

# Dvir Aran

## List of Publications by Year in descending order

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Version: 2024-02-01

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	Implementation of machine learning models for the prediction of vaginal birth after cesarean delivery. <i>Journal of Maternal-Fetal and Neonatal Medicine</i> , 2022, 35, 3677-3683.	1.5	14
2	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.. <i>Journal of Clinical Oncology</i> , 2022, 40, e21519-e21519.	1.6	0
3	Real-world data comparing FOLFIRINOX versus gemcitabine nab-paclitaxel as first-line treatment of metastatic pancreatic ductal adenocarcinoma patients in the United States.. <i>Journal of Clinical Oncology</i> , 2022, 40, e16271-e16271.	1.6	0
4	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.. <i>Journal of Clinical Oncology</i> , 2022, 40, e18767-e18767.	1.6	1
5	Real-world data comparing third and subsequent line regimens for treatment of metastatic triple-negative breast cancer in the United States.. <i>Journal of Clinical Oncology</i> , 2022, 40, e18765-e18765.	1.6	0
6	Comparison of FOLFIRINOX vs Gemcitabine Plus Nab-Paclitaxel as First-Line Chemotherapy for Metastatic Pancreatic Ductal Adenocarcinoma. <i>JAMA Network Open</i> , 2022, 5, e2216199.	5.9	21
7	CNS fibroblasts form a fibrotic scar in response to immune cell infiltration. <i>Nature Neuroscience</i> , 2021, 24, 234-244.	14.8	120
8	Extracting insights from heterogeneous tissues. <i>Nature Computational Science</i> , 2021, 1, 247-248.	8.0	1
9	Molecular programs of fibrotic change in aging human lung. <i>Nature Communications</i> , 2021, 12, 6309.	12.8	33
10	Development and validation of a machine learning model for prediction of shoulder dystocia. <i>Ultrasound in Obstetrics and Gynecology</i> , 2020, 56, 588-596.	1.7	34
11	Prior presumed coronavirus infection reduces COVID-19 risk: A cohort study. <i>Journal of Infection</i> , 2020, 81, 923-930.	3.3	39
12	629: MFMU Calculator versus machine learning techniques for predicting VBAC success â€œ Which model works best?. <i>American Journal of Obstetrics and Gynecology</i> , 2020, 222, S401-S402.	1.3	0
13	Intratumoral CD4+ T Cells Mediate Anti-tumor Cytotoxicity in Human Bladder Cancer. <i>Cell</i> , 2020, 181, 1612-1625.e13.	28.9	436
14	Cell-Type Enrichment Analysis of Bulk Transcriptomes Using xCell. <i>Methods in Molecular Biology</i> , 2020, 2120, 263-276.	0.9	86
15	Human splice factors contribute to latent HIV infection in primary cell models and blood CD4+ T cells from ART-treated individuals. <i>PLoS Pathogens</i> , 2020, 16, e1009060.	4.7	18
16	Comprehensive transcriptomic analysis of cell lines as models of primary tumors across 22 tumor types. <i>Nature Communications</i> , 2019, 10, 3574.	12.8	111
17	Heterogeneity in HIV and cellular transcription profiles in cell line models of latent and productive infection: implications for HIV latency. <i>Retrovirology</i> , 2019, 16, 32.	2.0	35
18	657: Improving the prediction of shoulder dystocia using artificial intelligence â€œ a novel approach. <i>American Journal of Obstetrics and Gynecology</i> , 2019, 220, S435-S436.	1.3	1

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19	Reference-based analysis of lung single-cell sequencing reveals a transitional profibrotic macrophage. <i>Nature Immunology</i> , 2019, 20, 163-172.	14.5	2,330
20	CD161 contributes to prenatal immune suppression of IFN- $\gamma$ -producing PLZF+ T cells. <i>Journal of Clinical Investigation</i> , 2019, 129, 3562-3577.	8.2	55
21	Global Transcriptome Analysis of RNA Abundance Regulation by ADAR in Lung Adenocarcinoma. <i>EBioMedicine</i> , 2018, 27, 167-175.	6.1	23
22	Abstract 2398: Tumor cell-adipocyte gap junctions activate lipolysis in breast cancer. , 2018, , .		0
23	Comprehensive analysis of normal adjacent to tumor transcriptomes. <i>Nature Communications</i> , 2017, 8, 1077.	12.8	394
24	Precision annotation of digital samples in NCBI's gene expression omnibus. <i>Scientific Data</i> , 2017, 4, 170125.	5.3	44
25	Cancer Cell's Autonomous Parainflammation Mimics Immune Cell Infiltration. <i>Cancer Research</i> , 2017, 77, 3740-3744.	0.9	12
26	xCell: digitally portraying the tissue cellular heterogeneity landscape. <i>Genome Biology</i> , 2017, 18, 220.	8.8	2,572
27	Widespread parainflammation in human cancer. <i>Genome Biology</i> , 2016, 17, 145.	8.8	87
28	Digitally deconvolving the tumor microenvironment. <i>Genome Biology</i> , 2016, 17, 175.	8.8	20
29	Cross-tissue Analysis of Gene and Protein Expression in Normal and Cancer Tissues. <i>Scientific Reports</i> , 2016, 6, 24799.	3.3	155
30	Embryonic Stem Cell (ES)-Specific Enhancers Specify the Expression Potential of ES Genes in Cancer. <i>PLoS Genetics</i> , 2016, 12, e1005840.	3.5	10
31	Systematic pan-cancer analysis of tumour purity. <i>Nature Communications</i> , 2015, 6, 8971.	12.8	937
32	Premature aging of leukocyte DNA methylation is associated with type 2 diabetes prevalence. <i>Clinical Epigenetics</i> , 2015, 7, 35.	4.1	34
33	S-6. <i>Cytokine</i> , 2014, 70, 22.	3.2	1
34	Unmasking risk loci: <sc>DNA</sc> methylation illuminates the biology of cancer predisposition. <i>BioEssays</i> , 2014, 36, 184-190.	2.5	16
35	DNA methylation of distal regulatory sites characterizes dysregulation of cancer genes. <i>Genome Biology</i> , 2013, 14, R21.	9.6	288
36	Aging is associated with highly defined epigenetic changes in the human epidermis. <i>Epigenetics and Chromatin</i> , 2013, 6, 36.	3.9	72

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37	DNA Methylation of Transcriptional Enhancers and Cancer Predisposition. <i>Cell</i> , 2013, 154, 11-13.	28.9	156
38	Genome-wide survey reveals predisposing diabetes type 2-related DNA methylation variations in human peripheral blood. <i>Human Molecular Genetics</i> , 2012, 21, 371-383.	2.9	317
39	Replication timing-related and gene body-specific methylation of active human genes. <i>Human Molecular Genetics</i> , 2011, 20, 670-680.	2.9	256