kappa$ B pathways. <i>Scientific Reports</i> , 2017, 7, 15441.	3.3	49
10	Patient similarity network of newly diagnosed multiple myeloma identifies patient subgroups with distinct genetic features and clinical implications. <i>Science Advances</i> , 2021, 7, eabg9551.	10.3	49
11	microRNA editing in seed region aligns with cellular changes in hypoxic conditions. <i>Nucleic Acids Research</i> , 2016, 44, 6298-6308.	14.5	41
12	A phase 2 study of panobinostat with lenalidomide and weekly dexamethasone in myeloma. <i>Blood Advances</i> , 2017, 1, 1575-1583.	5.2	39
13	KRAS induces lung tumorigenesis through microRNAs modulation. <i>Cell Death and Disease</i> , 2018, 9, 219.	6.3	39
14	Quaking and miR-155 interactions in inflammation and leukemogenesis. <i>Oncotarget</i> , 2015, 6, 24599-24610.	1.8	37
15	A Network Analysis of Multiple Myeloma Related Gene Signatures. <i>Cancers</i> , 2019, 11, 1452.	3.7	23
16	Precision Medicine for Relapsed Multiple Myeloma on the Basis of an Integrative Multiomics Approach. <i>JCO Precision Oncology</i> , 2018, 2018, 1-17.	3.0	20
17	MiREDiBase, a manually curated database of validated and putative editing events in microRNAs. <i>Scientific Data</i> , 2021, 8, 199.	5.3	18
18	Computational Prediction of microRNA Targets. <i>Advances in Experimental Medicine and Biology</i> , 2015, 887, 231-252.	1.6	14

#	ARTICLE	IF	CITATIONS
19	A Phase II Study of Panobinostat with Lenalidomide and Weekly Dexamethasone in Myeloma. <i>Blood</i> , 2015, 126, 4226-4226.	1.4	14
20	MAGE-A inhibit apoptosis and promote proliferation in multiple myeloma through regulation of BIM and p21Cip1. <i>Oncotarget</i> , 2020, 11, 727-739.	1.8	12
21	A phase II study of pomalidomide, daily oral cyclophosphamide, and dexamethasone in relapsed/refractory multiple myeloma. <i>Leukemia and Lymphoma</i> , 2020, 61, 2208-2215.	1.3	7
22	A Three-Gene Signature Predicts Response to Selinexor in Multiple Myeloma. <i>JCO Precision Oncology</i> , 2022, , .	3.0	7
23	SOX11 Inhibitors Are Cytotoxic in Mantle Cell Lymphoma. <i>Clinical Cancer Research</i> , 2021, 27, 4652-4663.	7.0	6
24	Clinical Outcomes and Treatment Strategies for Relapsed/Refractory Myeloma Patients after Relapse on BCMA-Targeted CAR T. <i>Blood</i> , 2021, 138, 2704-2704.	1.4	6
25	Optimal Supportive Care With Selinexor Improves Outcomes in Patients With Relapsed/Refractory Multiple Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2021, 21, e975-e984.	0.4	5
26	Single-Cell Profiling Reveals Contribution of Tumor Extrinsic and Intrinsic Factors to BCMA-Targeted CAR-T Cell Efficacy in Multiple Myeloma. <i>Blood</i> , 2021, 138, 326-326.	1.4	5
27	Large-Scale Mass Cytometry Reveals Significant Activation of Innate and Adaptive Immunity in Bone Marrow Tumor Microenvironment of Ibrdomide-Treated Myeloma Patients. <i>Blood</i> , 2021, 138, 730-730.	1.4	4
28	MAGE-a Mediate Resistance to Chemotherapy in Multiple Myeloma through Regulation of Bcl-2 Proteins. <i>Blood</i> , 2016, 128, 3277-3277.	1.4	3
29	A Machine Learning Approach Identifies a 30-Gene Model That Predicts Sensitivity to Selinexor in Multiple Myeloma. <i>Blood</i> , 2019, 134, 3101-3101.	1.4	2
30	(Distinct) origins of IgM myeloma. <i>Blood</i> , 2021, 138, 1914-1915.	1.4	2
31	Pathogenic Germline Variants in Multiple Myeloma. <i>Blood</i> , 2021, 138, 399-399.	1.4	2
32	Editorial: Bioinformatics of Non-Coding RNAs with Applications to Biomedicine: Recent Advances and Open Challenges. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 156.	4.1	1
33	MicroRNA profiling of blastic plasmacytoid dendritic cell neoplasm and myeloid sarcoma. <i>Hematological Oncology</i> , 2020, 38, 831-833.	1.7	1
34	Integrative Network Analysis of Newly Diagnosed Multiple Myeloma Identifies a Novel RNA-Seq Based High Riskgene Signature. <i>Blood</i> , 2016, 128, 3285-3285.	1.4	1
35	Transcriptomic Correlates of Response to Selinexor in Multiple Myeloma Reveal a Predictive Signature. <i>Blood</i> , 2021, 138, 457-457.	1.4	1
36	Aberrant Cell Cycle Programming Confers Rapid Lethality in the EuSOX11+ CCND1 MCL Mouse Model. <i>Blood</i> , 2020, 136, 6-7.	1.4	1

#	ARTICLE	IF	CITATIONS
37	Continuous genomic monitoring of multiple myeloma patients to identify patients of high risk for poor prognosis.. Journal of Clinical Oncology, 2021, 39, e20035-e20035.	1.6	0
38	Towards a Network-Based Molecular Taxonomy of Newly Diagnosed Multiple Myeloma. Blood, 2015, 126, 840-840.	1.4	0
39	Aberrant a-to-I RNA Editing and Prognostic Impact of Adar in Multiple Myeloma Patients with 1q Amplification. Blood, 2016, 128, 357-357.	1.4	0
40	Mutation Burden in Multiple Myeloma Is Captured By Gene Expression Profiles. Blood, 2016, 128, 4450-4450.	1.4	0
41	MAGE-A3 Promotes Chemotherapy Resistance and Proliferation in Multiple Myeloma through Regulation of BIM and p21Cip1. Blood, 2018, 132, 4464-4464.	1.4	0
42	Development of a Neoantigen Prediction Tool for Patient Stratification in Immuno-Oncology Trials. Blood, 2018, 132, 2215-2215.	1.4	0
43	Title: Genomic and Systemic Metabolism Differences Associated with Racial Disparities in Multiple Myeloma. Blood, 2021, 138, 1601-1601.	1.4	0