Izhak Haviv

List of Publications by Year in descending order

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84 papers

6,358 citations

36 h-index 71 g-index

86 all docs 86 docs citations

86 times ranked 12653 citing authors

#	Article	IF	CITATIONS
1	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
2	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
3	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
4	Cardiacâ€peripheral transvenous gradients of microRNA expression in systolic heart failure patients. ESC Heart Failure, 2020, 7, 835-843.	3.1	14
5	Differential microRNAs expression in calcified versus rheumatic aortic valve disease. Journal of Cardiac Surgery, 2020, 35, 1508-1513.	0.7	6
6	Dysregulation of the cohesin subunit RAD21 by Hepatitis C virus mediates host–virus interactions. Nucleic Acids Research, 2019, 47, 2455-2471.	14.5	7
7	Hepatitis C virus leaves an epigenetic signature post cure of infection by direct-acting antivirals. PLoS Genetics, 2019, 15, e1008181.	3.5	109
8	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
9	Interactions within the MHC contribute to the genetic architecture of celiac disease. PLoS ONE, 2017, 12, e0172826.	2.5	16
10	Abstract 5564: The interplay between etiology-dependent genomic and epigenetic signatures: The paradigm of liver cancer. , 2017, , .		0
11	Abstract 1190: Comprehensive high-throughput screen for combination therapies to block acquired resistance to targeted drugs., 2017,,.		O
12	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
13	Tracking the origins and drivers of subclonal metastatic expansion in prostate cancer. Nature Communications, 2015, 6, 6605.	12.8	312
14	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
15	Comparative microRNA profiling of sporadic and BRCA1 associated basal-like breast cancers. BMC Cancer, 2015, 15, 506.	2.6	12
16	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
17	Tracking clonal diversity in metastatic prostate cancer progression Journal of Clinical Oncology, 2015, 33, 193-193.	1.6	0
18	Abstract 4980: Rational design of combination therapies and block of acquired targeted drug resistance. , 2015, , .		0

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19	Promoting Precision Cancer Medicine through a Community-Driven Knowledgebase. Journal of Personalized Medicine, 2014, 4, 475-488.	2.5	3
20	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
21	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
22	Vascular histone deacetylation by pharmacological HDAC inhibition. Genome Research, 2014, 24, 1271-1284.	5.5	79
23	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
24	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
25	Widespread FRA1-Dependent Control of Mesenchymal Transdifferentiation Programs in Colorectal Cancer Cells. PLoS ONE, 2014, 9, e88950.	2.5	69
26	Abstract 1060: Integrated target discovery in the EMPathy Breast Cancer Network - Multidimensional analysis of epithelial mesenchymal plasticity (EMP) in experimental systems., 2014,,.		0
27	Discovery and analysis of consistent active sub-networks in cancers. BMC Bioinformatics, 2013, 14, S7.	2.6	12
28	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
29	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
30	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
31	Determining epithelial contribution to <i>in vivo</i> mesenchymal tumour expression signature using species-specific microarray profiling analysis of xenografts. Genetical Research, 2013, 95, 14-29.	0.9	2
32	Plasma Lipid Profiling Shows Similar Associations with Prediabetes and Type 2 Diabetes. PLoS ONE, 2013, 8, e74341.	2.5	247
33	Abstract B093: Discovery of microRNAs associated with breast cancer EMT using bioinformatics and next-generation sequencing. , 2013, , .		0
34	Abstract B092: Beta-blockade of breast cancer metastasis: Receptor regulation and downstream signaling pathways. , 2013, , .		0
35	Vascular Normalization by Loss of Siah2 Results in Increased Chemotherapeutic Efficacy. Cancer Research, 2012, 72, 1694-1704.	0.9	49
36	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

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37	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
38	Soiling the Seed: Microenvironment and Epithelial Mesenchymal Plasticity. Cancer Microenvironment, 2012, 5, 1-3.	3.1	8
39	Genome-wide analysis distinguishes hyperglycemia regulated epigenetic signatures of primary vascular cells. Genome Research, 2011, 21, 1601-1615.	5.5	198
40	The social aspects of EMT-MET plasticity. Nature Medicine, 2011, 17, 1048-1049.	30.7	71
41	Appraisal of progenitor markers in the context of molecular classification of breast cancers. Breast Cancer Research, 2011, 13, 102.	5.0	7
42	Meta-analysis of gene expression microarrays with missing replicates. BMC Bioinformatics, 2011, 12, 84.	2.6	2
43	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
44	Opposing effects of monomeric and pentameric C-reactive protein on endothelial progenitor cells. Basic Research in Cardiology, 2011, 106, 879-95.	5.9	18
45	Replication of epistatic DNA loci in two case-control GWAS studies using OPE algorithm. BMC Bioinformatics, 2011, 12, .	2.6	1
46	Genetic changes in tumour microenvironments. Journal of Pathology, 2011, 223, 450-458.	4.5	31
47	Plasma Lipidomic Analysis of Stable and Unstable Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2011, 31, 2723-2732.	2.4	265
48	Epigenetic Regulation of Cell Type–Specific Expression Patterns in the Human Mammary Epithelium. PLoS Genetics, 2011, 7, e1001369.	3.5	96
49	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
50	Abstract 3428: Coordinated regulation of mesenchymal epithelial transition in the PMC42-LA breast cancer cell line variant., 2011,,.		0
51	Using Gene Ontology annotations in exploratory microarray clustering to understand cancer etiology. Pattern Recognition Letters, 2010, 31, 2138-2146.	4.2	16
52	Prediction of breast cancer prognosis using gene set statistics provides signature stability and biological context. BMC Bioinformatics, 2010, 11, 277.	2.6	87
53	A bi-ordering approach to linking gene expression with clinical annotations in gastric cancer. BMC Bioinformatics, 2010, 11, 477.	2.6	3
54	is-rSNP: a novel technique for in silico regulatory SNP detection. BMC Bioinformatics, 2010, 11, .	2.6	2

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55	Combining target enrichment with barcode multiplexing for high throughput SNP discovery. BMC Genomics, 2010, 11, 641.	2.8	24
56	MIRAGAA—a methodology for finding coordinated effects of microRNA expression changes and genome aberrations in cancer. Bioinformatics, 2010, 26, 161-167.	4.1	15
57	Evaluation of Candidate Stromal Epithelial Cross-Talk Genes Identifies Association between Risk of Serous Ovarian Cancer and TERT, a Cancer Susceptibility "Hot-Spot― PLoS Genetics, 2010, 6, e1001016.	3.5	48
58	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
59	is-rSNP: a novel technique for <i>iin silico</i> regulatory SNP detection. Bioinformatics, 2010, 26, i524-i530.	4.1	115
60	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
61	Simple SVM based whole-genome segmentation. Nature Precedings, 2009, , .	0.1	3
62	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
63	Origin of carcinoma associated fibroblasts. Cell Cycle, 2009, 8, 589-595.	2.6	104
64	Clonal Mutations in the Cancer-Associated Fibroblasts: The Case against Genetic Coevolution. Cancer Research, 2009, 69, 6765-6769.	0.9	70
65	Co-evolution of tumor cells and their microenvironment. Trends in Genetics, 2009, 25, 30-38.	6.7	544
66	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
67	Novel Molecular Subtypes of Serous and Endometrioid Ovarian Cancer Linked to Clinical Outcome. Clinical Cancer Research, 2008, 14, 5198-5208.	7.0	1,312
68	Breast-Cancer Stromal Cells withTP53Mutations. New England Journal of Medicine, 2008, 358, 1634-1636.	27.0	43
69	Gene Ontology Assisted Exploratory Microarray Clustering and Its Application to Cancer. Lecture Notes in Computer Science, 2008, , 400-411.	1.3	0
70	Breast-Cancer Stromal Cells with <i>TP53 </i> Mutations and Nodal Metastases. New England Journal of Medicine, 2007, 357, 2543-2551.	27.0	288
71	Incessant ovulation, inflammation and epithelial ovarian carcinogenesis: Revisiting old hypotheses. Molecular and Cellular Endocrinology, 2006, 247, 4-21.	3.2	162
72	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

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73	Current and potential uses for DNA microarrays in transplantation medicine: lessons from other disciplines. Tissue Antigens, 2003, 62, 93-103.	1.0	3
74	Distinctive patterns of gene expression in premalignant gastric mucosa and gastric cancer. Cancer Research, 2003, 63, 2569-77.	0.9	172
75	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
76	Microarray analysis of VEGF-responsive genes in myometrial endothelial cells. Molecular Human Reproduction, 2002, 8, 855-863.	2.8	57
77	DNA microarrays for assessing ovarian cancer gene expression. Molecular and Cellular Endocrinology, 2002, 191, 121-126.	3.2	24
78	A Composite Polyadenylation Signal with TATA Box Function. Molecular and Cellular Biology, 2000, 20, 834-841.	2.3	15
79	Hepatitis B Virus pX Targets TFIIB in Transcription Coactivation. Molecular and Cellular Biology, 1998, 18, 1562-1569.	2.3	137
80	pX, the HBV-encoded coactivator, suppresses the phenotypes of TBP and TAFII250Âmutants. Genes and Development, 1998, 12, 1217-1226.	5.9	29
81	The X protein of hepatitis B virus coactivates potent activation domains. Molecular and Cellular Biology, 1995, 15, 1079-1085.	2.3	95
82	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
83	The X Protein of Hepatitis B Virus Has a ribo/deoxy ATPase Activity. Virology, 1994, 202, 401-407.	2.4	41
84	An NF1 Motif Plays a Central Role in Hepatitis B Virus Enhancer. Virology, 1994, 204, 600-608.	2.4	24