

Determining cell type abundance and expression from bulk

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Computational approaches for characterizing the tumor immune microenvironment. <i>Immunology</i> , 2019, 158, 70-84.	2.0	30
3	Tissue-specific deconvolution of immune cell composition by integrating bulk and single-cell transcriptomes. <i>Bioinformatics</i> , 2020, 36, 819-827.	1.8	13
4	An elastic-net logistic regression approach to generate classifiers and gene signatures for types of immune cells and T helper cell subsets. <i>BMC Bioinformatics</i> , 2019, 20, 433.	1.2	31
5	Next-generation computational tools for interrogating cancer immunity. <i>Nature Reviews Genetics</i> , 2019, 20, 724-746.	7.7	131
6	ADAPTS: Automated deconvolution augmentation of profiles for tissue specific cells. <i>PLoS ONE</i> , 2019, 14, e0224693.	1.1	19
7	RNA-seq from archival FFPE breast cancer samples: molecular pathway fidelity and novel discovery. <i>BMC Medical Genomics</i> , 2019, 12, 195.	0.7	35
8	Identification of non-cancer cells from cancer transcriptomic data. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2020, 1863, 194445.	0.9	7
9	The TMEM106B FTL-protective variant, rs1990621, is also associated with increased neuronal proportion. <i>Acta Neuropathologica</i> , 2020, 139, 45-61.	3.9	51
10	Prognostic value and immune cell infiltration of hypoxic phenotype-related gene signatures in glioblastoma microenvironment. <i>Journal of Cellular and Molecular Medicine</i> , 2020, 24, 13235-13247.	1.6	12
11	Identification of Immune-Related Cells and Genes in Tumor Microenvironment of Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 1770.	1.3	7
12	Efficient Propagation of Circulating Tumor Cells: A First Step for Probing Tumor Metastasis. <i>Cancers</i> , 2020, 12, 2784.	1.7	14
13	<i>KEAP1/NFE2L2</i> Mutations Predict Lung Cancer Radiation Resistance That Can Be Targeted by Glutaminase Inhibition. <i>Cancer Discovery</i> , 2020, 10, 1826-1841.	7.7	93
14	Elevated expression of <i>FREM1</i> in breast cancer indicates favorable prognosis and high-level immune infiltration status. <i>Cancer Medicine</i> , 2020, 9, 9554-9570.	1.3	20
15	The prognostic value of TMB and the relationship between TMB and immune infiltration in head and neck squamous cell carcinoma: A gene expression-based study. <i>Oral Oncology</i> , 2020, 110, 104943.	0.8	63
16	The murine Microenvironment Cell Population counter method to estimate abundance of tissue-infiltrating immune and stromal cell populations in murine samples using gene expression. <i>Genome Medicine</i> , 2020, 12, 86.	3.6	63
17	Predicting the clinical outcome of melanoma using an immune-related gene pairs signature. <i>PLoS ONE</i> , 2020, 15, e0240331.	1.1	9
18	Single-cell RNA sequencing highlights the role of inflammatory cancer-associated fibroblasts in bladder urothelial carcinoma. <i>Nature Communications</i> , 2020, 11, 5077.	5.8	281
19	UEG Week 2020 Oral Presentations. <i>United European Gastroenterology Journal</i> , 2020, 8, 8-142.	1.6	10

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20	Stromal Expression of the Core Clock Gene Period 2 Is Essential for Tumor Initiation and Metastatic Colonization. <i>Frontiers in Cell and Developmental Biology</i> , 2020, 8, 587697.	1.8	15
21	Prognostic alternative splicing signature reveals the landscape of immune infiltration in Pancreatic Cancer. <i>Journal of Cancer</i> , 2020, 11, 6530-6544.	1.2	9
22	Progressive Multiple Sclerosis Transcriptome Deconvolution Indicates Increased M2 Macrophages in Inactive Lesions. <i>European Neurology</i> , 2020, 83, 433-435.	0.6	5
23	Prefrontal Cortex Transcriptomic Deconvolution Implicates Monocyte Infiltration in Parkinson's Disease. <i>Neurodegenerative Diseases</i> , 2020, 20, 110-112.	0.8	6
24	Noninvasive Early Identification of Therapeutic Benefit from Immune Checkpoint Inhibition. <i>Cell</i> , 2020, 183, 363-376.e13.	13.5	206
25	An Unsupervised Strategy for Identifying Epithelial-Mesenchymal Transition State Metrics in Breast Cancer and Melanoma. <i>Science</i> , 2020, 23, 101080.	1.9	8
26	Ageing hallmarks exhibit organ-specific temporal signatures. <i>Nature</i> , 2020, 583, 596-602.	13.7	317
27	RNA Identification of PRIME Cells Predicting Rheumatoid Arthritis Flares. <i>New England Journal of Medicine</i> , 2020, 383, 218-228.	13.9	111
28	Immune Phenotypes of Nasopharyngeal Cancer. <i>Cancers</i> , 2020, 12, 3428.	1.7	7
29	Correlation of tumor-infiltrating immune cells of melanoma with overall survival by immunogenomic analysis. <i>Cancer Medicine</i> , 2020, 9, 8444-8456.	1.3	22
30	Identification of Epithelial-Mesenchymal Transition-Related lncRNA With Prognosis and Molecular Subtypes in Clear Cell Renal Cell Carcinoma. <i>Frontiers in Oncology</i> , 2020, 10, 591254.	1.3	26
31	Melanoma Persister Cells Are Tolerant to BRAF/MEK Inhibitors via ACOX1-Mediated Fatty Acid Oxidation. <i>Cell Reports</i> , 2020, 33, 108421.	2.9	77
32	SSMD: a semi-supervised approach for a robust cell type identification and deconvolution of mouse transcriptomics data. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	3
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37	Plasma-derived extracellular vesicle analysis and deconvolution enable prediction and tracking of melanoma checkpoint blockade outcome. <i>Science Advances</i> , 2020, 6, .	4.7	37

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39	Deep learning-based cell composition analysis from tissue expression profiles. <i>Science Advances</i> , 2020, 6, eaba2619.	4.7	113
40	Neonatal genetics of gene expression reveal potential origins of autoimmune and allergic disease risk. <i>Nature Communications</i> , 2020, 11, 3761.	5.8	22
41	Comprehensive molecular comparison of BRCA1 hypermethylated and BRCA1 mutated triple negative breast cancers. <i>Nature Communications</i> , 2020, 11, 3747.	5.8	53
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43	MethylResolver—a method for deconvoluting bulk DNA methylation profiles into known and unknown cell contents. <i>Communications Biology</i> , 2020, 3, 422.	2.0	33
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63	Transcriptome of the Southern Muriqui <i>Brachyteles arachnoides</i> (Primates:Platyrrhini), a Critically Endangered New World Monkey: Evidence of Adaptive Evolution. <i>Frontiers in Genetics</i> , 2020, 11, 831.	1.1	1
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72	Blood and Salivary Amphiregulin Levels as Biomarkers for Asthma. <i>Frontiers in Medicine</i> , 2020, 7, 561866.	1.2	9
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76	Prognostic value of intratumoral lymphocyte-to-monocyte ratio and M0 macrophage enrichment in tumor immune microenvironment of melanoma. <i>Melanoma Management</i> , 2020, 7, MMT51.	0.1	14
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83	Deep Into Breast Cancer Heterogeneity to Increase Immunotherapeutic Effectiveness. <i>JCO Precision Oncology</i> , 2020, 4, 1267-1268.	1.5	2
84	Pituitary Tumor Transforming Gene 1 Orchestrates Gene Regulatory Variation in Mouse Ventral Midbrain During Aging. <i>Frontiers in Genetics</i> , 2020, 11, 566734.	1.1	4
85	Novel Molecular Subtypes Associated With 5mC Methylation and Their Role in Hepatocellular Carcinoma Immunotherapy. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 562441.	1.6	12
86	Transcriptomic Deconvolution of Dorsal Striata Reveals Increased Monocyte Fractions in Bipolar Disorder. <i>Complex Psychiatry</i> , 2020, 6, 83-88.	1.3	2
87	Single-cell genomic profile-based analysis of tissue differentiation in colorectal cancer. <i>Science China Life Sciences</i> , 2021, 64, 1311-1325.	2.3	4
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93	Use of Single-Cell -Omic Technologies to Study the Gastrointestinal Tract and Diseases, From Single Cell Identities to Patient Features. <i>Gastroenterology</i> , 2020, 159, 453-466.e1.	0.6	17
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128	Downregulation of EOMES drives T cell exhaustion via abolishing EOMES-mediated repression of inhibitory receptors of T cells in liver cancer. <i>Journal of Cellular and Molecular Medicine</i> , 2021, 25, 161-169.	1.6	10
129	Specific MiRNAs in naïve T cells associated with Hepatitis C Virus-induced Hepatocellular Carcinoma. <i>Journal of Cancer</i> , 2021, 12, 1-9.	1.2	7
130	Transcriptomic organization of the human brain in post-traumatic stress disorder. <i>Nature Neuroscience</i> , 2021, 24, 24-33.	7.1	106
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146	Identification novel prognostic signatures for Head and Neck Squamous Cell Carcinoma based on ceRNA network construction and immune infiltration analysis. <i>International Journal of Medical Sciences</i> , 2021, 18, 1297-1311.	1.1	18
147	Circadian rhythm-associated clinical relevance and Tumor Microenvironment of Non-small Cell Lung Cancer. <i>Journal of Cancer</i> , 2021, 12, 2582-2597.	1.2	17

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149	Shaping of genome by long noncoding RNAs. , 2021, , 357-372.		0
150	Relevance of Immune Infiltration and Clinical Outcomes in Pancreatic Ductal Adenocarcinoma Subtypes. <i>Frontiers in Oncology</i> , 2020, 10, 575264.	1.3	14
152	A novel immune-related genes signature after bariatric surgery is histologically associated with non-alcoholic fatty liver disease. <i>Adipocyte</i> , 2021, 10, 424-434.	1.3	16
153	Immune modulation resulting from MR-guided high intensity focused ultrasound in a model of murine breast cancer. <i>Scientific Reports</i> , 2021, 11, 927.	1.6	48
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155	Diagnostic blood RNA profiles for human acute spinal cord injury. <i>Journal of Experimental Medicine</i> , 2021, 218, .	4.2	31
156	Combination of CD47 and CD68 expression predicts survival in eastern-Asian patients with non-small cell lung cancer. <i>Journal of Cancer Research and Clinical Oncology</i> , 2021, 147, 739-747.	1.2	8
157	Age-associated Ligand-receptor Interactions Imputed from Nasopharyngeal Transcriptomes of COVID-19 Patients. <i>Immunological Investigations</i> , 2021, , 1-8.	1.0	1
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159	Identification of an immune overdrive high-risk subpopulation with aberrant expression of FOXP3 and CTLA4 in colorectal cancer. <i>Oncogene</i> , 2021, 40, 2130-2145.	2.6	15
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1225	Identification of immune cell infiltration and diagnostic biomarkers in unstable atherosclerotic plaques by integrated bioinformatics analysis and machine learning. <i>Frontiers in Immunology</i> , 0, 13, .	2.2	17
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1353	Identification of mutational signature for lung adenocarcinoma prognosis and immunotherapy prediction. <i>Journal of Molecular Medicine</i> , 0, , .	1.7	0
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1374	Deep autoencoder for interpretable tissue-adaptive deconvolution and cell-type-specific gene analysis. <i>Nature Communications</i> , 2022, 13, .	5.8	16
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1379	TIMEDB: tumor immune micro-environment cell composition database with automatic analysis and interactive visualization. <i>Nucleic Acids Research</i> , 2023, 51, D1417-D1424.	6.5	7
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