

# Matteo Floris

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

2,288  
citations

346980

22  
h-index

263392

45  
g-index

55  
all docs

55  
docs citations

55  
times ranked

5161  
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-coding <i>scn</i> RNAs in malaria infection. <i>Wiley Interdisciplinary Reviews RNA</i> , 2022, 13, e1697.	3.2	11
2	Systematic identification of NF90 target RNAs by iCLIP analysis. <i>Scientific Reports</i> , 2022, 12, 364.	1.6	3
3	<i>PRF1</i> mutation alters immune system activation, inflammation, and risk of autoimmunity. <i>Multiple Sclerosis Journal</i> , 2021, 27, 1332-1340.	1.4	13
4	Peptidomimetics in Silico. <i>Molecular Informatics</i> , 2021, 40, e2000087.	1.4	5
5	Sex-Biased Expression of Pharmacogenes across Human Tissues. <i>Biomolecules</i> , 2021, 11, 1206.	1.8	5
6	A Deeper Insight into Evolutionary Patterns and Phylogenetic History of ASFV Epidemics in Sardinia (Italy) through Extensive Genomic Sequencing. <i>Viruses</i> , 2021, 13, 1994.	1.5	15
7	First Genomic Evidence of Dual African Swine Fever Virus Infection: Case Report from Recent and Historical Outbreaks in Sardinia. <i>Viruses</i> , 2021, 13, 2145.	1.5	4
8	Coexpression of CD163 and CD141 identifies human circulating IL-10-producing dendritic cells (DC-10). <i>Cellular and Molecular Immunology</i> , 2020, 17, 95-107.	4.8	54
9	African Swine Fever Circulation among Free-Ranging Pigs in Sardinia: Data from the Eradication Program. <i>Vaccines</i> , 2020, 8, 549.	2.1	25
10	Long Noncoding RNAs and Circular RNAs in Autoimmune Diseases. <i>Biomolecules</i> , 2020, 10, 1044.	1.8	75
11	Evolutionarily Selected Overexpression of the Cytokine BAFF Enhances Mucosal Immune Response Against <i>P. falciparum</i> . <i>Frontiers in Immunology</i> , 2020, 11, 575103.	2.2	4
12	Overview of the First 6 Months of Clinical Trials for COVID-19 Pharmacotherapy: The Most Studied Drugs. <i>Frontiers in Public Health</i> , 2020, 8, 497.	1.3	14
13	Complex genetic signatures in immune cells underlie autoimmunity and inform therapy. <i>Nature Genetics</i> , 2020, 52, 1036-1045.	9.4	153
14	A Sardinian founder mutation in glycoprotein Ib platelet subunit beta ( GP1BB ) that impacts thrombocytopenia. <i>British Journal of Haematology</i> , 2020, 191, e124-e128.	1.2	2
15	Histologic subtyping affecting outcome of triple negative breast cancer: a large Sardinian population-based analysis. <i>BMC Cancer</i> , 2020, 20, 491.	1.1	18
16	MTHFR, XRCC1 and OGG1 genetic polymorphisms in breast cancer: a case-control study in a population from North Sardinia. <i>BMC Cancer</i> , 2020, 20, 234.	1.1	16
17	The evolution of African swine fever virus in Sardinia (1978 to 2014) as revealed by whole genome sequencing and comparative analysis. <i>Transboundary and Emerging Diseases</i> , 2020, 67, 1971.	1.3	18
18	Direct-to-Consumer Nutrigenetics Testing: An Overview. <i>Nutrients</i> , 2020, 12, 566.	1.7	27

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19	Colorectal cancer-derived extracellular vesicles induce transformation of fibroblasts into colon carcinoma cells. <i>Journal of Experimental and Clinical Cancer Research</i> , 2019, 38, 257.	3.5	39
20	Genetic-Driven Druggable Target Identification and Validation. <i>Trends in Genetics</i> , 2018, 34, 558-570.	2.9	44
21	Molecular Similarity in Computational Toxicology. <i>Methods in Molecular Biology</i> , 2018, 1800, 171-179.	0.4	5
22	miRNA-135b Contributes to Triple Negative Breast Cancer Molecular Heterogeneity: Different Expression Profile in Basal-like Versus non-Basal-like Phenotypes. <i>International Journal of Medical Sciences</i> , 2018, 15, 536-548.	1.1	31
23	Clinical and pathological factors influencing survival in a large cohort of triple-negative breast cancer patients. <i>BMC Cancer</i> , 2018, 18, 56.	1.1	63
24	Overexpression of the Cytokine BAFF and Autoimmunity Risk. <i>New England Journal of Medicine</i> , 2017, 376, 1615-1626.	13.9	301
25	Fragment Prioritization on a Large Mutagenicity Dataset. <i>Molecular Informatics</i> , 2017, 36, 1600133.	1.4	10
26	Severe <i>Toxoplasma gondii</i> infection in a member of a NFKB2-deficient family with T and B cell dysfunction. <i>Clinical Immunology</i> , 2017, 183, 273-277.	1.4	32
27	In Silico 3D Modeling of Binding Activities. <i>Methods in Molecular Biology</i> , 2016, 1425, 23-35.	0.4	4
28	Height-reducing variants and selection for short stature in Sardinia. <i>Nature Genetics</i> , 2015, 47, 1352-1356.	9.4	96
29	A generalizable definition of chemical similarity for read-across. <i>Journal of Cheminformatics</i> , 2014, 6, 39.	2.8	75
30	BAT2 and BAT3 polymorphisms as novel genetic risk factors for rejection after HLA-related SCT. <i>Bone Marrow Transplantation</i> , 2014, 49, 1400-1404.	1.3	6
31	An alternative QSAR-based approach for predicting the bioconcentration factor for regulatory purposes. <i>ALTEX: Alternatives To Animal Experimentation</i> , 2014, 31, 23-36.	0.9	41
32	MMsDusty: an Alternative InChI-Based Tool to Minimize Chemical Redundancy. <i>Molecular Informatics</i> , 2013, 32, 681-684.	1.4	2
33	Implementing the "Best Template Searching" tool into Adenosiland platform. <i>In Silico Pharmacology</i> , 2013, 1, 25.	1.8	10
34	Genetic Variants Regulating Immune Cell Levels in Health and Disease. <i>Cell</i> , 2013, 155, 242-256.	13.5	295
35	Overlapping syndromes in laminopathies: a meta-analysis of the reported literature. <i>Acta Myologica</i> , 2013, 32, 7-17.	1.5	33
36	Adenosiland: Walking through adenosine receptors landscape. <i>European Journal of Medicinal Chemistry</i> , 2012, 58, 248-257.	2.6	29

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37	HLA-DRB1-DQB1 Haplotypes Confer Susceptibility and Resistance to Multiple Sclerosis in Sardinia. PLoS ONE, 2012, 7, e33972.	1.1	34
38	Mimicking Peptides in Silico. Molecular Informatics, 2012, 31, 12-20.	1.4	23
39	A A386G biallelic GPIbA gene mutation with anomalous behavior: a new mechanism suggested for Bernard-Soulier syndrome pathogenesis. Haematologica, 2011, 96, 1878-1882.	1.7	14
40	Aberrant splicing in the <i>LMNA</i> gene caused by a novel mutation on the polypyrimidine tract of intron 5. Muscle and Nerve, 2011, 43, 688-693.	1.0	10
41	ClickMD: an intuitive web-oriented molecular dynamics platform. Future Medicinal Chemistry, 2011, 3, 923-931.	1.1	4
42	Swimming into peptidomimetic chemical space using pepMMsMIMIC. Nucleic Acids Research, 2011, 39, W261-W269.	6.5	49
43	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. Bioinformatics, 2011, 27, 1625-1629.	1.8	12
44	Support Vector Machine (SVM) as Alternative Tool to Assign Acute Aquatic Toxicity Warning Labels to Chemicals. Molecular Informatics, 2010, 29, 51-64.	1.4	11
45	MMsINC: a large-scale chemoinformatics database. Nucleic Acids Research, 2009, 37, D284-D290.	6.5	71
46	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. BMC Genomics, 2009, 10, 601.	1.2	28
47	Splice-mediated Variants of Proteins (SpliVaP) – data and characterization of changes in signatures among protein isoforms due to alternative splicing. BMC Genomics, 2008, 9, 453.	1.2	8
48	MMsINC: A New Public Large-Scale Chemoinformatics Database System. , 2008, , .		1
49	The mepsMAP Server. Mapping Epitopes on Protein Surface: Mining Annotated Proteins. IEEE Transactions on Nanobioscience, 2007, 6, 155-161.	2.2	0
50	The MEPS server for identifying protein conformational epitopes. BMC Bioinformatics, 2007, 8, S6.	1.2	21
51	Recent Developments of the Chemistry Development Kit (CDK) - An Open-Source Java Library for Chemo- and Bioinformatics. Current Pharmaceutical Design, 2006, 12, 2111-2120.	0.9	418