Peng Qiu

List of Publications by Year
in descending order

97	7,561	159585	66911
papers	citations	30	78
		h-index	g-index

114	114	114	13442
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. Science, 2011, 332, 687-696.	12.6	2,097
2	Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. Nature Biotechnology, 2011, 29, 886-891.	17.5	905
3	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
4	Data-analysis strategies for image-based cell profiling. Nature Methods, 2017, 14, 849-863.	19.0	535
5	TCGA-Assembler: open-source software for retrieving and processing TCGA data. Nature Methods, 2014, 11, 599-600.	19.0	366
6	COSMID: A Web-based Tool for Identifying and Validating CRISPR/Cas Off-target Sites. Molecular Therapy - Nucleic Acids, 2014, 3, e214.	5.1	315
7	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
8	Embracing the dropouts in single-cell RNA-seq analysis. Nature Communications, 2020, 11, 1169.	12.8	204
9	Novel BET protein proteolysis-targeting chimera exerts superior lethal activity than bromodomain inhibitor (BETi) against post-myeloproliferative neoplasm secondary (s) AML cells. Leukemia, 2017, 31, 1951-1961.	7.2	151
10	Aging progression of human gut microbiota. BMC Microbiology, 2019, 19, 236.	3.3	151
11	PSGL-1/selectin and ICAM-1/CD18 interactions are involved in macrophage-induced drug resistance in myeloma. Leukemia, 2013, 27, 702-710.	7.2	123
12	Correlation Patterns Between DNA Methylation and Gene Expression in The Cancer Genome Atlas. Cancer Informatics, 2019, 18, 117693511982877.	1.9	120
13	Visualization and cellular hierarchy inference of single-cell data using SPADE. Nature Protocols, 2016, 11, 1264-1279.	12.0	99
14	Model Reduction by Manifold Boundaries. Physical Review Letters, 2014, 113, 098701.	7.8	98
15	Individual Motile CD4+ T Cells Can Participate in Efficient Multikilling through Conjugation to Multiple Tumor Cells. Cancer Immunology Research, 2015, 3, 473-482.	3.4	85
16	Single‐cell mass cytometry reveals intracellular survival/proliferative signaling in FLT3‐ITD‐mutated AML stem/progenitor cells. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 346-356.	1.5	83
17	BET protein bromodomain inhibitor-based combinations are highly active against post-myeloproliferative neoplasm secondary AML cells. Leukemia, 2017, 31, 678-687.	7.2	77
18	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. Immunity, 2015, 42, 591-592.	14.3	67

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19	A benchmark for evaluation of algorithms for identification of cellular correlates of clinical outcomes. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2016, 89, 16-21.	1.5	65
20	Dependence network modeling for biomarker identification. Bioinformatics, 2007, 23, 198-206.	4.1	64
21	Bridging Mechanistic and Phenomenological Models of Complex Biological Systems. PLoS Computational Biology, 2016, 12, e1004915.	3.2	54
22	Immunotherapy via PD-L1â€"presenting biomaterials leads to long-term islet graft survival. Science Advances, 2020, 6, eaba5573.	10.3	54
23	Fast calculation of pairwise mutual information for gene regulatory network reconstruction. Computer Methods and Programs in Biomedicine, 2009, 94, 177-180.	4.7	52
24	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
25	Microfluidic generation of transient cell volume exchange for convectively driven intracellular delivery of large macromolecules. Materials Today, 2018, 21, 703-712.	14.2	51
26	CytoSPADE: high-performance analysis and visualization of high-dimensional cytometry data. Bioinformatics, 2012, 28, 2400-2401.	4.1	44
27	Discovering Biological Progression Underlying Microarray Samples. PLoS Computational Biology, 2011, 7, e1001123.	3.2	42
28	Toward deterministic and semiautomated SPADE analysis. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2017, 91, 281-289.	1.5	37
29	Ensemble dependence model for classification and prediction of cancer and normal gene expression data. Bioinformatics, 2005, 21, 3114-3121.	4.1	36
30	Targeting nuclear Î²-catenin as therapy for post-myeloproliferative neoplasm secondary AML. Leukemia, 2019, 33, 1373-1386.	7.2	32
31	Optimal experiment selection for parameter estimation in biological differential equation models. BMC Bioinformatics, 2012, 13, 181.	2.6	31
32	Inferential modeling and predictive feedback control in real-time motion compensation using the treatment couch during radiotherapy. Physics in Medicine and Biology, 2007, 52, 5831-5854.	3.0	29
33	Inferring Phenotypic Properties from Single-Cell Characteristics. PLoS ONE, 2012, 7, e37038.	2.5	28
34	Dual delivery of IL-10 and AT-RvD1 from PEG hydrogels polarize immune cells towards pro-regenerative phenotypes. Biomaterials, 2021, 268, 120475.	11.4	27
35	Leveraging TCGA gene expression data to build predictive models for cancer drug response. BMC Bioinformatics, 2020, 21, 364.	2.6	26
36	Risk-associated alterations in marrow T cells in pediatric leukemia. JCI Insight, 2020, 5, .	5.0	23

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37	Biophysical subsets of embryonic stem cells display distinct phenotypic and morphological signatures. PLoS ONE, 2018, 13, e0192631.	2.5	20
38	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
39	Improving the sensitivity of sample clustering by leveraging gene co-expression networks in variable selection. BMC Bioinformatics, 2014, 15, 153.	2.6	18
40	Beyond Autoantibodies: Biologic Roles of Human Autoreactive B Cells in Rheumatoid Arthritis Revealed by RNAâ€Sequencing. Arthritis and Rheumatology, 2019, 71, 529-541.	5.6	17
41	Blockade of glutamine-dependent cell survival augments antitumor efficacy of CPI-613 in head and neck cancer. Journal of Experimental and Clinical Cancer Research, 2021, 40, 393.	8.6	17
42	Identification of gene-drug interactions that impact patient survival in TCGA. BMC Bioinformatics, 2016, 17, 409.	2.6	16
43	Urinary detection of early responses to checkpoint blockade and of resistance to it via protease-cleaved antibody-conjugated sensors. Nature Biomedical Engineering, 2022, 6, 310-324.	22.5	16
44	GDISC: a web portal for integrative analysis of geneâ€"drug interaction for survival in cancer. Bioinformatics, 2017, 33, 1426-1428.	4.1	15
45	Analyzing immune response to engineered hydrogels by hierarchical clustering of inflammatory cell subsets. Science Advances, 2022, 8, eabd8056.	10.3	15
46	Identification of markers associated with global changes in DNA methylation regulation in cancers. BMC Bioinformatics, 2012, 13, S7.	2.6	13
47	Harnessing lipid signaling pathways to target specialized pro-angiogenic neutrophil subsets for regenerative immunotherapy. Science Advances, 2020, 6, .	10.3	13
48	Accurately tracking single-cell movement trajectories in microfluidic cell sorting devices. PLoS ONE, 2018, 13, e0192463.	2.5	13
49	Identification of thresholds for dichotomizing DNA methylation data. Eurasip Journal on Bioinformatics and Systems Biology, 2013, 2013, 8.	1.4	12
50	Computational prediction of manually gated rare cells in flow cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2015, 87, 594-602.	1.5	12
51	Peripheral blood blast clearance is an independent prognostic factor for survival and response to acute myeloid leukemia induction chemotherapy. American Journal of Hematology, 2016, 91, 1221-1226.	4.1	12
52	Long short-term memory recurrent neural networks for antibacterial peptide identification. , 2017, , .		12
53	Modulating local S1P receptor signaling as a regenerative immunotherapy after volumetric muscle loss injury. Journal of Biomedical Materials Research - Part A, 2021, 109, 695-712.	4.0	12
54	Polynomial model approach for resynchronization analysis of cell-cycle gene expression data. Bioinformatics, 2006, 22, 959-966.	4.1	10

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55	Simultaneous Class Discovery and Classification of Microarray Data Using Spectral Analysis. Journal of Computational Biology, 2009, 16, 935-944.	1.6	10
56	Reconstructing Directed Signed Gene Regulatory Network From Microarray Data. IEEE Transactions on Biomedical Engineering, 2011, 58, 3518-3521.	4.2	9
57	Experimental design and model reduction in systems biology. Quantitative Biology, 2018, 6, 287-306.	0.5	9
58	GLaMST: grow lineages along minimum spanning tree for b cell receptor sequencing data. BMC Genomics, 2020, 21, 583.	2.8	8
59	Identifying gene expression patterns associated with drug-specific survival in cancer patients. Scientific Reports, 2021, 11, 5004.	3.3	8
60	Classification of Antibacterial Peptides using Long Short-Term Memory Recurrent Neural Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 17, 1-1.	3.0	7
61	Reducing the Computational Complexity of Information Theoretic Approaches for Reconstructing Gene Regulatory Networks. Journal of Computational Biology, 2010, 17, 169-176.	1.6	6
62	TreeVis: A MATLAB-based tool for tree visualization. Computer Methods and Programs in Biomedicine, 2013, 109, 74-76.	4.7	6
63	Deconvolving multiplexed protease signatures with substrate reduction and activity clustering. PLoS Computational Biology, 2019, 15, e1006909.	3.2	6
64	Nanofiber-Based Delivery of Bioactive Lipids Promotes Pro-regenerative Inflammation and Enhances Muscle Fiber Growth After Volumetric Muscle Loss. Frontiers in Bioengineering and Biotechnology, 2021, 9, 650289.	4.1	6
65	3D material cytometry (3DMaC): a very high-replicate, high-throughput analytical method using microfabricated, shape-specific, cell-material niches. Lab on A Chip, 2017, 17, 2861-2872.	6.0	5
66	A robust method for QRS detection based on modified p-spectrum. , 2008, , .		4
67	An Activity-Subspace Approach for Estimating the Integrated Input Function and Relative Distribution Volume in PET Parametric Imaging. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 25-36.	3.2	4
68	Unfold High-Dimensional Clouds for Exhaustive Gating of Flow Cytometry Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1045-1051.	3.0	4
69	Case series of patients with acute myeloid leukemia receiving hypomethylation therapy and retrospectively found to have **_IDH1_** or **_IDH2_** mutations. Leukemia and Lymphoma, 2014, 55, 1431-1434.	1.3	4
70	Bayesian Hierarchical Models for Protein Networks in Single-Cell Mass Cytometry. Cancer Informatics, 2014, 13s4, CIN.S13984.	1.9	4
71	Unsupervised Discovery of Subspace Trends. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 2131-2145.	13.9	4
72	Quantifying the relative importance of experimental data points in parameter estimation. BMC Systems Biology, 2018, 12, 103.	3.0	4

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73	BM-SNP: A Bayesian Model for SNP Calling Using High Throughput Sequencing Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 1038-1044.	3.0	3
74	Spectral feature selection and its application in high dimensional gene expression studies. , 2014, , .		3
75	Graph-based extraction of shape features for leaf classification. , 2017, , .		3
76	Automatically generate twoâ€dimensional gating hierarchy from clustered cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2018, 93, 1039-1050.	1.5	3
77	JSOM: Jointly-evolving self-organizing maps for alignment of biological datasets and identification of related clusters. PLoS Computational Biology, 2021, 17, e1008804.	3.2	3
78	Unsupervised inference of arbor morphology progression for microglia from confocal microscope images. , 2013, , .		2
79	Single-Cell Mass Cytometry Reveals Phenotypic and Functional Heterogeneity In Acute Myeloid Leukemia At Diagnosis and In Remission. Blood, 2013, 122, 1311-1311.	1.4	2
80	Mixture principal component analysis for distribution volume parametric imaging in brain PET studies. , 2006, , .		1
81	Toward exhaustive gating of flow cytometry data. , 2012, , .		1
82	Integrative analysis of methylation and gene expression data in TCGA. , 2012, , .		1
83	An iterative algorithm for sampling from manifolds. , 2014, , .		1
84	Shape-to-graph mapping method for efficient characterization and classification of complex geometries in biological images. PLoS Computational Biology, 2020, 16, e1007758.	3.2	1
85	Single-Cell Mass Cytometry Characterizes Phenotypic and Functional Heterogeneity in Acute Myeloid Leukemia at Diagnosis, in Remission and Relapse. Blood, 2018, 132, 912-912.	1.4	1
86	Feature selection algorithms for predicting preeclampsia: A comparative approach. , 2020, , .		1
87	Integrative analysis of TCGA data identifies miRNAs as drug-specific survival biomarkers. Scientific Reports, 2022, 12, 6785.	3.3	1
88	Discover Trend and Progression Underlying High-Dimensional Data. , 0, , 445-459.		0
89	Therapy Related Cellular Changes as a Tool for Prognosis in AML. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S120.	0.4	0
90	The relative importance of data points in systems biology and parameter estimation. , 2017, , .		0

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91	Correlating Mechanical and Gene Expression Data on the Single Cell Level to Investigate Metastasis. Biophysical Journal, 2020, 118, 189a.	0.5	0
92	Inference of Networks from Large Datasets. , 2021, , 17-25.		0
93	Dynamics and Prognostic Impact of Peripheral Blood Blast Clearance in Patients with Acute Myeloid Leukemia (AML) Receiving FLT3 Inhibitor Therapy in Combination with Induction Chemotherapy. Blood, 2012, 120, 1417-1417.	1.4	0
94	Differential Prognostic Impact Of Peripheral Blood Blast Clearance In AML Based On Type Of Therapy and FLT3 Mutation Status. Blood, 2013, 122, 2584-2584.	1.4	0
95	Image-based early predictions of functional properties in cell manufacturing. , 2020, , .		0
96	Prediction of Functional Markers of Mass Cytometry Data via Deep Learning. Emerging Topics in Statistics and Biostatistics, 2020, , 95-104.	0.1	0
97	17â€¦Activity sensors for noninvasive monitoring of immune response and tumor resistance during immune checkpoint blockade therapy. , 2020, , .		0