

Peng Jiang

List of Publications by Year in descending order

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Version: 2024-02-01

34
papers

7,404
citations

257357

24
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434063

31
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all docs

36
docs citations

36
times ranked

9182
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. <i>Nature Medicine</i> , 2018, 24, 1550-1558.	15.2	2,791
2	Comprehensive analyses of tumor immunity: implications for cancer immunotherapy. <i>Genome Biology</i> , 2016, 17, 174.	3.8	1,768
3	A major chromatin regulator determines resistance of tumor cells to T cell-mediated killing. <i>Science</i> , 2018, 359, 770-775.	6.0	641
4	Large-scale public data reuse to model immunotherapy response and resistance. <i>Genome Medicine</i> , 2020, 12, 21.	3.6	514
5	SPICi: a fast clustering algorithm for large biological networks. <i>Bioinformatics</i> , 2010, 26, 1105-1111.	1.8	210
6	Tumors exploit FTO-mediated regulation of glycolytic metabolism to evade immune surveillance. <i>Cell Metabolism</i> , 2021, 33, 1221-1233.e11.	7.2	138
7	Cistrome Cancer: A Web Resource for Integrative Gene Regulation Modeling in Cancer. <i>Cancer Research</i> , 2017, 77, e19-e22.	0.4	130
8	The Cutoff protein regulates piRNA cluster expression and piRNA production in the <i>Drosophila</i> germline. <i>EMBO Journal</i> , 2011, 30, 4601-4615.	3.5	110
9	Therapeutically Increasing MHC-I Expression Potentiates Immune Checkpoint Blockade. <i>Cancer Discovery</i> , 2021, 11, 1524-1541.	7.7	103
10	Integrin $\alpha 6 \beta 1$ -TGF $\beta 2$ -SOX4 Pathway Drives Immune Evasion in Triple-Negative Breast Cancer. <i>Cancer Cell</i> , 2021, 39, 54-67.e9.	7.7	99
11	Inference of transcriptional regulation in cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 7731-7736.	3.3	84
12	Systematic investigation of cytokine signaling activity at the tissue and single-cell levels. <i>Nature Methods</i> , 2021, 18, 1181-1191.	9.0	82
13	In vivo CRISPR screens identify the E3 ligase Cop1 as a modulator of macrophage infiltration and cancer immunotherapy target. <i>Cell</i> , 2021, 184, 5357-5374.e22.	13.5	79
14	Cytokine and Chemokine Signals of T-Cell Exclusion in Tumors. <i>Frontiers in Immunology</i> , 2020, 11, 594609.	2.2	66
15	Big data mining yields novel insights on cancer. <i>Nature Genetics</i> , 2015, 47, 103-104.	9.4	64
16	Immunostimulatory Cancer-Associated Fibroblast Subpopulations Can Predict Immunotherapy Response in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2022, 28, 2094-2109.	3.2	60
17	Estrogen-regulated feedback loop limits the efficacy of estrogen receptor-targeted breast cancer therapy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 7869-7878.	3.3	55
18	Functional Interactions Between microRNAs and RNA Binding Proteins. <i>MicroRNA (Shariqah, United)</i> Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5	6.6	54

#	ARTICLE	IF	CITATIONS
19	Network analysis of gene essentiality in functional genomics experiments. <i>Genome Biology</i> , 2015, 16, 239.	3.8	50
20	Improved design and analysis of CRISPR knockout screens. <i>Bioinformatics</i> , 2018, 34, 4095-4101.	1.8	44
21	CARM1 Inhibition Enables Immunotherapy of Resistant Tumors by Dual Action on Tumor Cells and T Cells. <i>Cancer Discovery</i> , 2021, 11, 2050-2071.	7.7	43
22	Genome-Scale Signatures of Gene Interaction from Compound Screens Predict Clinical Efficacy of Targeted Cancer Therapies. <i>Cell Systems</i> , 2018, 6, 343-354.e5.	2.9	40
23	Computational Assessment of the Cooperativity between RNA Binding Proteins and MicroRNAs in Transcript Decay. <i>PLoS Computational Biology</i> , 2013, 9, e1003075.	1.5	30
24	Inhibition of MAN2A1 Enhances the Immune Response to Anti-PD-L1 in Human Tumors. <i>Clinical Cancer Research</i> , 2020, 26, 5990-6002.	3.2	28
25	Big Data Approaches for Modeling Response and Resistance to Cancer Drugs. <i>Annual Review of Biomedical Data Science</i> , 2018, 1, 1-27.	2.8	27
26	A T cell resilience model associated with response to immunotherapy in multiple tumor types. <i>Nature Medicine</i> , 2022, 28, 1421-1431.	15.2	23
27	CCAT: Combinatorial Code Analysis Tool for transcriptional regulation. <i>Nucleic Acids Research</i> , 2014, 42, 2833-2847.	6.5	22
28	Clonal tracing reveals diverse patterns of response to immune checkpoint blockade. <i>Genome Biology</i> , 2020, 21, 263.	3.8	15
29	CRISPR Screens Identify Essential Cell Growth Mediators in BRAF Inhibitor-resistant Melanoma. <i>Genomics, Proteomics and Bioinformatics</i> , 2020, 18, 26-40.	3.0	14
30	Myeloid-Derived Suppressive Cell Expansion Promotes Melanoma Growth and Autoimmunity by Inhibiting CD40/IL27 Regulation in Macrophages. <i>Cancer Research</i> , 2021, 81, 5977-5990.	0.4	14
31	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	3.2	6
32	<i>In vivo</i> CRISPR Screens Identify E3 Ligase Cop1 as a Modulator of Macrophage Infiltration and Cancer Immunotherapy Target. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0
33	Cross-Site Concordance Evaluation of Tumor DNA and RNA Sequencing Platforms for the CIMAC-CIDC Network. <i>Clinical Cancer Research</i> , 2021, 27, 5049-5061.	3.2	0
34	Discover immunotherapy biomarkers from single-cell cytometry data. <i>Patterns</i> , 2021, 2, 100384.	3.1	0