

Vera Pancaldi

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

2,834
citations

394421

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243625

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71
all docs

71
docs citations

71
times ranked

7943
citing authors

#	ARTICLE	IF	CITATIONS
1	The antitumoral activity of TLR7 ligands is corrupted by the microenvironment of pancreatic tumors. <i>Molecular Therapy</i> , 2022, 30, 1553-1563.	8.2	3
2	OUP accepted manuscript. <i>Nucleic Acids Research</i> , 2021, 49, 11005-11021.	14.5	14
3	Mitochondrial metabolism supports resistance to IDH mutant inhibitors in acute myeloid leukemia. <i>Journal of Experimental Medicine</i> , 2021, 218, .	8.5	56
4	Low Replicative Stress Triggers Cell-Type Specific Inheritable Advanced Replication Timing. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4959.	4.1	3
5	Tysseandâ€™fast and accurate reconstruction of spatial networks from bioimages. <i>Bioinformatics</i> , 2021, 37, 3989-3991.	4.1	5
6	Community-wide hackathons to identify central themes in single-cell multi-omics. <i>Genome Biology</i> , 2021, 22, 220.	8.8	9
7	Activation of Vitamin D Receptor Pathway Enhances Differentiating Capacity in Acute Myeloid Leukemia with Isocitrate Dehydrogenase Mutations. <i>Cancers</i> , 2021, 13, 5243.	3.7	6
8	Chromatin Network Analyses: Towards Structure-Function Relationships in Epigenomics. <i>Frontiers in Bioinformatics</i> , 2021, 1, .	2.1	6
9	Abstract PO-043: Cytidine deaminase protects pancreatic cancer cells from replicative stress and drive response to DNA-targeting drugs. , 2021, , .		0
10	Supporting Clinical Decision-Making during the SARS-CoV-2 Pandemic through a Global Research Commitment: The TERA-VOLT Experience. <i>Cancer Cell</i> , 2020, 38, 602-604.	16.8	6
11	Eomes-Dependent Loss of the Co-activating Receptor CD226 Restrains CD8+ T Cell Anti-tumor Functions and Limits the Efficacy of Cancer Immunotherapy. <i>Immunity</i> , 2020, 53, 824-839.e10.	14.3	85
12	Chromatin network markers of leukemia. <i>Bioinformatics</i> , 2020, 36, i455-i463.	4.1	8
13	How Has the COVID-19 Pandemic Changed How You Will Approach Research and Lab Work in the Future?. <i>Cell Systems</i> , 2020, 11, 550-554.	6.2	0
14	Insights on TAM Formation from a Boolean Model of Macrophage Polarization Based on In Vitro Studies. <i>Cancers</i> , 2020, 12, 3664.	3.7	12
15	TERA-VOLT: Thoracic Cancers International COVID-19 Collaboration. <i>Cancer Cell</i> , 2020, 37, 742-745.	16.8	51
16	COVID-19 in patients with thoracic malignancies (TERA-VOLT): first results of an international, registry-based, cohort study. <i>Lancet Oncology</i> , The, 2020, 21, 914-922.	10.7	503
17	Interpreting molecular similarity between patients as a determinant of disease comorbidity relationships. <i>Nature Communications</i> , 2020, 11, 2854.	12.8	20
18	Using GARDEN-NET and ChAseR to explore human haematopoietic 3D chromatin interaction networks. <i>Nucleic Acids Research</i> , 2020, 48, 4066-4080.	14.5	18

#	ARTICLE	IF	CITATIONS
19	Unveiling new disease, pathway, and gene associations via multi-scale neural network. PLoS ONE, 2020, 15, e0231059.	2.5	18
20	CovMulNet19, Integrating Proteins, Diseases, Drugs, and Symptoms: A Network Medicine Approach to COVID-19. Network and Systems Medicine, 2020, 3, 130-141.	2.5	15
21	Thoracic Cancers International COVID-19 Collaboration (TERAVOLT): Impact of type of cancer therapy and COVID therapy on survival.. Journal of Clinical Oncology, 2020, 38, LBA1111-LBA1111.	1.6	34
22	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
23	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
24	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
25	Unveiling new disease, pathway, and gene associations via multi-scale neural network. , 2020, 15, e0231059.		0
26	ChiCMaxima: a robust and simple pipeline for detection and visualization of chromatin looping in Capture Hi-C. Genome Biology, 2019, 20, 102.	8.8	25
27	Molecular Inverse Comorbidity between Alzheimer's Disease and Lung Cancer: New Insights from Matrix Factorization. International Journal of Molecular Sciences, 2019, 20, 3114.	4.1	11
28	Transcriptomic metaanalyses of autistic brains reveals shared gene expression and biological pathway abnormalities with cancer. Molecular Autism, 2019, 10, 17.	4.9	30
29	Epigenetic and Transcriptional Variability Shape Phenotypic Plasticity. BioEssays, 2018, 40, 1700148.	2.5	71
30	Genome-wide analysis of differential transcriptional and epigenetic variability across human immune cell types. Genome Biology, 2017, 18, 18.	8.8	97
31	Automatic identification of informative regions with epigenomic changes associated to hematopoiesis. Nucleic Acids Research, 2017, 45, 9244-9259.	14.5	19
32	Integrating epigenomic data and 3D genomic structure with a new measure of chromatin assortativity. Genome Biology, 2016, 17, 152.	8.8	46
33	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	28.9	404
34	Genetic Drivers of Epigenetic and Transcriptional Variation in Human Immune Cells. Cell, 2016, 167, 1398-1414.e24.	28.9	573
35	Chromatin Regulators as a Guide for Cancer Treatment Choice. Molecular Cancer Therapeutics, 2016, 15, 1768-1777.	4.1	18
36	Abstract LB-129: Epigenetic regulators to predict docetaxel sensitivity; a guide for treatment choice. , 2016, , .		0

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37	AnGeLi: A Tool for the Analysis of Gene Lists from Fission Yeast. <i>Frontiers in Genetics</i> , 2015, 6, 330.	2.3	65
38	Whole-genome fingerprint of the DNA methylome during human B cell differentiation. <i>Nature Genetics</i> , 2015, 47, 746-756.	21.4	278
39	A Boolean gene regulatory model of heterosis and speciation. <i>BMC Evolutionary Biology</i> , 2015, 15, 24.	3.2	22
40	Higher gene expression variability in the more aggressive subtype of chronic lymphocytic leukemia. <i>Genome Medicine</i> , 2015, 7, 8.	8.2	57
41	Abstract LB-155: Epigenetic profiling of chemotherapy sensitivity. , 2015, , .		0
42	Biological noise to get a sense of direction: an analogy between chemotaxis and stress response. <i>Frontiers in Genetics</i> , 2014, 5, 52.	2.3	1
43	Systematic screen for mutants resistant to TORC1 inhibition in fission yeast reveals genes involved in cellular ageing and growth. <i>Biology Open</i> , 2014, 3, 161-171.	1.2	55
44	Characterization of the DNA Methylome during Human B-Cell Differentiation. <i>Blood</i> , 2014, 124, 4346-4346.	1.4	0
45	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , 2013, 9, 1697.	2.9	21
46	Predicting the Fission Yeast Protein Interaction Network. <i>G3: Genes, Genomes, Genetics</i> , 2012, 2, 453-467.	1.8	29
47	Topology of functional networks predicts physical binding of proteins. <i>Bioinformatics</i> , 2012, 28, 2137-2145.	4.1	5
48	A Gene Regulatory Network Simulation of Heterosis. <i>Lecture Notes in Computer Science</i> , 2012, , 12-16.	1.3	2
49	In silico characterization and prediction of global proteinâ€mRNA interactions in yeast. <i>Nucleic Acids Research</i> , 2011, 39, 5826-5836.	14.5	55
50	Meta-analysis of genome regulation and expression variability across hundreds of environmental and genetic perturbations in fission yeast. <i>Molecular BioSystems</i> , 2010, 6, 543-552.	2.9	36
51	Hierarchical coarse-graining transform. <i>Physical Review E</i> , 2009, 79, 036704.	2.1	2
52	Preface to the special issue â€Complexity in the Oil Industry 2007â€ Computational Geosciences, 2009, 13, 151-154.	2.4	0
53	Wavelet-based upscaling of advection equations. <i>Physica A: Statistical Mechanics and Its Applications</i> , 2008, 387, 4760-4770.	2.6	3
54	Permeability up-scaling using Haar Wavelets. <i>Transport in Porous Media</i> , 2007, 67, 395-412.	2.6	11

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55	Upscaling of the Saturation Equation. , 2007, , .		0