Matteo Floris

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9281510/publications.pdf

Version: 2024-02-01

304743 233421 2,288 51 22 45 citations h-index g-index papers 55 55 55 4685 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Recent Developments of the Chemistry Development Kit (CDK) - An Open-Source Java Library for Chemoand Bioinformatics. Current Pharmaceutical Design, 2006, 12, 2111-2120.	1.9	418
2	Overexpression of the Cytokine BAFF and Autoimmunity Risk. New England Journal of Medicine, 2017, 376, 1615-1626.	27.0	301
3	Genetic Variants Regulating Immune Cell Levels in Health and Disease. Cell, 2013, 155, 242-256.	28.9	295
4	Complex genetic signatures in immune cells underlie autoimmunity and inform therapy. Nature Genetics, 2020, 52, 1036-1045.	21.4	153
5	Height-reducing variants and selection for short stature in Sardinia. Nature Genetics, 2015, 47, 1352-1356.	21.4	96
6	A generalizable definition of chemical similarity for read-across. Journal of Cheminformatics, 2014, 6, 39.	6.1	75
7	Long Noncoding RNAs and Circular RNAs in Autoimmune Diseases. Biomolecules, 2020, 10, 1044.	4.0	75
8	MMsINC: a large-scale chemoinformatics database. Nucleic Acids Research, 2009, 37, D284-D290.	14.5	71
9	Clinical and pathological factors influencing survival in a large cohort of triple-negative breast cancer patients. BMC Cancer, 2018, 18, 56.	2.6	63
10	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
11	Swimming into peptidomimetic chemical space using pepMMsMIMIC. Nucleic Acids Research, 2011, 39, W261-W269.	14.5	49
12	Genetic-Driven Druggable Target Identification and Validation. Trends in Genetics, 2018, 34, 558-570.	6.7	44
13	An alternative QSAR-based approach for predicting the bioconcentration factor for regulatory purposes. ALTEX: Alternatives To Animal Experimentation, 2014, 31, 23-36.	1.5	41
14	Colorectal cancer-derived extracellular vesicles induce transformation of fibroblasts into colon carcinoma cells. Journal of Experimental and Clinical Cancer Research, 2019, 38, 257.	8.6	39
15	HLA-DRB1-DQB1 Haplotypes Confer Susceptibility and Resistance to Multiple Sclerosis in Sardinia. PLoS ONE, 2012, 7, e33972.	2.5	34
16	Overlapping syndromes in laminopathies: a meta-analysis of the reported literature. Acta Myologica, 2013, 32, 7-17.	1.5	33
17	Severe Toxoplasma gondii infection in a member of a NFKB2-deficient family with T and B cell dysfunction. Clinical Immunology, 2017, 183, 273-277.	3.2	32
18	miRNA-135b Contributes to <i>Triple Negative Breast Cancer</i> Molecular Heterogeneity: Different Expression Profile in <i>Basal-like</i> Versus <i>non-Basal-like</i> Phenotypes. International Journal of Medical Sciences, 2018, 15, 536-548.	2.5	31

#	Article	IF	CITATIONS
19	Adenosiland: Walking through adenosine receptors landscape. European Journal of Medicinal Chemistry, 2012, 58, 248-257.	5.5	29
20	Dissecting the dynamics of dysregulation of cellular processes in mouse mammary gland tumor. BMC Genomics, 2009, 10, 601.	2.8	28
21	Direct-to-Consumer Nutrigenetics Testing: An Overview. Nutrients, 2020, 12, 566.	4.1	27
22	African Swine Fever Circulation among Free-Ranging Pigs in Sardinia: Data from the Eradication Program. Vaccines, 2020, 8, 549.	4.4	25
23	Mimicking Peptides… In Silico. Molecular Informatics, 2012, 31, 12-20.	2.5	23
24	The MEPS server for identifying protein conformational epitopes. BMC Bioinformatics, 2007, 8, S6.	2.6	21
25	Histologic subtyping affecting outcome of triple negative breast cancer: a large Sardinian population-based analysis. BMC Cancer, 2020, 20, 491.	2.6	18
26	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
27	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
28	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
29	A A386G biallelic GPIb gene mutation with anomalous behavior: a new mechanism suggested for Bernard-Soulier syndrome pathogenesis. Haematologica, 2011, 96, 1878-1882.	3.5	14
30	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
31	<i>PRF1</i> mutation alters immune system activation, inflammation, and risk of autoimmunity. Multiple Sclerosis Journal, 2021, 27, 1332-1340.	3.0	13
32	MAISTAS: a tool for automatic structural evaluation of alternative splicing products. Bioinformatics, 2011, 27, 1625-1629.	4.1	12
33	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
34	Nonâ€coding <scp>RNAs</scp> in malaria infection. Wiley Interdisciplinary Reviews RNA, 2022, 13, e1697.	6.4	11
35	Aberrant splicing in the $\langle i \rangle$ LMNA $\langle i \rangle$ gene caused by a novel mutation on the polypyrimidine tract of intron 5. Muscle and Nerve, 2011, 43, 688-693.	2.2	10
36	Implementing the "Best Template Searching―tool into Adenosiland platform. In Silico Pharmacology, 2013, 1, 25.	3.3	10

#	Article	IF	Citations
37	Fragment Prioritization on a Large Mutagenicity Dataset. Molecular Informatics, 2017, 36, 1600133.	2.5	10
38	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.	2.8	8
39	BAT2 and BAT3 polymorphisms as novel genetic risk factors for rejection after HLA-related SCT. Bone Marrow Transplantation, 2014, 49, 1400-1404.	2.4	6
40	Molecular Similarity in Computational Toxicology. Methods in Molecular Biology, 2018, 1800, 171-179.	0.9	5
41	Peptidomimetics in Silico. Molecular Informatics, 2021, 40, e2000087.	2.5	5
42	Sex-Biased Expression of Pharmacogenes across Human Tissues. Biomolecules, 2021, 11, 1206.	4.0	5
43	ClickMD: an intuitive web-oriented molecular dynamics platform. Future Medicinal Chemistry, 2011, 3, 923-931.	2.3	4
44	In Silico 3D Modeling of Binding Activities. Methods in Molecular Biology, 2016, 1425, 23-35.	0.9	4
45	Evolutionarily Selected Overexpression of the Cytokine BAFF Enhances Mucosal Immune Response Against P. falciparum. Frontiers in Immunology, 2020, 11, 575103.	4.8	4
46	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
47	Systematic identification of NF90 target RNAs by iCLIP analysis. Scientific Reports, 2022, 12, 364.	3.3	3
48	MMsDusty: an Alternative InChlâ€Based Tool to Minimize Chemical Redundancy. Molecular Informatics, 2013, 32, 681-684.	2.5	2
49	A Sardinian founder mutation in glycoprotein lb platelet subunit beta (GP1BB) that impacts thrombocytopenia. British Journal of Haematology, 2020, 191, e124-e128.	2.5	2
50	MMsINC®: A New Public Large-Scale Chemoinformatics Database System. , 2008, , .		1
51	The mepsMAP Server. Mapping Epitopes on Protein Surface: Mining Annotated Proteins. IEEE Transactions on Nanobioscience, 2007, 6, 155-161.	3.3	0