

Nicolas Alcala

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

610
citations

840776

11
h-index

752698

20
g-index

28
all docs

28
docs citations

28
times ranked

1214
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential Orthopedia Homeobox expression in pulmonary carcinoids is associated with changes in <scp>DNA</scp> methylation. International Journal of Cancer, 2022, 150, 1987-1997.	5.1	4
2	Mathematical constraints on <i>F</i>_{<i>ST</i>}: multiallelic markers in arbitrarily many populations. Philosophical Transactions of the Royal Society B: Biological Sciences, 2022, 377, 20200414.	4.0	7
3	<scp>FSTRUCT</scp>: An <i>F</i>_{ST}-based tool for measuring ancestry variation in inference of population structure. Molecular Ecology Resources, 2022, 22, 2614-2626.	4.8	6
4	Challenges in lung and thoracic pathology: molecular advances in the classification of pleural mesotheliomas. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2021, 478, 73-80.	2.8	11
5	EURACAN/IASLC Proposals for Updating the Histologic Classification of Pleural Mesothelioma: Towards a More Multidisciplinary Approach. Journal of Thoracic Oncology, 2020, 15, 29-49.	1.1	106
6	A molecular map of lung neuroendocrine neoplasms. GigaScience, 2020, 9, .	6.4	17
7	Needlestack: an ultra-sensitive variant caller for multi-sample next generation sequencing data. NAR Genomics and Bioinformatics, 2020, 2, lqaa021.	3.2	5
8	Use of stochastic patch occupancy models in the California red-legged frog for Bayesian inference regarding past events and future persistence. Conservation Biology, 2019, 33, 685-696.	4.7	2
9	Integrative and comparative genomic analyses identify clinically relevant pulmonary carcinoid groups and unveil the supra-carcinoids. Nature Communications, 2019, 10, 3407.	12.8	132
10	Coalescent Theory of Migration Network Motifs. Molecular Biology and Evolution, 2019, 36, 2358-2374.	8.9	4
11	Redefining malignant pleural mesothelioma types as a continuum uncovers immune-vascular interactions. EBioMedicine, 2019, 48, 191-202.	6.1	55
12	, Jost's <i>D</i>, and <scp><i>F</i>_{ST}</scp> are similarly constrained by allele frequencies: A mathematical, simulation, and empirical study. Molecular Ecology, 2019, 28, 1624-1636.	3.9	19
13	Mathematical Constraints on <i>F</i>ST: Biallelic Markers in Arbitrarily Many Populations. Genetics, 2017, 206, 1581-1600.	2.9	25
14	Network analysis for species management in rivers networks: Application to the Loire River. Biological Conservation, 2017, 210, 26-36.	4.1	9
15	Host shift and cospeciation rate estimation from co-phylogenies. Ecology Letters, 2017, 20, 1014-1024.	6.4	34
16	The Genomic Signature of Population Reconnection Following Isolation: From Theory to HIV. G3: Genes, Genomes, Genetics, 2016, 6, 107-120.	1.8	17
17	Genetic consequences of population expansions and contractions in the common hippopotamus (<i>Hippopotamus amphibius</i>) since the Late Pleistocene. Molecular Ecology, 2015, 24, 2507-2520.	3.9	18
18	On the transition of genetic differentiation from isolation to panmixia: What we can learn from and. Theoretical Population Biology, 2014, 93, 75-84.	1.1	71

#	ARTICLE	IF	CITATIONS
19	Turnover and accumulation of genetic diversity across large time-scale cycles of isolation and connection of populations. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2014, 281, 20141369.	2.6	30
20	Peak and Persistent Excess of Genetic Diversity Following an Abrupt Migration Increase. <i>Genetics</i> , 2013, 193, 953-971.	2.9	30