Peng Qiu

List of Publications by Year
in descending order

97 papers	7,561 citations	159585 30 h-index	66911 78 g-index
114 all docs	114 docs citations	114 times ranked	13442 citing authors

#	Article	IF	Citations
1	Analyzing immune response to engineered hydrogels by hierarchical clustering of inflammatory cell subsets. Science Advances, 2022, 8, eabd8056.	10.3	15
2	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
3	Integrative analysis of TCGA data identifies miRNAs as drug-specific survival biomarkers. Scientific Reports, 2022, 12, 6785.	3.3	1
4	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
5	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
6	Inference of Networks from Large Datasets. , 2021, , 17-25.		0
7	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
8	Identifying gene expression patterns associated with drug-specific survival in cancer patients. Scientific Reports, 2021, 11, 5004.	3.3	8
9	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
10	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
11	Leveraging TCGA gene expression data to build predictive models for cancer drug response. BMC Bioinformatics, 2020, 21, 364.	2.6	26
12	Correlating Mechanical and Gene Expression Data on the Single Cell Level to Investigate Metastasis. Biophysical Journal, 2020, 118, 189a.	0.5	0
13	Harnessing lipid signaling pathways to target specialized pro-angiogenic neutrophil subsets for regenerative immunotherapy. Science Advances, 2020, 6, .	10.3	13
14	Immunotherapy via PD-L1â€"presenting biomaterials leads to long-term islet graft survival. Science Advances, 2020, 6, eaba5573.	10.3	54
15	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
16	GLaMST: grow lineages along minimum spanning tree for b cell receptor sequencing data. BMC Genomics, 2020, 21, 583.	2.8	8
17	Embracing the dropouts in single-cell RNA-seq analysis. Nature Communications, 2020, 11, 1169.	12.8	204
18	Risk-associated alterations in marrow T cells in pediatric leukemia. JCI Insight, 2020, 5, .	5.0	23

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19	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
20	Image-based early predictions of functional properties in cell manufacturing. , 2020, , .		0
21	Feature selection algorithms for predicting preeclampsia: A comparative approach. , 2020, , .		1
22	Prediction of Functional Markers of Mass Cytometry Data via Deep Learning. Emerging Topics in Statistics and Biostatistics, 2020, , 95-104.	0.1	0
23	17…Activity sensors for noninvasive monitoring of immune response and tumor resistance during immune checkpoint blockade therapy. , 2020, , .		0
24	Aging progression of human gut microbiota. BMC Microbiology, 2019, 19, 236.	3.3	151
25	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
26	Correlation Patterns Between DNA Methylation and Gene Expression in The Cancer Genome Atlas. Cancer Informatics, 2019, 18, 117693511982877.	1.9	120
27	Quantitative Proteome Landscape of the NCI-60 Cancer Cell Lines. IScience, 2019, 21, 664-680.	4.1	52
28	Deconvolving multiplexed protease signatures with substrate reduction and activity clustering. PLoS Computational Biology, 2019, 15, e1006909.	3.2	6
29	Targeting nuclear Î²-catenin as therapy for post-myeloproliferative neoplasm secondary AML. Leukemia, 2019, 33, 1373-1386.	7.2	32
30	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
31	Microfluidic generation of transient cell volume exchange for convectively driven intracellular delivery of large macromolecules. Materials Today, 2018, 21, 703-712.	14.2	51
32	Experimental design and model reduction in systems biology. Quantitative Biology, 2018, 6, 287-306.	0.5	9
33	Quantifying the relative importance of experimental data points in parameter estimation. BMC Systems Biology, 2018, 12, 103.	3.0	4
34	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
35	Biophysical subsets of embryonic stem cells display distinct phenotypic and morphological signatures. PLoS ONE, 2018, 13, e0192631.	2.5	20
36	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

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37	Accurately tracking single-cell movement trajectories in microfluidic cell sorting devices. PLoS ONE, 2018, 13, e0192463.	2.5	13
38	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
39	GDISC: a web portal for integrative analysis of gene–drug interaction for survival in cancer. Bioinformatics, 2017, 33, 1426-1428.	4.1	15
40	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
41	Data-analysis strategies for image-based cell profiling. Nature Methods, 2017, 14, 849-863.	19.0	535
42	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
43	BET protein bromodomain inhibitor-based combinations are highly active against post-myeloproliferative neoplasm secondary AML cells. Leukemia, 2017, 31, 678-687.	7.2	77
44	Graph-based extraction of shape features for leaf classification. , 2017, , .		3
45	Long short-term memory recurrent neural networks for antibacterial peptide identification. , 2017, , .		12
46	The relative importance of data points in systems biology and parameter estimation. , 2017, , .		0
47	Bridging Mechanistic and Phenomenological Models of Complex Biological Systems. PLoS Computational Biology, 2016, 12, e1004915.	3.2	54
48	Identification of gene-drug interactions that impact patient survival in TCGA. BMC Bioinformatics, 2016, 17, 409.	2.6	16
49	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
50	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
51	Visualization and cellular hierarchy inference of single-cell data using SPADE. Nature Protocols, 2016, 11, 1264-1279.	12.0	99
52	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
53	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
54	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

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55	Thinking Outside the Gate: Single-Cell Assessments in Multiple Dimensions. Immunity, 2015, 42, 591-592.	14.3	67
56	Unsupervised Discovery of Subspace Trends. IEEE Transactions on Pattern Analysis and Machine Intelligence, 2015, 37, 2131-2145.	13.9	4
57	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
58	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
59	COSMID: A Web-based Tool for Identifying and Validating CRISPR/Cas Off-target Sites. Molecular Therapy - Nucleic Acids, 2014, 3, e214.	5.1	315
60	An iterative algorithm for sampling from manifolds. , 2014, , .		1
61	Spectral feature selection and its application in high dimensional gene expression studies. , 2014, , .		3
62	Therapy Related Cellular Changes as a Tool for Prognosis in AML. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S120.	0.4	0
63	A community computational challenge to predict the activity of pairs of compounds. Nature Biotechnology, 2014, 32, 1213-1222.	17.5	264
64	Model Reduction by Manifold Boundaries. Physical Review Letters, 2014, 113, 098701.	7.8	98
65	Improving the sensitivity of sample clustering by leveraging gene co-expression networks in variable selection. BMC Bioinformatics, 2014, 15, 153.	2.6	18
66	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
67	A community effort to assess and improve drug sensitivity prediction algorithms. Nature Biotechnology, 2014, 32, 1202-1212.	17.5	653
68	TCGA-Assembler: open-source software for retrieving and processing TCGA data. Nature Methods, 2014, 11, 599-600.	19.0	366
69	Bayesian Hierarchical Models for Protein Networks in Single-Cell Mass Cytometry. Cancer Informatics, 2014, 13s4, CIN.S13984.	1.9	4
70	Identification of thresholds for dichotomizing DNA methylation data. Eurasip Journal on Bioinformatics and Systems Biology, 2013, 2013, 8.	1.4	12
71	TreeVis: A MATLAB-based tool for tree visualization. Computer Methods and Programs in Biomedicine, 2013, 109, 74-76.	4.7	6
72	Unsupervised inference of arbor morphology progression for microglia from confocal microscope images. , 2013, , .		2

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73	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
74	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
75	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
76	Toward exhaustive gating of flow cytometry data. , 2012, , .		1
77	CytoSPADE: high-performance analysis and visualization of high-dimensional cytometry data. Bioinformatics, 2012, 28, 2400-2401.	4.1	44
78	Optimal experiment selection for parameter estimation in biological differential equation models. BMC Bioinformatics, 2012, 13, 181.	2.6	31
79	Integrative analysis of methylation and gene expression data in TCGA. , 2012, , .		1
80	Identification of markers associated with global changes in DNA methylation regulation in cancers. BMC Bioinformatics, 2012, 13, S7.	2.6	13
81	Inferring Phenotypic Properties from Single-Cell Characteristics. PLoS ONE, 2012, 7, e37038.	2.5	28
82	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
83	Extracting a cellular hierarchy from high-dimensional cytometry data with SPADE. Nature Biotechnology, 2011, 29, 886-891.	17.5	905
84	Reconstructing Directed Signed Gene Regulatory Network From Microarray Data. IEEE Transactions on Biomedical Engineering, 2011, 58, 3518-3521.	4.2	9
85	Single-Cell Mass Cytometry of Differential Immune and Drug Responses Across a Human Hematopoietic Continuum. Science, 2011, 332, 687-696.	12.6	2,097
86	Discovering Biological Progression Underlying Microarray Samples. PLoS Computational Biology, 2011, 7, e1001123.	3.2	42
87	Reducing the Computational Complexity of Information Theoretic Approaches for Reconstructing Gene Regulatory Networks. Journal of Computational Biology, 2010, 17, 169-176.	1.6	6
88	Simultaneous Class Discovery and Classification of Microarray Data Using Spectral Analysis. Journal of Computational Biology, 2009, 16, 935-944.	1.6	10
89	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
90	Fast calculation of pairwise mutual information for gene regulatory network reconstruction. Computer Methods and Programs in Biomedicine, 2009, 94, 177-180.	4.7	52

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91	A robust method for QRS detection based on modified p-spectrum. , 2008, , .		4
92	Dependence network modeling for biomarker identification. Bioinformatics, 2007, 23, 198-206.	4.1	64
93	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
94	Polynomial model approach for resynchronization analysis of cell-cycle gene expression data. Bioinformatics, 2006, 22, 959-966.	4.1	10
95	Mixture principal component analysis for distribution volume parametric imaging in brain PET studies. , 2006, , .		1
96	Ensemble dependence model for classification and prediction of cancer and normal gene expression data. Bioinformatics, 2005, 21, 3114-3121.	4.1	36
97	Discover Trend and Progression Underlying High-Dimensional Data. , 0, , 445-459.		0