

Tomislav Maricic

List of Publications by Year in descending order

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Version: 2024-02-01

31
papers

8,781
citations

361045

20
h-index

610482

24
g-index

39
all docs

39
docs citations

39
times ranked

10217
citing authors

#	ARTICLE	IF	CITATIONS
1	Improved gRNA secondary structures allow editing of target sites resistant to CRISPR-Cas9 cleavage. Nature Communications, 2022, 13, 489.	5.8	35
2	Genetic determinants of mannose-binding lectin activity predispose to thromboembolic complications in critical COVID-19. Nature Immunology, 2022, 23, 861-864.	7.0	7
3	Point-of-care bulk testing for SARS-CoV-2 by combining hybridization capture with improved colorimetric LAMP. Nature Communications, 2021, 12, 1467.	5.8	81
4	Reduced purine biosynthesis in humans after their divergence from Neandertals. ELife, 2021, 10, .	2.8	12
5	Comment on "Reintroduction of the archaic variant of <i>NOVA1</i> in cortical organoids alters neurodevelopment". Science, 2021, 374, eabi6060.	6.0	19
6	Evaluating the feasibility of Cas9 overexpression in 3T3-L1 cells for generation of genetic knock-out adipocyte cell lines. Adipocyte, 2021, 10, 631-645.	1.3	0
7	A Neanderthal Sodium Channel Increases Pain Sensitivity in Present-Day Humans. Current Biology, 2020, 30, 3465-3469.e4.	1.8	33
8	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. PLoS ONE, 2020, 15, e0244824.	1.1	12
9	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
10	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
11	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
12	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
13	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
14	A direct RT-qPCR approach to test large numbers of individuals for SARS-CoV-2. , 2020, 15, e0244824.		0
15	Simultaneous precise editing of multiple genes in human cells. Nucleic Acids Research, 2019, 47, e116-e116.	6.5	85
16	Targeting repair pathways with small molecules increases precise genome editing in pluripotent stem cells. Nature Communications, 2018, 9, 2164.	5.8	122
17	A high-coverage Neanderthal genome from Vindija Cave in Croatia. Science, 2017, 358, 655-658.	6.0	501
18	Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. ELife, 2016, 5, .	2.8	200

#	ARTICLE	IF	CITATIONS
19	deML: robust demultiplexing of Illumina sequences using a likelihood-based approach. <i>Bioinformatics</i> , 2015, 31, 770-772.	1.8	184
20	A Recent Evolutionary Change Affects a Regulatory Element in the Human FOXP2 Gene. <i>Molecular Biology and Evolution</i> , 2013, 30, 844-852.	3.5	205
21	Analysis of Human Accelerated DNA Regions Using Archaic Hominin Genomes. <i>PLoS ONE</i> , 2012, 7, e32877.	1.1	38
22	Targeted Investigation of the Neandertal Genome by Array-Based Sequence Capture. <i>Science</i> , 2010, 328, 723-725.	6.0	255
23	A Draft Sequence of the Neandertal Genome. <i>Science</i> , 2010, 328, 710-722.	6.0	3,588
24	A Complete mtDNA Genome of an Early Modern Human from Kostenki, Russia. <i>Current Biology</i> , 2010, 20, 231-236.	1.8	252
25	Genetic history of an archaic hominin group from Denisova Cave in Siberia. <i>Nature</i> , 2010, 468, 1053-1060.	13.7	1,537
26	Multiplexed DNA Sequence Capture of Mitochondrial Genomes Using PCR Products. <i>PLoS ONE</i> , 2010, 5, e14004.	1.1	471
27	Optimization of 454 sequencing library preparation from small amounts of DNA permits sequence determination of both DNA strands. <i>BioTechniques</i> , 2009, 46, 51-57.	0.8	40
28	Targeted Retrieval and Analysis of Five Neandertal mtDNA Genomes. <i>Science</i> , 2009, 325, 318-321.	6.0	456
29	Primer Extension Capture: Targeted Sequence Retrieval from Heavily Degraded DNA Sources. <i>Journal of Visualized Experiments</i> , 2009, , 1573.	0.2	22
30	A Complete Neandertal Mitochondrial Genome Sequence Determined by High-Throughput Sequencing. <i>Cell</i> , 2008, 134, 416-426.	13.5	503
31	From micrograms to picograms: quantitative PCR reduces the material demands of high-throughput sequencing. <i>Nucleic Acids Research</i> , 2008, 36, e5-e5.	6.5	105