Eitan Rubin

List of Publications by Year
in descending order

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	A <scp>WIN</scp> Consortium phase I study exploring avelumab, palbociclib, and axitinib in advanced non‐small cell lung cancer. Cancer Medicine, 2022, 11, 2790-2800.	2.8	7
2	High levels of LINE-1 transposable elements expressed in Kaposi's sarcoma-associated herpesvirus-related primary effusion lymphoma. Oncogene, 2021, 40, 536-550.	5.9	2
3	Synthetic lethality-mediated precision oncology via the tumor transcriptome. Cell, 2021, 184, 2487-2502.e13.	28.9	60
4	Digital Display Precision Predictor: the prototype of a global biomarker model to guide treatments with targeted therapy and predict progression-free survival. Npj Precision Oncology, 2021, 5, 33.	5.4	5
5	Results of an early second PCR test performed on SARS-CoV-2 positive patients may support risk assessment for severe COVID-19. Scientific Reports, 2021, 11, 20463.	3.3	1
6	Direct comparison shows that mRNA-based diagnostics incorporate information which cannot be learned directly from genomic mutations. BMC Bioinformatics, 2020, 21, 196.	2.6	2
7	Identification of Tumor Antigens in the HLA Peptidome of Patient-derived Xenograft Tumors in Mouse. Molecular and Cellular Proteomics, 2020, 19, 1360-1374.	3.8	12
8	Gray whale transcriptome reveals longevity adaptations associated with DNA repair and ubiquitination. Aging Cell, 2020, 19, e13158.	6.7	27
9	BORIS/CTCFL promotes a switch from a proliferative towards an invasive phenotype in melanoma cells. Cell Death Discovery, 2020, 6, 1.	4.7	59
10	PICOT binding to chromatin-associated EED negatively regulates cyclin D2 expression by increasing H3K27me3 at the CCND2 gene promoter. Cell Death and Disease, 2019, 10, 685.	6.3	6
11	Genomic and transcriptomic profiling expands precision cancer medicine: the WINTHER trial. Nature Medicine, 2019, 25, 751-758.	30.7	362
12	PCM-SABRE: a platform for benchmarking and comparing outcome prediction methods in precision cancer medicine. BMC Bioinformatics, 2017, 18, 40.	2.6	9
13	NKp44 and NKp30 splice variant profiles in decidua and tumor tissues: a comparative viewpoint. Oncotarget, 2016, 7, 70912-70923.	1.8	14
14	Survival in acute myeloid leukemia is associated with NKp44 splice variants. Oncotarget, 2016, 7, 32933-32945.	1.8	27
15	A simplified interventional mapping system (SIMS) for the selection of combinations of targeted treatments in non-small cell lung cancer. Oncotarget, 2015, 6, 14139-14152.	1.8	22
16	Extracting tumor tissue immune status from expression profiles: correlating renal cancer prognosis with tumor-associated immunome. Oncotarget, 2015, 6, 33191-33205.	1.8	3
17	Promoting Precision Cancer Medicine through a Community-Driven Knowledgebase. Journal of Personalized Medicine, 2014, 4, 475-488.	2.5	3
18	Redefining meaningful age groups in the context of disease. Age, 2013, 35, 2357-2366.	3.0	61

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19	Suicidal Thoughts Are Associated with Platelet Counts in Adolescent Inpatients. Journal of Child and Adolescent Psychopharmacology, 2013, 23, 49-53.	1.3	8
20	The Mouse Age Phenome Knowledgebase and Disease-Specific Inter-Species Age Mapping. PLoS ONE, 2013, 8, e81114.	2.5	30
21	A Novel â€œReactomicsâ€•Approach for Cancer Diagnostics. Sensors, 2012, 12, 5572-5585.	3.8	5
22	Tight coevolution of proliferating cell nuclear antigen (PCNA)-partner interaction networks in fungi leads to interspecies network incompatibility. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E406-14.	7.1	37
23	Array-Based Disease Diagnostics Using Lipid/Polydiacetylene Vesicles Encapsulated in a Solâ€"Gel Matrix. Analytical Chemistry, 2012, 84, 5925-5931.	6.5	33
24	Two Patterns of Adipokine and Other Biomarker Dynamics in a Long-Term Weight Loss Intervention. Diabetes Care, 2012, 35, 342-349.	8.6	114
25	The age-phenome database. SpringerPlus, 2012, 1, 4.	1.2	4
26	Mitochondrial DNA heteroplasmy in diabetes and normal adults: role of acquired and inherited mutational patterns in twins. Human Molecular Genetics, 2012, 21, 4214-4224.	2.9	79
27	Unsupervised Analysis of Classical Biomedical Markers: Robustness and Medical Relevance of Patient Clustering Using Bioinformatics Tools. PLoS ONE, 2012, 7, e29578.	2.5	8
28	CHILD: a new tool for detecting low-abundance insertions and deletions in standard sequence traces. Nucleic Acids Research, 2011, 39, e47-e47.	14.5	12
29	MitoBamAnnotator: A web-based tool for detecting and annotating heteroplasmy in human mitochondrial DNA sequences. Mitochondrion, 2011, 11, 924-928.	3.4	26
30	Serum Apolipoproteins C-I and C-III Are Reduced in Stomach Cancer Patients: Results from MALDI-Based Peptidome and Immuno-Based Clinical Assays. PLoS ONE, 2011, 6, e14540.	2.5	43
31	Towards an Age-Phenome Knowledge-base. BMC Bioinformatics, 2011, 12, 229.	2.6	9
32	Ethnic differences in age-related changes of postpartum hemoglobin levels. Archives of Gynecology and Obstetrics, 2011, 283, 173-178.	1.7	2
33	The Neural/Immune Gene Ontology: clipping the Gene Ontology for neurological and immunological systems. BMC Bioinformatics, 2010, 11, 458.	2.6	23
34	mtDNA mutation pattern in tumors and human evolution are shaped by similar selective constraints. Genome Research, 2009, 19, 576-580.	5.5	31
35	Reverse translational bioinformatics: a bioinformatics assay of age, gender and clinical biomarkers. Summit on Translational Bioinformatics, 2008, 2008, 11-5.	0.7	5
36	Comparative Cross-Species Alternative Splicing in Plants. Plant Physiology, 2007, 144, 1632-1641.	4.8	73

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37	The Realistic Modeling of Biological Systems: A Workshop Synopsis. Complexus, 2006, 3, 217-230.	0.6	6
38	List mania: interpreting microarray results with the L2L server. Briefings in Bioinformatics, 2006, 7, 121-122.	6.5	1
39	Circumventing the cut-off for enrichment analysis. Briefings in Bioinformatics, 2006, 7, 202-203.	6.5	8
40	Applying Instructional Design Theories to Bioinformatics Education in Microarray Analysis and Primer Design Workshops. CBE: Life Sciences Education, 2005, 4, 199-206.	0.7	16
41	Intron retention is a major phenomenon in alternative splicing inArabidopsis. Plant Journal, 2004, 39, 877-885.	5.7	297
42	Biases and complex patterns in the residues flanking protein N-glycosylation sites. Glycobiology, 2003, 14, 95-101.	2.5	111
43	Binding of. Molecular Genetics and Genomics, 1996, 251, 436.	2.4	0