

# Matteo Floris

## List of Publications by Year in descending order

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Version: 2024-02-01

51  
papers

2,288  
citations

304743  
22  
h-index

233421  
45  
g-index

55  
all docs

55  
docs citations

55  
times ranked

4685  
citing authors

#	ARTICLE	IF	CITATIONS
1	Non-coding <i>scRNA</i> s in malaria infection. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1697.	6.4	11
2	Systematic identification of NF90 target RNAs by iCLIP analysis. Scientific Reports, 2022, 12, 364.	3.3	3
3	<i>PRF1</i> mutation alters immune system activation, inflammation, and risk of autoimmunity. Multiple Sclerosis Journal, 2021, 27, 1332-1340.	3.0	13
4	Peptidomimetics in Silico. Molecular Informatics, 2021, 40, e2000087.	2.5	5
5	Sex-Biased Expression of Pharmacogenes across Human Tissues. Biomolecules, 2021, 11, 1206.	4.0	5
6	A Deeper Insight into Evolutionary Patterns and Phylogenetic History of ASFV Epidemics in Sardinia (Italy) through Extensive Genomic Sequencing. Viruses, 2021, 13, 1994.	3.3	15
7	First Genomic Evidence of Dual African Swine Fever Virus Infection: Case Report from Recent and Historical Outbreaks in Sardinia. Viruses, 2021, 13, 2145.	3.3	4
8	Coexpression of CD163 and CD141 identifies human circulating IL-10-producing dendritic cells (DC-10). Cellular and Molecular Immunology, 2020, 17, 95-107.	10.5	54
9	African Swine Fever Circulation among Free-Ranging Pigs in Sardinia: Data from the Eradication Program. Vaccines, 2020, 8, 549.	4.4	25
10	Long Noncoding RNAs and Circular RNAs in Autoimmune Diseases. Biomolecules, 2020, 10, 1044.	4.0	75
11	Evolutionarily Selected Overexpression of the Cytokine BAFF Enhances Mucosal Immune Response Against <i>P. falciparum</i> . Frontiers in Immunology, 2020, 11, 575103.	4.8	4
12	Overview of the First 6 Months of Clinical Trials for COVID-19 Pharmacotherapy: The Most Studied Drugs. Frontiers in Public Health, 2020, 8, 497.	2.7	14
13	Complex genetic signatures in immune cells underlie autoimmunity and inform therapy. Nature Genetics, 2020, 52, 1036-1045.	21.4	153
14	A Sardinian founder mutation in glycoprotein Ib platelet subunit beta ( GP1BB ) that impacts thrombocytopenia. British Journal of Haematology, 2020, 191, e124-e128.	2.5	2
15	Histologic subtyping affecting outcome of triple negative breast cancer: a large Sardinian population-based analysis. BMC Cancer, 2020, 20, 491.	2.6	18
16	MTHFR, XRCC1 and OGG1 genetic polymorphisms in breast cancer: a case-control study in a population from North Sardinia. BMC Cancer, 2020, 20, 234.	2.6	16
17	The evolution of African swine fever virus in Sardinia (1978 to 2014) as revealed by whole genome sequencing and comparative analysis. Transboundary and Emerging Diseases, 2020, 67, 1971.	3.0	18
18	Direct-to-Consumer Nutrigenetics Testing: An Overview. Nutrients, 2020, 12, 566.	4.1	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.	8.6	39
20	Genetic-Driven Druggable Target Identification and Validation. <i>Trends in Genetics</i> , 2018, 34, 558-570.	6.7	44
21	Molecular Similarity in Computational Toxicology. <i>Methods in Molecular Biology</i> , 2018, 1800, 171-179.	0.9	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.	2.5	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.	2.6	63
24	Overexpression of the Cytokine BAFF and Autoimmunity Risk. <i>New England Journal of Medicine</i> , 2017, 376, 1615-1626.	27.0	301
25	Fragment Prioritization on a Large Mutagenicity Dataset. <i>Molecular Informatics</i> , 2017, 36, 1600133.	2.5	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.	3.2	32
27	In Silico 3D Modeling of Binding Activities. <i>Methods in Molecular Biology</i> , 2016, 1425, 23-35.	0.9	4
28	Height-reducing variants and selection for short stature in Sardinia. <i>Nature Genetics</i> , 2015, 47, 1352-1356.	21.4	96
29	A generalizable definition of chemical similarity for read-across. <i>Journal of Cheminformatics</i> , 2014, 6, 39.	6.1	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.	2.4	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.	1.5	41
32	MMsDusty: an Alternative InChI-Based Tool to Minimize Chemical Redundancy. <i>Molecular Informatics</i> , 2013, 32, 681-684.	2.5	2
33	Implementing the "Best Template Searching" tool into Adenosiland platform. <i>In Silico Pharmacology</i> , 2013, 1, 25.	3.3	10
34	Genetic Variants Regulating Immune Cell Levels in Health and Disease. <i>Cell</i> , 2013, 155, 242-256.	28.9	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.	5.5	29

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37	HLA-DRB1-DQB1 Haplotypes Confer Susceptibility and Resistance to Multiple Sclerosis in Sardinia. PLoS ONE, 2012, 7, e33972.	2.5	34
38	Mimicking Peptidesâ€ In Silico. Molecular Informatics, 2012, 31, 12-20.	2.5	23
39	A A386G biallelic GPIbÂ gene mutation with anomalous behavior: a new mechanism suggested for Bernard-Soulier syndrome pathogenesis. Haematologica, 2011, 96, 1878-1882.	3.5	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.	2.2	10
41	ClickMD: an intuitive web-oriented molecular dynamics platform. Future Medicinal Chemistry, 2011, 3, 923-931.	2.3	4
42	Swimming into peptidomimetic chemical space using pepMMsMIMIC. Nucleic Acids Research, 2011, 39, W261-W269.	14.5	49
43	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. Bioinformatics, 2011, 27, 1625-1629.	4.1	12
44	Support Vector Machine (SVM) as Alternative Tool to Assign Acute Aquatic Toxicity Warning Labels to Chemicals. Molecular Informatics, 2010, 29, 51-64.	2.5	11
45	MMsINC: a large-scale chemoinformatics database. Nucleic Acids Research, 2009, 37, D284-D290.	14.5	71
46	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. BMC Genomics, 2009, 10, 601.	2.8	28
47	Splice-mediated Variants of Proteins (SpliVaP) â€“ data and characterization of changes in signatures among protein isoforms due to alternative splicing. BMC Genomics, 2008, 9, 453.	2.8	8
48	MMsINC&#x0AE;; 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.	3.3	0
50	The MEPS server for identifying protein conformational epitopes. BMC Bioinformatics, 2007, 8, S6.	2.6	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.	1.9	418