

Jose M C Tubio

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8875699/publications.pdf>

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	High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015, 348, 880-886.	12.6	1,431
2	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
3	The evolutionary history of lethal metastatic prostate cancer. <i>Nature</i> , 2015, 520, 353-357.	27.8	1,185
4	Genome Sequence of <i>Aedes aegypti</i> , a Major Arbovirus Vector. <i>Science</i> , 2007, 316, 1718-1723.	12.6	1,025
5	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
6	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	12.8	741
7	Highly evolvable malaria vectors: The genomes of 16 <i>Anopheles</i> mosquitoes. <i>Science</i> , 2015, 347, 1258-1262.	12.6	492
8	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
9	Genomic insights into the <i>Ixodes scapularis</i> tick vector of Lyme disease. <i>Nature Communications</i> , 2016, 7, 10507.	12.8	450
10	Sequencing of <i>Culex quinquefasciatus</i> Establishes a Platform for Mosquito Comparative Genomics. <i>Science</i> , 2010, 330, 86-88.	12.6	424
11	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
12	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. <i>Science</i> , 2021, 372, .	12.6	358
13	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251-1253.	12.6	348
14	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
15	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
16	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019, 176, 1282-1294.e20.	28.9	298
17	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
18	Extensive heterogeneity in somatic mutation and selection in the human bladder. <i>Science</i> , 2020, 370, 75-82.	12.6	195

#	ARTICLE	IF	CITATIONS
19	A second transmissible cancer in Tasmanian devils. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 374-379.	7.1	192
20	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	12.8	183
21	Frequent mutation of the major cartilage collagen gene COL2A1 in chondrosarcoma. Nature Genetics, 2013, 45, 923-926.	21.4	180
22	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	12.6	144
23	Vitamin B12-dependent taurine synthesis regulates growth and bone mass. Journal of Clinical Investigation, 2014, 124, 2988-3002.	8.2	124
24	Genome analysis of a major urban malaria vector mosquito, Anopheles stephensi. Genome Biology, 2014, 15, 459.	8.8	119
25	The Origins and Vulnerabilities of Two Transmissible Cancers in Tasmanian Devils. Cancer Cell, 2018, 33, 607-619.e15.	16.8	88
26	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	12.8	86
27	When catastrophe strikes a cell. Nature, 2011, 470, 476-477.	27.8	77
28	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
29	Characterisation of the genomic landscape of <i>CRLF2</i> -rearranged acute lymphoblastic leukemia. Genes Chromosomes and Cancer, 2017, 56, 363-372.	2.8	49
30	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. Scientific Reports, 2018, 8, 13537.	3.3	49
31	Sporadic and reversible chromothripsis in chronic lymphocytic leukemia revealed by longitudinal genomic analysis. Leukemia, 2013, 27, 2376-2379.	7.2	29
32	VAV2 signaling promotes regenerative proliferation in both cutaneous and head and neck squamous cell carcinoma. Nature Communications, 2020, 11, 4788.	12.8	27
33	Aberrant integration of Hepatitis B virus DNA promotes major restructuring of human hepatocellular carcinoma genome architecture. Nature Communications, 2021, 12, 6910.	12.8	27
34	Structural and Evolutionary Analyses of the Ty3/gypsy Group of LTR Retrotransposons in the Genome of <i>Anopheles gambiae</i> . Molecular Biology and Evolution, 2005, 22, 29-39.	8.9	26
35	Somatic structural variation and cancer. Briefings in Functional Genomics, 2015, 14, 339-351.	2.7	26
36	Mitochondrial genome sequencing of marine leukaemias reveals cancer contagion between clam species in the Seas of Southern Europe. ELife, 2022, 11, .	6.0	22

#	ARTICLE	IF	CITATIONS
37	<i>CDKN2A</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
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. <i>Blood</i> , 2013, 122, 399-399.	1.4	0