Abel Gonzalez-Perez

List of Publications by Year
in descending order

65 papers	17,778 citations	66234 42 h-index	106150 65 g-index
80 all docs	80 docs citations	80 times ranked	29147 citing authors

#	ARTICLE	IF	CITATIONS
1	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
2	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
3	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	13.5	1,518
4	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
5	Whole-genome landscapes of major melanoma subtypes. Nature, 2017, 545, 175-180.	13.7	1,068
6	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
7	Non-coding recurrent mutations in chronic lymphocytic leukaemia. Nature, 2015, 526, 519-524.	13.7	749
8	Improving the Assessment of the Outcome of Nonsynonymous SNVs with a Consensus Deleteriousness Score, Condel. American Journal of Human Genetics, 2011, 88, 440-449.	2.6	736
9	A compendium of mutational cancer driver genes. Nature Reviews Cancer, 2020, 20, 555-572.	12.8	605
10	IntOGen-mutations identifies cancer drivers across tumor types. Nature Methods, 2013, 10, 1081-1082.	9.0	517
11	Comprehensive identification of mutational cancer driver genes across 12 tumor types. Scientific Reports, 2013, 3, 2650.	1.6	437
12	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
13	OncodriveCLUST: exploiting the positional clustering of somatic mutations to identify cancer genes. Bioinformatics, 2013, 29, 2238-2244.	1.8	397
14	Cancer Genome Interpreter annotates the biological and clinical relevance of tumor alterations. Genome Medicine, 2018, 10, 25.	3.6	366
15	Functional impact bias reveals cancer drivers. Nucleic Acids Research, 2012, 40, e169-e169.	6.5	304
16	Pathway and network analysis of cancer genomes. Nature Methods, 2015, 12, 615-621.	9.0	297
17	In Silico Prescription of Anticancer Drugs to Cohorts of 28 Tumor Types Reveals Targeting Opportunities. Cancer Cell, 2015, 27, 382-396.	7.7	290
18	Nucleotide excision repair is impaired by binding of transcription factors to DNA. Nature, 2016, 532, 264-267.	13.7	274

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19	A Pan-cancer Landscape of Interactions between Solid Tumors and Infiltrating Immune Cell Populations. Clinical Cancer Research, 2018, 24, 3717-3728.	3.2	267
20	Gitools: Analysis and Visualisation of Genomic Data Using Interactive Heat-Maps. PLoS ONE, 2011, 6, e19541.	1.1	252
21	OncodriveFML: a general framework to identify coding and non-coding regions with cancer driver mutations. Genome Biology, 2016, 17, 128.	3.8	251
22	The mutational footprints of cancer therapies. Nature Genetics, 2019, 51, 1732-1740.	9.4	212
23	Independent Component Analysis Uncovers the Landscape of the Bladder Tumor Transcriptome and Reveals Insights into Luminal and Basal Subtypes. Cell Reports, 2014, 9, 1235-1245.	2.9	181
24	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. Genome Research, 2014, 24, 212-226.	2.4	175
25	Computational approaches to identify functional genetic variants in cancer genomes. Nature Methods, 2013, 10, 723-729.	9.0	161
26	Reduced mutation rate in exons due to differential mismatch repair. Nature Genetics, 2017, 49, 1684-1692.	9.4	139
27	Notch signal strength controls cell fate in the haemogenic endothelium. Nature Communications, 2015, 6, 8510.	5.8	135
28	Local Determinants of the Mutational Landscape of the Human Genome. Cell, 2019, 177, 101-114.	13.5	132
29	The road ahead in genetics and genomics. Nature Reviews Genetics, 2020, 21, 581-596.	7.7	118
30	Somatic and Germline Mutation Periodicity Follow the Orientation of the DNA Minor Groove around Nucleosomes. Cell, 2018, 175, 1074-1087.e18.	13.5	103
31	IntOGen: integration and data mining of multidimensional oncogenomic data. Nature Methods, 2010, 7, 92-93.	9.0	102
32	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. Genome Biology, 2013, 14, r106.	13.9	102
33	PARADIGM-SHIFT predicts the function of mutations in multiple cancers using pathway impact analysis. Bioinformatics, 2012, 28, i640-i646.	1.8	94
34	Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation. Genome Medicine, 2012, 4, 89.	3.6	91
35	Mutational landscape of RNA-binding proteins in human cancers. RNA Biology, 2018, 15, 115-129.	1.5	87
36	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	9.4	81

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37	Visualizing multidimensional cancer genomics data. Genome Medicine, 2013, 5, 9.	3.6	79
38	Comparison of algorithms for the detection of cancer drivers at subgene resolution. Nature Methods, 2017, 14, 782-788.	9.0	72
39	Increased mitochondrial function downstream from KDM5A histone demethylase rescues differentiation in pRB-deficient cells. Genes and Development, 2015, 29, 1817-1834.	2.7	63
40	In silico saturation mutagenesis of cancer genes. Nature, 2021, 596, 428-432.	13.7	61
41	OncodriveROLE classifies cancer driver genes in loss of function and activating mode of action. Bioinformatics, 2014, 30, i549-i555.	1.8	49
42	Identification of Cdca7 as a novel Notch transcriptional target involved in hematopoietic stem cell emergence. Journal of Experimental Medicine, 2014, 211, 2411-2423.	4.2	46
43	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers. Bioinformatics, 2019, 35, 4788-4790.	1.8	41
44	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline. Nature, 2022, 602, 623-631.	13.7	38
45	Pervasive lesion segregation shapes cancer genome evolution. Nature, 2020, 583, 265-270.	13.7	36
46	Systematic analysis of alterations in the ubiquitin proteolysis system reveals its contribution to driver mutations in cancer. Nature Cancer, 2020, 1, 122-135.	5.7	30
47	Oncodrive-CIS: A Method to Reveal Likely Driver Genes Based on the Impact of Their Copy Number Changes on Expression. PLoS ONE, 2013, 8, e55489.	1.1	29
48	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. Scientific Reports, 2016, 6, 24570.	1.6	29
49	The evolution of hematopoietic cells under cancer therapy. Nature Communications, 2021, 12, 4803.	5.8	28
50	NF-îºB directly mediates epigenetic deregulation of common microRNAs in Epstein-Barr virus-mediated transformation of B-cells and in lymphomas. Nucleic Acids Research, 2014, 42, 11025-11039.	6.5	27
51	Variable interplay of UV-induced DNA damage and repair at transcription factor binding sites. Nucleic Acids Research, 2021, 49, 891-901.	6.5	23
52	jHeatmap: an interactive heatmap viewer for the web. Bioinformatics, 2014, 30, 1757-1758.	1.8	22
53	An Intronic microRNA Links Rb/E2F and EGFR Signaling. PLoS Genetics, 2014, 10, e1004493.	1.5	21
54	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. European Journal of Cancer, 2019, 120, 54-64.	1.3	18

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55	Mutational signatures impact the evolution of anti-EGFR antibody resistance in colorectal cancer. Nature Ecology and Evolution, 2021, 5, 1024-1032.	3.4	16
56	The evolution of relapse of adult T cell acute lymphoblastic leukemia. Genome Biology, 2020, 21, 284.	3.8	13
57	Are carcinogens direct mutagens?. Nature Genetics, 2020, 52, 1137-1138.	9.4	13
58	The Ubiquity of the Insulin Superfamily Across the Eukaryotes Detected Using a Bioinformatics Approach. OMICS A Journal of Integrative Biology, 2011, 15, 439-447.	1.0	10
59	Circuits of cancer drivers revealed by convergent misregulation of transcription factor targets across tumor types. Genome Medicine, 2016, 8, 6.	3.6	10
60	Cytoplasmic accumulation of NCoR in malignant melanoma: consequences of altered gene repression and prognostic significance. Oncotarget, 2015, 6, 9284-9294.	0.8	8
61	DeepMP: a deep learning tool to detect DNA base modifications on Nanopore sequencing data. Bioinformatics, 2022, 38, 1235-1243.	1.8	8
62	Rational design of cancer gene panels with OncoPaD. Genome Medicine, 2016, 8, 98.	3.6	5
63	Altered oncomodules underlie chromatin regulatory factors driver mutations. Oncotarget, 2016, 7, 30748-30759.	0.8	3
64	Predicting disease variants using biodiversity and machine learning. Nature Biotechnology, 2022, 40, 27-28.	9.4	3
65	Abstract LB-401: Functional impact bias reveals cancer drivers. , 2012, , .		1