

Eitan Rubin

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

1,664
citations

394421

19
h-index

302126

39
g-index

47
all docs

47
docs citations

47
times ranked

3424
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic and transcriptomic profiling expands precision cancer medicine: the WINTHER trial. <i>Nature Medicine</i> , 2019, 25, 751-758.	30.7	362
2	Intron retention is a major phenomenon in alternative splicing in <i>Arabidopsis</i> . <i>Plant Journal</i> , 2004, 39, 877-885.	5.7	297
3	Two Patterns of Adipokine and Other Biomarker Dynamics in a Long-Term Weight Loss Intervention. <i>Diabetes Care</i> , 2012, 35, 342-349.	8.6	114
4	Biases and complex patterns in the residues flanking protein N-glycosylation sites. <i>Glycobiology</i> , 2003, 14, 95-101.	2.5	111
5	Mitochondrial DNA heteroplasmy in diabetes and normal adults: role of acquired and inherited mutational patterns in twins. <i>Human Molecular Genetics</i> , 2012, 21, 4214-4224.	2.9	79
6	Comparative Cross-Species Alternative Splicing in Plants. <i>Plant Physiology</i> , 2007, 144, 1632-1641.	4.8	73
7	Redefining meaningful age groups in the context of disease. <i>Age</i> , 2013, 35, 2357-2366.	3.0	61
8	Synthetic lethality-mediated precision oncology via the tumor transcriptome. <i>Cell</i> , 2021, 184, 2487-2502.e13.	28.9	60
9	BORIS/CTCFL promotes a switch from a proliferative towards an invasive phenotype in melanoma cells. <i>Cell Death Discovery</i> , 2020, 6, 1.	4.7	59
10	Serum Apolipoproteins C-I and C-III Are Reduced in Stomach Cancer Patients: Results from MALDI-Based Peptidome and Immuno-Based Clinical Assays. <i>PLoS ONE</i> , 2011, 6, e14540.	2.5	43
11	Tight coevolution of proliferating cell nuclear antigen (PCNA)-partner interaction networks in fungi leads to interspecies network incompatibility. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E406-14.	7.1	37
12	Array-Based Disease Diagnostics Using Lipid/Polydiacetylene Vesicles Encapsulated in a Solâ€“Gel Matrix. <i>Analytical Chemistry</i> , 2012, 84, 5925-5931.	6.5	33
13	mtDNA mutation pattern in tumors and human evolution are shaped by similar selective constraints. <i>Genome Research</i> , 2009, 19, 576-580.	5.5	31
14	The Mouse Age Phenome Knowledgebase and Disease-Specific Inter-Species Age Mapping. <i>PLoS ONE</i> , 2013, 8, e81114.	2.5	30
15	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. <i>Aging Cell</i> , 2020, 19, e13158.	6.7	27
16	Survival in acute myeloid leukemia is associated with NKp44 splice variants. <i>Oncotarget</i> , 2016, 7, 32933-32945.	1.8	27
17	MitoBamAnnotator: A web-based tool for detecting and annotating heteroplasmy in human mitochondrial DNA sequences. <i>Mitochondrion</i> , 2011, 11, 924-928.	3.4	26
18	The Neural/Immune Gene Ontology: clipping the Gene Ontology for neurological and immunological systems. <i>BMC Bioinformatics</i> , 2010, 11, 458.	2.6	23

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19	A simplified interventional mapping system (SIMS) for the selection of combinations of targeted treatments in non-small cell lung cancer. <i>Oncotarget</i> , 2015, 6, 14139-14152.	1.8	22
20	Applying Instructional Design Theories to Bioinformatics Education in Microarray Analysis and Primer Design Workshops. <i>CBE: Life Sciences Education</i> , 2005, 4, 199-206.	0.7	16
21	NKp44 and NKp30 splice variant profiles in decidua and tumor tissues: a comparative viewpoint. <i>Oncotarget</i> , 2016, 7, 70912-70923.	1.8	14
22	CHILD: a new tool for detecting low-abundance insertions and deletions in standard sequence traces. <i>Nucleic Acids Research</i> , 2011, 39, e47-e47.	14.5	12
23	Identification of Tumor Antigens in the HLA Peptidome of Patient-derived Xenograft Tumors in Mouse. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 1360-1374.	3.8	12
24	Towards an Age-Phenome Knowledge-base. <i>BMC Bioinformatics</i> , 2011, 12, 229.	2.6	9
25	PCM-SABRE: a platform for benchmarking and comparing outcome prediction methods in precision cancer medicine. <i>BMC Bioinformatics</i> , 2017, 18, 40.	2.6	9
26	Circumventing the cut-off for enrichment analysis. <i>Briefings in Bioinformatics</i> , 2006, 7, 202-203.	6.5	8
27	Suicidal Thoughts Are Associated with Platelet Counts in Adolescent Inpatients. <i>Journal of Child and Adolescent Psychopharmacology</i> , 2013, 23, 49-53.	1.3	8
28	Unsupervised Analysis of Classical Biomedical Markers: Robustness and Medical Relevance of Patient Clustering Using Bioinformatics Tools. <i>PLoS ONE</i> , 2012, 7, e29578.	2.5	8
29	A <sc>WIN</sc> Consortium phase I study exploring avelumab, palbociclib, and axitinib in advanced nonâ€small cell lung cancer. <i>Cancer Medicine</i> , 2022, 11, 2790-2800.	2.8	7
30	The Realistic Modeling of Biological Systems: A Workshop Synopsis. <i>Complexus</i> , 2006, 3, 217-230.	0.6	6
31	PICOT binding to chromatin-associated EED negatively regulates cyclin D2 expression by increasing H3K27me3 at the CCND2 gene promoter. <i>Cell Death and Disease</i> , 2019, 10, 685.	6.3	6
32	A Novel â€œReactomicsâ€ Approach for Cancer Diagnostics. <i>Sensors</i> , 2012, 12, 5572-5585.	3.8	5
33	Digital Display Precision Predictor: the prototype of a global biomarker model to guide treatments with targeted therapy and predict progression-free survival. <i>Npj Precision Oncology</i> , 2021, 5, 33.	5.4	5
34	Reverse translational bioinformatics: a bioinformatics assay of age, gender and clinical biomarkers. <i>Summit on Translational Bioinformatics</i> , 2008, 2008, 11-5.	0.7	5
35	The age-phenome database. <i>SpringerPlus</i> , 2012, 1, 4.	1.2	4
36	Promoting Precision Cancer Medicine through a Community-Driven Knowledgebase. <i>Journal of Personalized Medicine</i> , 2014, 4, 475-488.	2.5	3

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37	Extracting tumor tissue immune status from expression profiles: correlating renal cancer prognosis with tumor-associated immunome. <i>Oncotarget</i> , 2015, 6, 33191-33205.	1.8	3
38	Ethnic differences in age-related changes of postpartum hemoglobin levels. <i>Archives of Gynecology and Obstetrics</i> , 2011, 283, 173-178.	1.7	2
39	Direct comparison shows that mRNA-based diagnostics incorporate information which cannot be learned directly from genomic mutations. <i>BMC Bioinformatics</i> , 2020, 21, 196.	2.6	2
40	High levels of LINE-1 transposable elements expressed in Kaposi's sarcoma-associated herpesvirus-related primary effusion lymphoma. <i>Oncogene</i> , 2021, 40, 536-550.	5.9	2
41	List mania: interpreting microarray results with the L2L server. <i>Briefings in Bioinformatics</i> , 2006, 7, 121-122.	6.5	1
42	Results of an early second PCR test performed on SARS-CoV-2 positive patients may support risk assessment for severe COVID-19. <i>Scientific Reports</i> , 2021, 11, 20463.	3.3	1
43	Binding of. <i>Molecular Genetics and Genomics</i> , 1996, 251, 436.	2.4	0