Izhak Haviv

List of Publications by Year
in descending order

84 papers	6,358 citations	101543 36 h-index	85541 71 g-index
86 all docs	86 docs citations	86 times ranked	12653 citing authors

#	Article	IF	Citations
1	Novel Molecular Subtypes of Serous and Endometrioid Ovarian Cancer Linked to Clinical Outcome. Clinical Cancer Research, 2008, 14, 5198-5208.	7.0	1,312
2	Co-evolution of tumor cells and their microenvironment. Trends in Genetics, 2009, 25, 30-38.	6.7	544
3	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. Nature Communications, 2015, 6, 6605.	12.8	312
4	Breast-Cancer Stromal Cells withTP53Mutations and Nodal Metastases. New England Journal of Medicine, 2007, 357, 2543-2551.	27.0	288
5	No evidence of clonal somatic genetic alterations in cancer-associated fibroblasts from human breast and ovarian carcinomas. Nature Genetics, 2008, 40, 650-655.	21.4	269
6	Plasma Lipidomic Analysis of Stable and Unstable Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2723-2732.	2.4	265
7	Plasma Lipid Profiling Shows Similar Associations with Prediabetes and Type 2 Diabetes. PLoS ONE, 2013, 8, e74341.	2.5	247
8	An Expression-Based Site of Origin Diagnostic Method Designed for Clinical Application to Cancer of Unknown Origin. Cancer Research, 2005, 65, 4031-4040.	0.9	206
9	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. Genome Research, 2011, 21, 1601-1615.	5.5	198
10	Distinctive patterns of gene expression in premalignant gastric mucosa and gastric cancer. Cancer Research, 2003, 63, 2569-77.	0.9	172
11	A Novel Mouse Model of Atherosclerotic Plaque Instability for Drug Testing and Mechanistic/Therapeutic Discoveries Using Gene and MicroRNA Expression Profiling. Circulation Research, 2013, 113, 252-265.	4.5	164
12	Incessant ovulation, inflammation and epithelial ovarian carcinogenesis: Revisiting old hypotheses. Molecular and Cellular Endocrinology, 2006, 247, 4-21.	3.2	162
13	Hepatitis B Virus pX Targets TFIIB in Transcription Coactivation. Molecular and Cellular Biology, 1998, 18, 1562-1569.	2.3	137
14	is-rSNP: a novel technique for in silico regulatory SNP detection. Bioinformatics, 2010, 26, i524-i530.	4.1	115
15	Hepatitis C virus leaves an epigenetic signature post cure of infection by direct-acting antivirals. PLoS Genetics, 2019, 15, e1008181.	3.5	109
16	Origin of carcinoma associated fibroblasts. Cell Cycle, 2009, 8, 589-595.	2.6	104
17	The Ubiquitin Ligase Component Siah1a Is Required for Completion of Meiosis I in Male Mice. Molecular and Cellular Biology, 2002, 22, 2294-2303.	2.3	99
18	Epigenetic Regulation of Cell Typeâ€“Specific Expression Patterns in the Human Mammary Epithelium. PLoS Genetics, 2011, 7, e1001369.	3.5	96

#	Article	IF	Citations
19	The X protein of hepatitis B virus coactivates potent activation domains. Molecular and Cellular Biology, 1995, 15, 1079-1085.	2.3	95
20	Prediction of breast cancer prognosis using gene set statistics provides signature stability and biological context. BMC Bioinformatics, 2010, 11, 277.	2.6	87
21	EBNA1 regulates cellular gene expression by binding cellular promoters. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 22421-22426.	7.1	83
22	Vascular histone deacetylation by pharmacological HDAC inhibition. Genome Research, 2014, 24, 1271-1284.	5.5	79
23	Molecular Profiling of Human Mammary Gland Links Breast Cancer Risk to a p27+ Cell Population with Progenitor Characteristics. Cell Stem Cell, 2013, 13, 117-130.	11.1	72
24	The social aspects of EMT-MET plasticity. Nature Medicine, 2011, 17, 1048-1049.	30.7	71
25	Clonal Mutations in the Cancer-Associated Fibroblasts: The Case against Genetic Coevolution. Cancer Research, 2009, 69, 6765-6769.	0.9	70
26	Widespread FRA1-Dependent Control of Mesenchymal Transdifferentiation Programs in Colorectal Cancer Cells. PLoS ONE, 2014, 9, e88950.	2.5	69
27	A Signature Predicting Poor Prognosis in Gastric and Ovarian Cancer Represents a Coordinated Macrophage and Stromal Response. Clinical Cancer Research, 2014, 20, 2761-2772.	7.0	60
28	Microarray analysis of VEGF-responsive genes in myometrial endothelial cells. Molecular Human Reproduction, 2002, 8, 855-863.	2.8	57
29	Image-guided sampling reveals increased stroma and lower glandular complexity in mammographically dense breast tissue. Breast Cancer Research and Treatment, 2011, 128, 505-516.	2.5	52
30	A novel role for the Pol I transcription factor UBTF in maintaining genome stability through the regulation of highly transcribed Pol II genes. Genome Research, 2015, 25, 201-212.	5.5	52
31	Vascular Normalization by Loss of Siah2 Results in Increased Chemotherapeutic Efficacy. Cancer Research, 2012, 72, 1694-1704.	0.9	49
32	Successful In Vitro Expansion and Differentiation of Cord Blood Derived CD34+ Cells into Early Endothelial Progenitor Cells Reveals Highly Differential Gene Expression. PLoS ONE, 2011, 6, e23210.	2.5	49
33	Evaluation of Candidate Stromal Epithelial Cross-Talk Genes Identifies Association between Risk of Serous Ovarian Cancer and TERT, a Cancer Susceptibility â€œHot-Spotâ€• PLoS Genetics, 2010, 6, e1001016.	3.5	48
34	Enhanced RAD21 cohesin expression confers poor prognosis in BRCA2 and BRCAX, but not BRCA1 familial breast cancers. Breast Cancer Research, 2012, 14, R69.	5.0	45
35	Breast-Cancer Stromal Cells withTP53Mutations. New England Journal of Medicine, 2008, 358, 1634-1636.	27.0	43
36	Canonical Androstenedione Reduction Is the Predominant Source of Signaling Androgens in Hormone-Refractory Prostate Cancer. Clinical Cancer Research, 2014, 20, 5547-5557.	7.0	43

#	Article	IF	Citations
37	The X Protein of Hepatitis B Virus Has a ribo/deoxy ATPase Activity. Virology, 1994, 202, 401-407.	2.4	41
38	Genetic changes in tumour microenvironments. Journal of Pathology, 2011, 223, 450-458.	4.5	31
39	pX, the HBV-encoded coactivator, suppresses the phenotypes of TBP and TAFII250Âmutants. Genes and Development, 1998, 12, 1217-1226.	5.9	29
40	An NF1 Motif Plays a Central Role in Hepatitis B Virus Enhancer. Virology, 1994, 204, 600-608.	2.4	24
41	DNA microarrays for assessing ovarian cancer gene expression. Molecular and Cellular Endocrinology, 2002, 191, 121-126.	3.2	24
42	Combining target enrichment with barcode multiplexing for high throughput SNP discovery. BMC Genomics, 2010, 11, 641.	2.8	24
43	Effects of Tamoxifen and oestrogen on histology and radiographic density in high and low mammographic density human breast tissues maintained in murine tissue engineering chambers. Breast Cancer Research and Treatment, 2014, 148, 303-314.	2.5	20
44	Can molecular profiling enhance radiotherapy? Impact of personalized targeted gold nanoparticles on radiosensitivity and imaging of adenoid cystic carcinoma. Theranostics, 2017, 7, 3962-3971.	10.0	20
45	Opposing effects of monomeric and pentameric C-reactive protein on endothelial progenitor cells. Basic Research in Cardiology, 2011, 106, 879-95.	5.9	18
46	Using Gene Ontology annotations in exploratory microarray clustering to understand cancer etiology. Pattern Recognition Letters, 2010, 31, 2138-2146.	4.2	16
47	Increased COX-2 expression in epithelial and stromal cells of high mammographic density tissues and in a xenograft model of mammographic density. Breast Cancer Research and Treatment, 2015, 153, 89-99.	2.5	16
48	Interactions within the MHC contribute to the genetic architecture of celiac disease. PLoS ONE, 2017, 12, e0172826.	2.5	16
49	A Composite Polyadenylation Signal with TATA Box Function. Molecular and Cellular Biology, 2000, 20, 834-841.	2.3	15
50	MIRAGAAâ€”a methodology for finding coordinated effects of microRNA expression changes and genome aberrations in cancer. Bioinformatics, 2010, 26, 161-167.	4.1	15
51	Cardiacâ€peripheral transvenous gradients of microRNA expression in systolic heart failure patients. ESC Heart Failure, 2020, 7, 835-843.	3.1	14
52	High and low mammographic density human breast tissues maintain histological differential in murine tissue engineering chambers. Breast Cancer Research and Treatment, 2012, 135, 177-187.	2.5	13
53	Dynamic changes in high and low mammographic density human breast tissues maintained in murine tissue engineering chambers during various murine peripartum states and over time. Breast Cancer Research and Treatment, 2013, 140, 285-297.	2.5	13
54	Discovery and analysis of consistent active sub-networks in cancers. BMC Bioinformatics, 2013, 14, S7.	2.6	12

#	Article	IF	Citations
55	Comparative microRNA profiling of sporadic and BRCA1 associated basal-like breast cancers. BMC Cancer, 2015, 15, 506.	2.6	12
56	IRS1 phosphorylation underlies the non-stochastic probability of cancer cells to persist during EGFR inhibition therapy. Nature Cancer, 2021, 2, 1055-1070.	13.2	9
57	Soiling the Seed: Microenvironment and Epithelial Mesenchymal Plasticity. Cancer Microenvironment, 2012, 5, 1-3.	3.1	8
58	Appraisal of progenitor markers in the context of molecular classification of breast cancers. Breast Cancer Research, 2011, 13, 102.	5.0	7
59	Dysregulation of the cohesin subunit RAD21 by Hepatitis C virus mediates hostâ€“virus interactions. Nucleic Acids Research, 2019, 47, 2455-2471.	14.5	7
60	Differential microRNAs expression in calcified versus rheumatic aortic valve disease. Journal of Cardiac Surgery, 2020, 35, 1508-1513.	0.7	6
61	MSH2-deficient prostate tumours have a distinct immune response and clinical outcome compared to MSH2-deficient colorectal or endometrial cancer. Prostate Cancer and Prostatic Diseases, 2021, 24, 1167-1180.	3.9	4
62	Current and potential uses for DNA microarrays in transplantation medicine: lessons from other disciplines. Tissue Antigens, 2003, 62, 93-103.	1.0	3
63	Simple SVM based whole-genome segmentation. Nature Precedings, 2009, , .	0.1	3
64	A bi-ordering approach to linking gene expression with clinical annotations in gastric cancer. BMC Bioinformatics, 2010, 11, 477.	2.6	3
65	Promoting Precision Cancer Medicine through a Community-Driven Knowledgebase. Journal of Personalized Medicine, 2014, 4, 475-488.	2.5	3
66	is-rSNP: a novel technique for in silico regulatory SNP detection. BMC Bioinformatics, 2010, 11, .	2.6	2
67	Meta-analysis of gene expression microarrays with missing replicates. BMC Bioinformatics, 2011, 12, 84.	2.6	2
68	Determining epithelial contribution to in vivo mesenchymal tumour expression signature using species-specific microarray profiling analysis of xenografts. Genetical Research, 2013, 95, 14-29.	0.9	2
69	Exploiting sequence similarity to validate the sensitivity of SNP arrays in detecting fine-scaled copy number variations. Bioinformatics, 2010, 26, 1007-1014.	4.1	1
70	Replication of epistatic DNA loci in two case-control GWAS studies using OPE algorithm. BMC Bioinformatics, 2011, 12, .	2.6	1
71	Using whole-genome sequencing to implicate the androgen receptor as the predominant driver of DNA breakpoints and fusion events in prostate cancer.. Journal of Clinical Oncology, 2014, 32, 67-67.	1.6	1
72	The X protein of HBV acts as a transcription coactivator both in vivo and in vitro. Journal of Cancer Research and Clinical Oncology, 1995, 121, S15-S15.	2.5	0

#	Article	IF	Citations
73	Assessing the involvement of the placental microbiome and virome in preeclampsia using non coding RNA sequencing. Journal of Perinatal Medicine, 2021, 49, 1071-1083.	1.4	0
74	Gene Ontology Assisted Exploratory Microarray Clustering and Its Application to Cancer. Lecture Notes in Computer Science, 2008, , 400-411.	1.3	0
75	DNA Methylation Profiling of Childhood Acute Lymphoblastic Leukaemia Using Illumina Infinium DNA Methylation27 Bead Arrays Identifies a Distinct DNA Methylation Signature Associated with Leukaemogenesis. Blood, 2010, 116, 4650-4650.	1.4	0
76	Abstract 3428: Coordinated regulation of mesenchymal epithelial transition in the PMC42-LA breast cancer cell line variant. , 2011, , .		0
77	Abstract B093: Discovery of microRNAs associated with breast cancer EMT using bioinformatics and next-generation sequencing. , 2013, , .		0
78	Abstract B092: Beta-blockade of breast cancer metastasis: Receptor regulation and downstream signaling pathways. , 2013, , .		0
79	Abstract 1060: Integrated target discovery in the EMPathy Breast Cancer Network - Multidimensional analysis of epithelial mesenchymal plasticity (EMP) in experimental systems. , 2014, , .		0
80	Tracking clonal diversity in metastatic prostate cancer progression.. Journal of Clinical Oncology, 2015, 33, 193-193.	1.6	0
81	Abstract 4980: Rational design of combination therapies and block of acquired targeted drug resistance. , 2015, , .		0
82	The impact of molecular profiling guided targeted gold nanoparticles on radiosensitivity of metastatic salivary gland adenoid cystic carcinoma.. Journal of Clinical Oncology, 2016, 34, e17558-e17558.	1.6	0
83	Abstract 5564: The interplay between etiology-dependent genomic and epigenetic signatures: The paradigm of liver cancer. , 2017, , .		0
84	Abstract 1190: Comprehensive high-throughput screen for combination therapies to block acquired resistance to targeted drugs. , 2017, , .		0