

Jose M C Tubio

List of Publications by Year in descending order

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Version: 2024-02-01

45
papers

12,708
citations

159585

30
h-index

233421

45
g-index

54
all docs

54
docs citations

54
times ranked

21642
citing authors

#	ARTICLE	IF	CITATIONS
1	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe. <i>ELife</i> , 2022, 11, .	6.0	22
2	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2. <i>Npj Genomic Medicine</i> , 2022, 7, 19.	3.8	2
3	Clinical significance of baseline Pan-Immune-Inflammation Value and its dynamics in metastatic colorectal cancer patients under first-line chemotherapy. <i>Scientific Reports</i> , 2022, 12, 6893.	3.3	9
4	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	12.6	358
5	Subclone Eradication Analysis Identifies Targets for Enhanced Cancer Therapy and Reveals L1 Retrotransposition as a Dynamic Source of Cancer Heterogeneity. <i>Cancer Research</i> , 2021, 81, 4901-4909.	0.9	6
6	<i><i>CDKN2A</i></i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). <i>Haematologica</i> , 2021, 106, 2918-2926.	3.5	18
7	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. <i>Nature Communications</i> , 2021, 12, 6910.	12.8	27
8	VAV2 signaling promotes regenerative proliferation in both cutaneous and head and neck squamous cell carcinoma. <i>Nature Communications</i> , 2020, 11, 4788.	12.8	27
9	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
10	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	21.4	275
11	Extensive heterogeneity in somatic mutation and selection in the human bladder. <i>Science</i> , 2020, 370, 75-82.	12.6	195
12	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	12.8	183
13	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019, 176, 1282-1294.e20.	28.9	298
14	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. <i>Cancer Cell</i> , 2018, 33, 607-619.e15.	16.8	88
15	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , 2018, 8, 13537.	3.3	49
16	Characterisation of the genomic landscape of <i>CRLF2</i>-rearranged acute lymphoblastic leukemia. <i>Genes Chromosomes and Cancer</i> , 2017, 56, 363-372.	2.8	49
17	Genomic insights into the Ixodes scapularis tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	12.8	450
18	A second transmissible cancer in Tasmanian devils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 374-379.	7.1	192

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19	High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015, 348, 880-886.	12.6	1,431
20	Genome of <i>Rhodnius prolixus</i> , an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 14936-14941.	7.1	329
21	Somatic structural variation and cancer. <i>Briefings in Functional Genomics</i> , 2015, 14, 339-351.	2.7	26
22	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. <i>Genome Research</i> , 2015, 25, 814-824.	5.5	69
23	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	27.8	1,185
24	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	12.6	492
25	Genome analysis of a major urban malaria vector mosquito, <i>Anopheles stephensi</i> . <i>Genome Biology</i> , 2014, 15, 459.	8.8	119
26	Processed pseudogenes acquired somatically during cancer development. <i>Nature Communications</i> , 2014, 5, 3644.	12.8	86
27	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	12.8	741
28	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	12.6	144
29	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014, 46, 116-125.	21.4	313
30	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251-1253.	12.6	348
31	Vitamin B12-dependent taurine synthesis regulates growth and bone mass. <i>Journal of Clinical Investigation</i> , 2014, 124, 2988-3002.	8.2	124
32	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. <i>Nature Genetics</i> , 2013, 45, 923-926.	21.4	180
33	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. <i>Leukemia</i> , 2013, 27, 2376-2379.	7.2	29
34	PeSV-Fisher: Identification of Somatic and Non-Somatic Structural Variants Using Next Generation Sequencing Data. <i>PLoS ONE</i> , 2013, 8, e63377.	2.5	17
35	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. <i>Blood</i> , 2013, 122, 399-399.	1.4	0
36	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893

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37	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
38	When catastrophe strikes a cell. <i>Nature</i> , 2011, 470, 476-477.	27.8	77
39	Correction for Kirkness et al., Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6335-6335.	7.1	7
40	Evolutionary Dynamics of the Ty3/Gypsy LTR Retrotransposons in the Genome of <i>Anopheles gambiae</i> . <i>PLoS ONE</i> , 2011, 6, e16328.	2.5	15
41	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	12.6	424
42	Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12168-12173.	7.1	482
43	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
44	Structural and Evolutionary Analyses of the Ty3/gypsy Group of LTR Retrotransposons in the Genome of <i>Anopheles gambiae</i> . <i>Molecular Biology and Evolution</i> , 2005, 22, 29-39.	8.9	26
45	Evolution of the mdg1 lineage of the Ty3/gypsy group of LTR retrotransposons in <i>Anopheles gambiae</i> . <i>Gene</i> , 2004, 330, 123-131.	2.2	9