

Doron Betel

List of Publications by Year in descending order

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Version: 2024-02-01

63
papers

10,026
citations

117571

34
h-index

149623

56
g-index

72
all docs

72
docs citations

72
times ranked

18941
citing authors

#	ARTICLE	IF	CITATIONS
1	An autoimmune stem-like CD8 T cell population drives type 1 diabetes. <i>Nature</i> , 2022, 602, 156-161.	13.7	85
2	TCR signal strength defines distinct mechanisms of T cell dysfunction and cancer evasion. <i>Journal of Experimental Medicine</i> , 2022, 219, .	4.2	64
3	Immunogenicity and therapeutic targeting of a public neoantigen derived from mutated PIK3CA. <i>Nature Medicine</i> , 2022, 28, 946-957.	15.2	50
4	Comparison of ACR-TIRADS to the ATA Guidelines for Thyroid Nodules: A Neck to Neck Comparison. , 2022, 1, 1-8.		1
5	Fully defined human pluripotent stem cell-derived microglia and tri-culture system model C3 production in Alzheimer's disease. <i>Nature Neuroscience</i> , 2021, 24, 343-354.	7.1	118
6	Biphasic Activation of WNT Signaling Facilitates the Derivation of Midbrain Dopamine Neurons from hESCs for Translational Use. <i>Cell Stem Cell</i> , 2021, 28, 343-355.e5.	5.2	100
7	Impact of Use of Antibiotics on Response to Immune Checkpoint Inhibitors and Tumor Microenvironment. <i>American Journal of Clinical Oncology: Cancer Clinical Trials</i> , 2021, 44, 247-253.	0.6	19
8	Discovery of Candidate DNA Methylation Cancer Driver Genes. <i>Cancer Discovery</i> , 2021, 11, 2266-2281.	7.7	42
9	Multicenter, randomized phase II study of neoadjuvant pembrolizumab plus chemotherapy and chemoradiotherapy in esophageal adenocarcinoma (EAC).. <i>Journal of Clinical Oncology</i> , 2021, 39, 4005-4005.	0.8	18
10	Selective BCL-X _L Antagonists Eliminate Infected Cells from a Primary-Cell Model of HIV Latency but Not from <i>Ex Vivo</i> Reservoirs. <i>Journal of Virology</i> , 2021, 95, e0242520.	1.5	10
11	Hippocampal Transcriptome Changes After Subarachnoid Hemorrhage in Mice. <i>Frontiers in Neurology</i> , 2021, 12, 691631.	1.1	4
12	Inducible and reversible inhibition of miRNA-mediated gene repression in vivo. <i>ELife</i> , 2021, 10, .	2.8	23
13	Selective STAT3 Degraders Dissect Peripheral T-Cell Lymphomas Vulnerabilities Empowering Personalized Regimens. <i>Blood</i> , 2021, 138, 865-865.	0.6	0
14	High-Resolution <i>In Vivo</i> Identification of miRNA Targets by Halo-Enhanced Ago2 Pull-Down. <i>Molecular Cell</i> , 2020, 79, 167-179.e11.	4.5	36
15	A Novel JAK1 Mutant Breast Implant-Associated Anaplastic Large Cell Lymphoma Patient-Derived Xenograft Fostering Pre-Clinical Discoveries. <i>Cancers</i> , 2020, 12, 1603.	1.7	11
16	Multicenter Phase II Study of Cabazitaxel in Advanced Gastroesophageal Cancer: Association of HER2 Expression and M2-Like Tumor-Associated Macrophages with Patient Outcome. <i>Clinical Cancer Research</i> , 2020, 26, 4756-4766.	3.2	7
17	A Multiplex Human Pluripotent Stem Cell Platform Defines Molecular and Functional Subclasses of Autism-Related Genes. <i>Cell Stem Cell</i> , 2020, 27, 35-49.e6.	5.2	56
18	Microtubule Engagement with Taxane Is Altered in Taxane-Resistant Gastric Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 3771-3783.	3.2	19

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19	Three-dimensional growth of breast cancer cells potentiates the anti-tumor effects of unacylated ghrelin and AZP-531. <i>ELife</i> , 2020, 9, .	2.8	7
20	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020, 136, 33-34.	0.6	0
21	TOX is a critical regulator of tumour-specific T cell differentiation. <i>Nature</i> , 2019, 571, 270-274.	13.7	697
22	A Comparison of Homogenization vs. Enzymatic Lysis for Microbiome Profiling in Clinical Endoscopic Biopsy Tissue Samples. <i>Frontiers in Microbiology</i> , 2019, 9, 3246.	1.5	9
23	Lipid Deprivation Induces a Stable, Naive-to-Primed Intermediate State of Pluripotency in Human PSCs. <i>Cell Stem Cell</i> , 2019, 25, 120-136.e10.	5.2	98
24	Genome-scale screens identify JNK–JUN signaling as a barrier for pluripotency exit and endoderm differentiation. <i>Nature Genetics</i> , 2019, 51, 999-1010.	9.4	90
25	Impact of antibiotic use on response to treatment with immune checkpoint inhibitors.. <i>Journal of Clinical Oncology</i> , 2019, 37, 143-143.	0.8	10
26	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018, 5, 180061.	2.4	152
27	Extracellular vesicles in DLBCL provide abundant clues to aberrant transcriptional programming and genomic alterations. <i>Blood</i> , 2018, 132, e13-e23.	0.6	23
28	“Same difference” comprehensive evaluation of four DNA methylation measurement platforms. <i>Epigenetics and Chromatin</i> , 2018, 11, 21.	1.8	27
29	Early-onset Colorectal Cancer is Distinct From Traditional Colorectal Cancer. <i>Clinical Colorectal Cancer</i> , 2017, 16, 293-299.e6.	1.0	117
30	CryoPause: A New Method to Immediately Initiate Experiments after Cryopreservation of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2017, 9, 355-365.	2.3	21
31	The Gastric Microbiome and Its Influence on Gastric Carcinogenesis. <i>Hematology/Oncology Clinics of North America</i> , 2017, 31, 389-408.	0.9	27
32	Encoding of Contextual Fear Memory Requires De Novo Proteins in the Prelimbic Cortex. <i>Biological Psychiatry: Cognitive Neuroscience and Neuroimaging</i> , 2017, 2, 158-169.	1.1	25
33	Circulating Plasma Levels of MicroRNA-21 and MicroRNA-221 Are Potential Diagnostic Markers for Primary Intrahepatic Cholangiocarcinoma. <i>PLoS ONE</i> , 2016, 11, e0163699.	1.1	52
34	Enhanced Reduced Representation Bisulfite Sequencing for Assessment of DNA Methylation at Base Pair Resolution. <i>Journal of Visualized Experiments</i> , 2015, , e52246.	0.2	89
35	Response to Zhou and Robinson. <i>Genome Biology</i> , 2015, 16, 223.	3.8	0
36	Multiplexing of ChIP-Seq Samples in an Optimized Experimental Condition Has Minimal Impact on Peak Detection. <i>PLoS ONE</i> , 2015, 10, e0129350.	1.1	0

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37	An allelic series of miR-17 ^{1/492} mutant mice uncovers functional specialization and cooperation among members of a microRNA polycistron. <i>Nature Genetics</i> , 2015, 47, 766-775.	9.4	101
38	Identification of low abundance microbiome in clinical samples using whole genome sequencing. <i>Genome Biology</i> , 2015, 16, 265.	3.8	90
39	Identification of the gastric microbiome from endoscopic biopsy samples using whole genome sequencing.. <i>Journal of Clinical Oncology</i> , 2015, 33, 8-8.	0.8	0
40	Characterization of DLBCL-Derived Exosomes and Investigation of Their Biological Properties. <i>Blood</i> , 2014, 124, 3021-3021.	0.6	8
41	Whole-genome sequencing (WGS) to identify <i>H. pylori</i> and its impact on the gastric microbiome.. <i>Journal of Clinical Oncology</i> , 2014, 32, 11070-11070.	0.8	0
42	Comprehensive evaluation of differential gene expression analysis methods for RNA-seq data. <i>Genome Biology</i> , 2013, 14, R95.	13.9	588
43	Neurophysiological Defects and Neuronal Gene Deregulation in <i>Drosophila</i> mir-124 Mutants. <i>PLoS Genetics</i> , 2012, 8, e1002515.	1.5	48
44	Genome-wide identification of miRNA targets by PAR-CLIP. <i>Methods</i> , 2012, 58, 94-105.	1.9	91
45	The expanding role of miR-302 ³⁶⁷ in pluripotency and reprogramming. <i>Cell Cycle</i> , 2012, 11, 1517-1523.	1.3	61
46	Genome-wide identification of microRNA targets in human ES cells reveals a role for miR-302 in modulating BMP response. <i>Genes and Development</i> , 2011, 25, 2173-2186.	2.7	175
47	Widespread regulatory activity of vertebrate microRNA* species. <i>Rna</i> , 2011, 17, 312-326.	1.6	293
48	Comprehensive modeling of microRNA targets predicts functional non-conserved and non-canonical sites. <i>Genome Biology</i> , 2010, 11, R90.	13.9	1,478
49	Genetic dissection of the miR-17 ^{1/492} cluster of microRNAs in Myc-induced B-cell lymphomas. <i>Genes and Development</i> , 2009, 23, 2806-2811.	2.7	425
50	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. <i>Nature Biotechnology</i> , 2009, 27, 549-555.	9.4	470
51	Characterization of Small RNAs in <i>Aplysia</i> Reveals a Role for miR-124 in Constraining Synaptic Plasticity through CREB. <i>Neuron</i> , 2009, 63, 803-817.	3.8	374
52	Structure-Templated Predictions of Novel Protein Interactions from Sequence Information. <i>PLoS Computational Biology</i> , 2007, 3, e182.	1.5	39
53	Computational Analysis of Mouse piRNA Sequence and Biogenesis. <i>PLoS Computational Biology</i> , 2007, 3, e222.	1.5	83
54	The microRNA.org resource: targets and expression. <i>Nucleic Acids Research</i> , 2007, 36, D149-D153.	6.5	2,280

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55	COMPUTATIONAL CHALLENGES IN THE STUDY OF SMALL REGULATORY RNAs – Session Introduction. , 2007, , .		0
56	Computational analysis of mouse piRNA sequence and biogenesis. PLoS Computational Biology, 2005, preprint, e222.	1.5	0
57	Analysis of domain correlations in yeast protein complexes. Bioinformatics, 2004, 20, i55-i62.	1.8	10
58	BIND: the Biomolecular Interaction Network Database. Nucleic Acids Research, 2003, 31, 248-250.	6.5	969
59	Cloning and expression of a novel UDP-GlcNAc:Î±-d-mannoside Î²1,2-N-acetylglucosaminyltransferase homologous to UDP-GlcNAc:Î±-3-d-mannoside Î²1,2-N-acetylglucosaminyltransferase I. Biochemical Journal, 2002, 361, 153.	1.7	43
60	Cloning and expression of a novel UDP-GlcNAc:Î±-d-mannoside Î²1,2-N-acetylglucosaminyltransferase homologous to UDP-GlcNAc:Î±-3-d-mannoside Î²1,2-N-acetylglucosaminyltransferase I. Biochemical Journal, 2002, 361, 153-162.	1.7	56
61	Kangaroo—a pattern-matching program for biological sequences. BMC Bioinformatics, 2002, 3, 20.	1.2	13
62	SeqHound: biological sequence and structure database as a platform for bioinformatics research. BMC Bioinformatics, 2002, 3, 32.	1.2	40
63	Mutation profiling of mismatch repair-deficient colorectal cancers using an in silico genome scan to identify coding microsatellites. Cancer Research, 2002, 62, 1284-8.	0.4	46