Francesca Finotello

List of Publications by Year
in descending order

53 papers	8,032 citations	185998 28 h-index	243296 44 g-index
62 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. Cell Reports, 2017, 18, 248-262.	2.9	2,953
2	Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. Genome Medicine, 2019, 11, 34.	3.6	732
3	Comprehensive evaluation of transcriptome-based cell-type quantification methods for immuno-oncology. Bioinformatics, 2019, 35, i436-i445.	1.8	576
4	Global genomic and transcriptomic analysis of human pancreatic islets reveals novel genes influencing glucose metabolism. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 13924-13929.	3.3	407
5	Quantifying tumor-infiltrating immune cells from transcriptomics data. Cancer Immunology, Immunotherapy, 2018, 67, 1031-1040.	2.0	292
6	Computational genomics tools for dissecting tumourâ€"immune cell interactions. Nature Reviews Genetics, 2016, 17, 441-458.	7.7	233
7	Mitochondrial DNA drives abscopal responses to radiation that are inhibited by autophagy. Nature Immunology, 2020, 21, 1160-1171.	7.0	214
8	Inferring causal molecular networks: empirical assessment through a community-based effort. Nature Methods, 2016, 13, 310-318.	9.0	209
9	Targeting immune checkpoints potentiates immunoediting and changes the dynamics of tumor evolution. Nature Communications, 2018, 9, 32.	5.8	193
10	Measuring differential gene expression with RNA-seq: challenges and strategies for data analysis. Briefings in Functional Genomics, 2015, 14, 130-142.	1.3	186
11	Neoantigens Generated by Individual Mutations and Their Role in Cancer Immunity and Immunotherapy. Frontiers in Immunology, 2017, 8, 1679.	2.2	171
12	Deviations of the immune cell landscape between healthy liver and hepatocellular carcinoma. Scientific Reports, 2018, 8, 6220.	1.6	155
13	Deconvoluting tumor-infiltrating immune cells from RNA-seq data using quanTIseq. Methods in Enzymology, 2020, 636, 261-285.	0.4	141
14	A Genome-Wide Association Study of Diabetic Kidney Disease in Subjects With Type 2 Diabetes. Diabetes, 2018, 67, 1414-1427.	0.3	136
15	Next-generation computational tools for interrogating cancer immunity. Nature Reviews Genetics, 2019, 20, 724-746.	7.7	131
16	Immunedeconv: An R Package for Unified Access to Computational Methods for Estimating Immune Cell Fractions from Bulk RNA-Sequencing Data. Methods in Molecular Biology, 2020, 2120, 223-232.	0.4	120
17	Scirpy: a Scanpy extension for analyzing single-cell T-cell receptor-sequencing data. Bioinformatics, 2020, 36, 4817-4818.	1.8	88
18	Neoantigen prediction and computational perspectives towards clinical benefit: recommendations from the ESMO Precision Medicine Working Group. Annals of Oncology, 2020, 31, 978-990.	0.6	87

#	Article	IF	Citations
19	CD39 Identifies the CD4+ Tumor-Specific T-cell Population in Human Cancer. Cancer Immunology Research, 2020, 8, 1311-1321.	1.6	84
20	TIminer: NGS data mining pipeline for cancer immunology and immunotherapy. Bioinformatics, 2017, 33, 3140-3141.	1.8	68
21	FunPat: function-based pattern analysis on RNA-seq time series data. BMC Genomics, 2015, 16, S2.	1.2	63
22	New strategies for cancer immunotherapy: targeting regulatory T cells. Genome Medicine, 2017, 9, 10.	3.6	62
23	Guadecitabine Plus Ipilimumab in Unresectable Melanoma: The NIBIT-M4 Clinical Trial. Clinical Cancer Research, 2019, 25, 7351-7362.	3.2	61
24	Measuring the diversity of the human microbiota with targeted next-generation sequencing. Briefings in Bioinformatics, 2018, 19, bbw119.	3.2	58
25	Multi-Omics Profiling of the Tumor Microenvironment: Paving the Way to Precision Immuno-Oncology. Frontiers in Oncology, 2018, 8, 430.	1.3	57
26	Reducing bias in RNA sequencing data: a novel approach to compute counts. BMC Bioinformatics, 2014, 15, S7.	1.2	51
27	Interpretable systems biomarkers predict response to immune-checkpoint inhibitors. Patterns, 2021, 2, 100293.	3.1	47
28	Optimizing PCR primers targeting the bacterial 16S ribosomal RNA gene. BMC Bioinformatics, 2018, 19, 343.	1.2	39
29	NeoFuse: predicting fusion neoantigens from RNA sequencing data. Bioinformatics, 2020, 36, 2260-2261.	1.8	32
30	Comparative analysis of algorithms for whole-genome assembly of pyrosequencing data. Briefings in Bioinformatics, 2012, 13, 269-280.	3.2	23
31	NKG2A is a late immune checkpoint on CD8 T cells and marks repeated stimulation and cell division. International Journal of Cancer, 2022, 150, 688-704.	2.3	22
32	Genomic comparative analysis and gene function prediction in infectious diseases: application to the investigation of a meningitis outbreak. BMC Infectious Diseases, 2013, 13, 554.	1.3	18
33	Hypoglycemia-induced EEG complexity changes in Type 1 diabetes assessed by fractal analysis algorithm. Biomedical Signal Processing and Control, 2017, 38, 168-173.	3.5	18
34	nextNEOpi: a comprehensive pipeline for computational neoantigen prediction. Bioinformatics, 2022, 38, 1131-1132.	1.8	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 IRE1Î± kinase inhibitor KIRA6 through HSP60 targeting. Cell Death and Differentiation, 2022, 29, 230-245.	5.0	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. Journal of Experimental and Clinical Cancer Research, 2021, 40, 240.	3.5	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. Methods in Molecular Biology, 2020, 2120, 129-145.	0.4	3
42	In Silico Cell-Type Deconvolution Methods in Cancer Immunotherapy. Methods in Molecular Biology, 2020, 2120, 213-222.	0.4	3
43	Draft Genome Sequences of Two Neisseria meningitidis Serogroup C Clinical Isolates. Journal of Bacteriology, 2010, 192, 5270-5271.	1.0	2
44	Mo1791 Colonic Microbiota and Gene Methylation in Colonic Carcinogenesis. Gastroenterology, 2014, 146, S-1072.	0.6	2
45	Analysis of High-Throughput RNA Bisulfite Sequencing Data. Methods in Molecular Biology, 2017, 1562, 143-154.	0.4	2
46	Editorial: Multi-omic Data Integration in Oncology. Frontiers in Oncology, 2020, 10, 1768.	1.3	2
47	A strategy to reduce technical variability and bias in RNA sequencing data. EMBnet Journal, 2012, 18, 65.	0.2	2
48	Mitochondrial DNA Drives Abscopal Responses to Radiation that are Inhibited by Autophagy. SSRN Electronic Journal, 0, , .	0.4	2
49	Predictive Systems Biomarkers of Response to Immune Checkpoint Inhibitors. SSRN Electronic Journal, 0, , .	0.4	0
50	Safety and immunobiological activity of guadecitabine sequenced with ipilimumab in metastatic melanoma patients: The phase Ib NIBIT-M4 study.. Journal of Clinical Oncology, 2019, 37, 2549-2549.	0.8	0
51	Abstract 666: A novel, highly selective PI3KÎ´ 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	35â€¦Chemokine-driven spatial organization of immune cell microaggregates marks oropharyngeal squamous cell carcinomas containing tumor-specific T cells. , 2021, 9, A41-A41.		0