

Roy Ronen

List of Publications by Year in descending order

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Version: 2024-02-01

14
papers

559
citations

840776

11
h-index

1199594

12
g-index

15
all docs

15
docs citations

15
times ranked

993
citing authors

#	ARTICLE	IF	CITATIONS
1	Safety, Feasibility, and Merits of Longitudinal Molecular Testing of Multiple Metastatic Sites to Inform mTNBC Patient Treatment in the Intensive Trial of Omics in Cancer. <i>JCO Precision Oncology</i> , 2022, 6, e2100280.	3.0	1
2	A Distributed Network for Intensive Longitudinal Monitoring in Metastatic Triple-Negative Breast Cancer. <i>Journal of the National Comprehensive Cancer Network: JNCCN</i> , 2016, 14, 8-17.	4.9	21
3	Senp1 drives hypoxia-induced polycythemia via GATA1 and Bcl-xL in subjects with Monge's disease. <i>Journal of Experimental Medicine</i> , 2016, 213, 2729-2744.	8.5	29
4	Predicting Carriers of Ongoing Selective Sweeps without Knowledge of the Favored Allele. <i>PLoS Genetics</i> , 2015, 11, e1005527.	3.5	19
5	Endothelin receptor B, a candidate gene from human studies at high altitude, improves cardiac tolerance to hypoxia in genetically engineered heterozygote mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 10425-10430.	7.1	45
6	Haplotype Allele Frequency (HAF) Score: Predicting Carriers of Ongoing Selective Sweeps Without Knowledge of the Adaptive Allele. <i>Lecture Notes in Computer Science</i> , 2015, , 276-280.	1.3	1
7	Abstract 16038: Heterozygous Endothelin Receptor Type B Knockout Confers Cardiac Resistance to Extreme Hypoxia in Mice. <i>Circulation</i> , 2015, 132, .	1.6	0
8	The Genetic Basis of Chronic Mountain Sickness. <i>Physiology</i> , 2014, 29, 403-412.	3.1	27
9	Whole genome sequencing of Ethiopian highlanders reveals conserved hypoxia tolerance genes. <i>Genome Biology</i> , 2014, 15, R36.	9.6	71
10	Whole-Genome Sequencing Uncovers the Genetic Basis of Chronic Mountain Sickness in Andean Highlanders. <i>American Journal of Human Genetics</i> , 2013, 93, 452-462.	6.2	115
11	Learning Natural Selection from the Site Frequency Spectrum. <i>Genetics</i> , 2013, 195, 181-193.	2.9	105
12	Novel insight into the non-coding repertoire through deep sequencing analysis. <i>Nucleic Acids Research</i> , 2012, 40, e86-e86.	14.5	17
13	Vaccinia virus infection suppresses the cell microRNA machinery. <i>Archives of Virology</i> , 2012, 157, 1719-1727.	2.1	23
14	miRNAkey: a software for microRNA deep sequencing analysis. <i>Bioinformatics</i> , 2010, 26, 2615-2616.	4.1	85