

Francesca Finotello

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

49
papers

3,655
citations

25
h-index

60
g-index

62
ext. papers

6,079
ext. citations

7.8
avg, IF

5.83
L-index

#	Paper	IF	Citations
49	CD161 expression and regulation defines rapidly responding effector CD4+ T cells associated with improved survival in HPV16-associated tumors. 2022 , 10,		3
48	35 Chemokine-driven spatial organization of immune cell microaggregates marks oropharyngeal squamous cell carcinomas containing tumor-specific T cells 2021 , 9, A41-A41		
47	NKG2A is a late immune checkpoint on CD8 T cells and marks repeated stimulation and cell division. <i>International Journal of Cancer</i> , 2021 ,	7.5	1
46	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	12.8	0
45	Interpretable systems biomarkers predict response to immune-checkpoint inhibitors. <i>Patterns</i> , 2021 , 2, 100293	5.1	4
44	Stress-induced inflammation evoked by immunogenic cell death is blunted by the IRE1 α kinase inhibitor KIRA6 through HSP60 targeting. <i>Cell Death and Differentiation</i> , 2021 ,	12.7	1
43	nextNEOpi: a comprehensive pipeline for computational neoantigen prediction. <i>Bioinformatics</i> , 2021 ,	7.2	1
42	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	10.3	29
41	In Silico Cell-Type Deconvolution Methods in Cancer Immunotherapy. <i>Methods in Molecular Biology</i> , 2020 , 2120, 213-222	1.4	
40	In Silico Prediction of Tumor Neoantigens with TIminer. <i>Methods in Molecular Biology</i> , 2020 , 2120, 129-145	1.4	1
39	NeoFuse: predicting fusion neoantigens from RNA sequencing data. <i>Bioinformatics</i> , 2020 , 36, 2260-2261	7.2	9
38	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. <i>Bioinformatics</i> , 2020 , 36, 4817-4818	7.2	28
37	CD39 Identifies the CD4 Tumor-Specific T-cell Population in Human Cancer. <i>Cancer Immunology Research</i> , 2020 , 8, 1311-1321	12.5	30
36	Mitochondrial DNA drives abscopal responses to radiation that are inhibited by autophagy. <i>Nature Immunology</i> , 2020 , 21, 1160-1171	19.1	94
35	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTIseq. <i>Methods in Enzymology</i> , 2020 , 636, 261-285	1.7	38
34	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	1.4	29
33	Next-generation computational tools for interrogating cancer immunity. <i>Nature Reviews Genetics</i> , 2019 , 20, 724-746	30.1	72

32	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. <i>Genome Medicine</i> , 2019 , 11, 34	14.4	243
31	Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. <i>Bioinformatics</i> , 2019 , 35, i436-i445	7.2	209
30	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	2.2	
29	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. <i>Clinical Cancer Research</i> , 2019 , 25, 7351-7362	12.9	33
28	Deviations of the immune cell landscape between healthy liver and hepatocellular carcinoma. <i>Scientific Reports</i> , 2018 , 8, 6220	4.9	99
27	Targeting immune checkpoints potentiates immunoediting and changes the dynamics of tumor evolution. <i>Nature Communications</i> , 2018 , 9, 32	17.4	104
26	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. <i>Diabetes</i> , 2018 , 67, 1414-1427	0.9	71
25	Quantifying tumor-infiltrating immune cells from transcriptomics data. <i>Cancer Immunology, Immunotherapy</i> , 2018 , 67, 1031-1040	7.4	164
24	Abstract CT059: Epigenetic tumor remodelling to improve the efficacy of immune checkpoint blockade: the NIBIT-M4 clinical trial 2018 ,		2
23	Measuring the diversity of the human microbiota with targeted next-generation sequencing. <i>Briefings in Bioinformatics</i> , 2018 , 19, 679-692	13.4	25
22	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. <i>BMC Bioinformatics</i> , 2018 , 19, 343	3.6	20
21	Multi-Omics Profiling of the Tumor Microenvironment: Paving the Way to Precision Immuno-Oncology. <i>Frontiers in Oncology</i> , 2018 , 8, 430	5.3	35
20	New strategies for cancer immunotherapy: targeting regulatory T cells. <i>Genome Medicine</i> , 2017 , 9, 10	14.4	35
19	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	4.9	14
18	Analysis of High-Throughput RNA Bisulfite Sequencing Data. <i>Methods in Molecular Biology</i> , 2017 , 1562, 143-154	1.4	0
17	Pan-cancer Immunogenomic Analyses Reveal Genotype-Immunophenotype Relationships and Predictors of Response to Checkpoint Blockade. <i>Cell Reports</i> , 2017 , 18, 248-262	10.6	1179
16	Tlminer: NGS data mining pipeline for cancer immunology and immunotherapy. <i>Bioinformatics</i> , 2017 , 33, 3140-3141	7.2	53
15	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. <i>Frontiers in Immunology</i> , 2017 , 8, 1679	8.4	113

14	Inferring causal molecular networks: empirical assessment through a community-based effort. <i>Nature Methods</i> , 2016 , 13, 310-8	21.6	158
13	Computational genomics tools for dissecting tumour-immune cell interactions. <i>Nature Reviews Genetics</i> , 2016 , 17, 441-58	30.1	172
12	Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. <i>Briefings in Functional Genomics</i> , 2015 , 14, 130-42	4.9	127
11	FunPat: function-based pattern analysis on RNA-seq time series data. <i>BMC Genomics</i> , 2015 , 16, S2	4.5	33
10	EEG signal features extraction based on fractal dimension. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , 2015 , 2015, 4154-7	0.9	4
9	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, 13924-9	11.5	297
8	Reducing bias in RNA sequencing data: a novel approach to compute counts. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 1, S7	3.6	23
7	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	4	17
6	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. <i>Briefings in Bioinformatics</i> , 2012 , 13, 269-80	13.4	21
5	A strategy to reduce technical variability and bias in RNA sequencing data. <i>EMBnet Journal</i> , 2012 , 18, 65	2.3	2
4	Draft genome sequences of two <i>Neisseria meningitidis</i> serogroup C clinical isolates. <i>Journal of Bacteriology</i> , 2010 , 192, 5270-1	3.5	2
3	Pan-cancer immunogenomic analyses reveal genotype-immunophenotype relationships and predictors of response to checkpoint blockade		30
2	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data		9
1	Comprehensive evaluation of computational cell-type quantification methods for immuno-oncology		3