

Yosef E Maruvka

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

6,400
citations

361413

20
h-index

454955

30
g-index

33
all docs

33
docs citations

33
times ranked

13911
citing authors

#	ARTICLE	IF	CITATIONS
1	Genomic predictors of response to PD-1 inhibition in children with germline DNA replication repair deficiency. <i>Nature Medicine</i> , 2022, 28, 125-135.	30.7	53
2	Diagenetic inheritance of germline <i>POLE</i> and <i>PMS2</i> pathogenic variants causes a unique condition associated with pediatric cancer predisposition. <i>Clinical Genetics</i> , 2022, 101, 442-447.	2.0	5
3	Radiation-related genomic profile of papillary thyroid carcinoma after the Chernobyl accident. <i>Science</i> , 2021, 372, .	12.6	85
4	DNA Polymerase and Mismatch Repair Exert Distinct Microsatellite Instability Signatures in Normal and Malignant Human Cells. <i>Cancer Discovery</i> , 2021, 11, 1176-1191.	9.4	46
5	Proteogenomic Landscape of Breast Cancer Tumorigenesis and Targeted Therapy. <i>Cell</i> , 2020, 183, 1436-1456.e31.	28.9	273
6	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. <i>Nature Communications</i> , 2020, 11, 4748.	12.8	27
7	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
8	Patient-Specific Tumor Growth Trajectories Determine Persistent and Resistant Cancer Cell Populations during Treatment with Targeted Therapies. <i>Cancer Research</i> , 2019, 79, 3776-3788.	0.9	32
9	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	27.8	2,149
10	Analyzing Frequently Mutated Genes and the Association With Tumor Mutation Load. <i>JAMA Oncology</i> , 2019, 5, 577.	7.1	16
11	Quantification of somatic mutation flow across individual cell division events by lineage sequencing. <i>Genome Research</i> , 2018, 28, 1901-1918.	5.5	24
12	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018, 560, 325-330.	27.8	662
13	A mutational signature reveals alterations underlying deficient homologous recombination repair in breast cancer. <i>Nature Genetics</i> , 2017, 49, 1476-1486.	21.4	427
14	Analysis of somatic microsatellite indels identifies driver events in human tumors. <i>Nature Biotechnology</i> , 2017, 35, 951-959.	17.5	106
15	Recurrent and functional regulatory mutations in breast cancer. <i>Nature</i> , 2017, 547, 55-60.	27.8	269
16	Mutational Strand Asymmetries in Cancer Genomes Reveal Mechanisms of DNA Damage and Repair. <i>Cell</i> , 2016, 164, 538-549.	28.9	363
17	Tumor cells can follow distinct evolutionary paths to become resistant to epidermal growth factor receptor inhibition. <i>Nature Medicine</i> , 2016, 22, 262-269.	30.7	768
18	Polyploidy can drive rapid adaptation in yeast. <i>Nature</i> , 2015, 519, 349-352.	27.8	376

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19	On the Validity of Using Increases in 5-Year Survival Rates to Measure Success in the Fight against Cancer. PLoS ONE, 2014, 9, e83100.	2.5	25
20	Model for macroevolutionary dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E2460-9.	7.1	28
21	First principles theories for last name dynamics. Physics of Life Reviews, 2013, 10, 422-423.	2.8	0
22	Comparing Algorithms That Reconstruct Cell Lineage Trees Utilizing Information on Microsatellite Mutations. PLoS Computational Biology, 2013, 9, e1003297.	3.2	16
23	Cell Lineage Analysis of the Mammalian Female Germline. PLoS Genetics, 2012, 8, e1002477.	3.5	60
24	The Birth-Death-Mutation Process: A New Paradigm for Fat Tailed Distributions. PLoS ONE, 2011, 6, e26480.	2.5	19
25	Slicing and Dicing the Genome: A Statistical Physics Approach to Population Genetics. Journal of Statistical Physics, 2011, 142, 1302-1316.	1.2	1
26	Recovering Population Parameters from a Single Gene Genealogy: An Unbiased Estimator of the Growth Rate. Molecular Biology and Evolution, 2011, 28, 1617-1631.	8.9	22
27	Colon Stem Cell and Crypt Dynamics Exposed by Cell Lineage Reconstruction. PLoS Genetics, 2011, 7, e1002192.	3.5	52
28	Polymorphism Data Can Reveal the Origin of Species Abundance Statistics. PLoS Computational Biology, 2009, 5, e1000359.	3.2	1
29	Nonlocal competition and the speciation transition on random networks. Physical Review E, 2008, 78, 031920.	2.1	2
30	Nonlocal competition and front propagation in branching-coalescence systems. Physical Review E, 2007, 75, 042901.	2.1	7
31	Nonlocal competition and logistic growth: Patterns, defects, and fronts. Physical Review E, 2006, 73, 011903.	2.1	40