

Francesca Finotello

List of Publications by Year in descending order

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53
papers

8,032
citations

186265

28
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243625

44
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all docs

62
docs citations

62
times ranked

12128
citing authors

#	ARTICLE	IF	CITATIONS
1	Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. <i>Cell Reports</i> , 2017, 18, 248-262.	6.4	2,953
2	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. <i>Genome Medicine</i> , 2019, 11, 34.	8.2	732
3	Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. <i>Bioinformatics</i> , 2019, 35, i436-i445.	4.1	576
4	Global genomic and transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 13924-13929.	7.1	407
5	Quantifying tumor-infiltrating immune cells from transcriptomics data. <i>Cancer Immunology, Immunotherapy</i> , 2018, 67, 1031-1040.	4.2	292
6	Computational genomics tools for dissecting tumour-immune cell interactions. <i>Nature Reviews Genetics</i> , 2016, 17, 441-458.	16.3	233
7	Mitochondrial DNA drives abscopal responses to radiation that are inhibited by autophagy. <i>Nature Immunology</i> , 2020, 21, 1160-1171.	14.5	214
8	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016, 13, 310-318.	19.0	209
9	Targeting immune checkpoints potentiates immunoeediting and changes the dynamics of tumor evolution. <i>Nature Communications</i> , 2018, 9, 32.	12.8	193
10	Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. <i>Briefings in Functional Genomics</i> , 2015, 14, 130-142.	2.7	186
11	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. <i>Frontiers in Immunology</i> , 2017, 8, 1679.	4.8	171
12	Deviations of the immune cell landscape between healthy liver and hepatocellular carcinoma. <i>Scientific Reports</i> , 2018, 8, 6220.	3.3	155
13	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTIseq. <i>Methods in Enzymology</i> , 2020, 636, 261-285.	1.0	141
14	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018, 67, 1414-1427.	0.6	136
15	Next-generation computational tools for interrogating cancer immunity. <i>Nature Reviews Genetics</i> , 2019, 20, 724-746.	16.3	131
16	Immunedeconv: An R Package for Unified Access to Computational Methods for Estimating Immune Cell Fractions from Bulk RNA-Sequencing Data. <i>Methods in Molecular Biology</i> , 2020, 2120, 223-232.	0.9	120
17	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. <i>Bioinformatics</i> , 2020, 36, 4817-4818.	4.1	88
18	Neoantigen prediction and computational perspectives towards clinical benefit: recommendations from the ESMO Precision Medicine Working Group. <i>Annals of Oncology</i> , 2020, 31, 978-990.	1.2	87

#	ARTICLE	IF	CITATIONS
19	CD39 Identifies the CD4+ Tumor-Specific T-cell Population in Human Cancer. <i>Cancer Immunology Research</i> , 2020, 8, 1311-1321.	3.4	84
20	Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. <i>Bioinformatics</i> , 2017, 33, 3140-3141.	4.1	68
21	FunPat: function-based pattern analysis on RNA-seq time series data. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	63
22	New strategies for cancer immunotherapy: targeting regulatory T cells. <i>Genome Medicine</i> , 2017, 9, 10.	8.2	62
23	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019, 25, 7351-7362.	7.0	61
24	Measuring the diversity of the human microbiota with targeted next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2018, 19, bbw119.	6.5	58
25	Multi-Omics Profiling of the Tumor Microenvironment: Paving the Way to Precision Immuno-Oncology. <i>Frontiers in Oncology</i> , 2018, 8, 430.	2.8	57
26	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014, 15, S7.	2.6	51
27	Interpretable systems biomarkers predict response to immune-checkpoint inhibitors. <i>Patterns</i> , 2021, 2, 100293.	5.9	47
28	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018, 19, 343.	2.6	39
29	NeoFuse: predicting fusion neoantigens from RNA sequencing data. <i>Bioinformatics</i> , 2020, 36, 2260-2261.	4.1	32
30	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012, 13, 269-280.	6.5	23
31	<sc>NKG2A</sc> is a late immune checkpoint on <sc>CD8</sc> T cells and marks repeated stimulation and cell division. <i>International Journal of Cancer</i> , 2022, 150, 688-704.	5.1	22
32	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. <i>BMC Infectious Diseases</i> , 2013, 13, 554.	2.9	18
33	Hypoglycemia-induced EEG complexity changes in Type 1 diabetes assessed by fractal analysis algorithm. <i>Biomedical Signal Processing and Control</i> , 2017, 38, 168-173.	5.7	18
34	nextNEOpI: a comprehensive pipeline for computational neoantigen prediction. <i>Bioinformatics</i> , 2022, 38, 1131-1132.	4.1	17
35	CD161 expression and regulation defines rapidly responding effector CD4+ T cells associated with improved survival in HPV16-associated tumors. , 2022, 10, e003995.		16
36	Tumor-specific T cells support chemokine-driven spatial organization of intratumoral immune microaggregates needed for long survival. , 2022, 10, e004346.		15

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37	Stress-induced inflammation evoked by immunogenic cell death is blunted by the IRE1 β kinase inhibitor KIRA6 through HSP60 targeting. <i>Cell Death and Differentiation</i> , 2022, 29, 230-245.	11.2	12
38	EEG signal features extraction based on fractal dimension. , 2015, 2015, 4154-7.		10
39	A vision of immuno-oncology: the Siena think tank of the Italian network for tumor biotherapy (NIBIT) foundation. <i>Journal of Experimental and Clinical Cancer Research</i> , 2021, 40, 240.	8.6	3
40	Abstract CT059: Epigenetic tumor remodelling to improve the efficacy of immune checkpoint blockade: the NIBIT-M4 clinical trial. , 2018, , .		3
41	In Silico Prediction of Tumor Neoantigens with TIminer. <i>Methods in Molecular Biology</i> , 2020, 2120, 129-145.	0.9	3
42	In Silico Cell-Type Deconvolution Methods in Cancer Immunotherapy. <i>Methods in Molecular Biology</i> , 2020, 2120, 213-222.	0.9	3
43	Draft Genome Sequences of Two <i>Neisseria meningitidis</i> Serogroup C Clinical Isolates. <i>Journal of Bacteriology</i> , 2010, 192, 5270-5271.	2.2	2
44	Mo1791 Colonic Microbiota and Gene Methylation in Colonic Carcinogenesis. <i>Gastroenterology</i> , 2014, 146, S-1072.	1.3	2
45	Analysis of High-Throughput RNA Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2017, 1562, 143-154.	0.9	2
46	Editorial: Multi-omic Data Integration in Oncology. <i>Frontiers in Oncology</i> , 2020, 10, 1768.	2.8	2
47	A strategy to reduce technical variability and bias in RNA sequencing data. <i>EMBnet Journal</i> , 2012, 18, 65.	0.6	2
48	Mitochondrial DNA Drives Abscopal Responses to Radiation that are Inhibited by Autophagy. <i>SSRN Electronic Journal</i> , 0, , .	0.4	2
49	Predictive Systems Biomarkers of Response to Immune Checkpoint Inhibitors. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
50	Safety and immunobiological activity of guadecitabine sequenced with ipilimumab in metastatic melanoma patients: The phase Ib NIBIT-M4 study.. <i>Journal of Clinical Oncology</i> , 2019, 37, 2549-2549.	1.6	0
51	Abstract 666: A novel, highly selective PI3K β inhibitor for the treatment of solid malignancies that express high levels of target protein as assessed by immunohistochemistry. , 2020, , .		0
52	Abstract B60: Perturbation biology of colorectal cancer organoids reveals patient-specific signaling rewiring and interference with immunity. , 2020, , .		0
53	35 β ...Chemokine-driven spatial organization of immune cell microaggregates marks oropharyngeal squamous cell carcinomas containing tumor-specific T cells. , 2021, 9, A41-A41.		0