Dvir Aran

List of Publications by Year
in descending order

39 papers	8,871 citations	331670 21 h-index	361022 35 g-index
51 all docs	51 docs citations	51 times ranked	17411 citing authors

#	Article	IF	Citations
1	xCell: digitally portraying the tissue cellular heterogeneity landscape. Genome Biology, 2017, 18, 220.	8.8	2,572
2	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. Nature Immunology, 2019, 20, 163-172.	14.5	2,330
3	Systematic pan-cancer analysis of tumour purity. Nature Communications, 2015, 6, 8971.	12.8	937
4	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. Cell, 2020, 181, 1612-1625.e13.	28.9	436
5	Comprehensive analysis of normal adjacent to tumor transcriptomes. Nature Communications, 2017, 8, 1077.	12.8	394
6	Genome-wide survey reveals predisposing diabetes type 2-related DNA methylation variations in human peripheral blood. Human Molecular Genetics, 2012, 21, 371-383.	2.9	317
7	DNA methylation of distal regulatory sites characterizes dysregulation of cancer genes. Genome Biology, 2013, 14, R21.	9.6	288
8	Replication timing-related and gene body-specific methylation of active human genes. Human Molecular Genetics, 2011, 20, 670-680.	2.9	256
9	DNA Methylation of Transcriptional Enhancers and Cancer Predisposition. Cell, 2013, 154, 11-13.	28.9	156
10	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. Scientific Reports, 2016, 6, 24799.	3.3	155
11	CNS fibroblasts form a fibrotic scar in response to immune cell infiltration. Nature Neuroscience, 2021, 24, 234-244.	14.8	120
12	Comprehensive transcriptomic analysis of cell lines as models of primary tumors across 22 tumor types. Nature Communications, 2019, 10, 3574.	12.8	111
13	Widespread parainflammation in human cancer. Genome Biology, 2016, 17, 145.	8.8	87
14	Cell-Type Enrichment Analysis of Bulk Transcriptomes Using xCell. Methods in Molecular Biology, 2020, 2120, 263-276.	0.9	86
15	Aging is associated with highly defined epigenetic changes in the human epidermis. Epigenetics and Chromatin, 2013, 6, 36.	3.9	72
16	CD161 contributes to prenatal immune suppression of IFN-Î³â€"producing PLZF+ T cells. Journal of Clinical Investigation, 2019, 129, 3562-3577.	8.2	55
17	Precision annotation of digital samples in NCBIâ€™s gene expression omnibus. Scientific Data, 2017, 4, 170125.	5.3	44
18	Prior presumed coronavirus infection reduces COVID-19 risk: A cohort study. Journal of Infection, 2020, 81, 923-930.	3.3	39

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19	Heterogeneity in HIV and cellular transcription profiles in cell line models of latent and productive infection: implications for HIV latency. Retrovirology, 2019, 16, 32.	2.0	35
20	Premature aging of leukocyte DNA methylation is associated with type 2 diabetes prevalence. Clinical Epigenetics, 2015, 7, 35.	4.1	34
21	Development and validation of a machine‐learning model for prediction of shoulder dystocia. Ultrasound in Obstetrics and Gynecology, 2020, 56, 588-596.	1.7	34
22	Molecular programs of fibrotic change in aging human lung. Nature Communications, 2021, 12, 6309.	12.8	33
23	Global Transcriptome Analysis of RNA Abundance Regulation by ADAR in Lung Adenocarcinoma. EBioMedicine, 2018, 27, 167-175.	6.1	23
24	Comparison of FOLFIRINOX vs Gemcitabine Plus Nab-Paclitaxel as First-Line Chemotherapy for Metastatic Pancreatic Ductal Adenocarcinoma. JAMA Network Open, 2022, 5, e2216199.	5.9	21
25	Digitally deconvolving the tumor microenvironment. Genome Biology, 2016, 17, 175.	8.8	20
26	Human splice factors contribute to latent HIV infection in primary cell models and blood CD4+ T cells from ART-treated individuals. PLoS Pathogens, 2020, 16, e1009060.	4.7	18
27	Unmasking risk loci: <scp>DNA</scp> methylation illuminates the biology of cancer predisposition. BioEssays, 2014, 36, 184-190.	2.5	16
28	Implementation of machine learning models for the prediction of vaginal birth after cesarean delivery. Journal of Maternal-Fetal and Neonatal Medicine, 2022, 35, 3677-3683.	1.5	14
29	Cancer Cell‐Autonomous Parainflammation Mimics Immune Cell Infiltration. Cancer Research, 2017, 77, 3740-3744.	0.9	12
30	Embryonic Stem Cell (ES)-Specific Enhancers Specify the Expression Potential of ES Genes in Cancer. PLoS Genetics, 2016, 12, e1005840.	3.5	10
31	S-6. Cytokine, 2014, 70, 22.	3.2	1
32	657: Improving the prediction of shoulder dystocia using artificial intelligence â€" a novel approach. American Journal of Obstetrics and Gynecology, 2019, 220, S435-S436.	1.3	1
33	Extracting insights from heterogeneous tissues. Nature Computational Science, 2021, 1, 247-248.	8.0	1
34	Real-world data comparing atezolizumab plus taxane therapy versus taxane alone as first-line treatment of metastatic triple-negative breast cancer patients in the United States.. Journal of Clinical Oncology, 2022, 40, e18767-e18767.	1.6	1
35	629: MFMU Calculator versus machine learning techniques for predicting VBAC success â€" Which model works best?. American Journal of Obstetrics and Gynecology, 2020, 222, S401-S402.	1.3	0
36	Abstract 2398: Tumor cell-adipocyte gap junctions activate lipolysis in breast cancer. , 2018, , .		0

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37	Real-world comparison of outcomes in the first line treatment of metastatic melanoma according to BRAF mutation status: Nivolumab and ipilimumab therapy vs. nivolumab monotherapy.. Journal of Clinical Oncology, 2022, 40, e21519-e21519.	1.6	0
38	Real-world data comparing FOLFIRINOX versus gemcitabine nab-paclitaxel as first-line treatment of metastatic pancreatic ductal adenocarcinoma patients in the United States.. Journal of Clinical Oncology, 2022, 40, e16271-e16271.	1.6	0
39	Real-world data comparing third and subsequent line regimens for treatment of metastatic triple-negative breast cancer in the United States.. Journal of Clinical Oncology, 2022, 40, e18765-e18765.	1.6	0