Abel Gonzalez-Perez

List of Publications by Citations

68	10,861	39	80
papers	citations	h-index	g-index

80	15,075	22.7	6.19
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
68	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
67	A Landscape of Pharmacogenomic Interactions in Cancer. *Cell*, **2016**, 166, 740-754	56.2	892
66	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
65	The repertoire of mutational signatures in human cancer. *Nature*, **2020**, 578, 94-101	50.4	849
64	Whole-genome landscapes of major melanoma subtypes. *Nature*, **2017**, 545, 175-180	50.4	662
63	Improving the assessment of the outcome of nonsynonymous SNVs with a consensus deleteriousness score, Condel. *American Journal of Human Genetics*, **2011**, 88, 440-9	11	599
62	Non-coding recurrent mutations in chronic lymphocytic leukaemia. *Nature*, **2015**, 526, 519-24	50.4	565
61	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *Nature Genetics*, **2015**, 47, 106-14	36.3	547
60	IntOGen-mutations identifies cancer drivers across tumor types. *Nature Methods*, **2013**, 10, 1081-2	21.6	374
59	Comprehensive identification of mutational cancer driver genes across 12 tumor types. *Scientific Reports*, **2013**, 3, 2650	4.9	350
58	OncodriveCLUST: exploiting the positional clustering of somatic mutations to identify cancer genes. *Bioinformatics*, **2013**, 29, 2238-44	7.2	276
57	Functional impact bias reveals cancer drivers. *Nucleic Acids Research*, **2012**, 40, e169	20.1	238
56	In silico prescription of anticancer drugs to cohorts of 28 tumor types reveals targeting opportunities. *Cancer Cell*, **2015**, 27, 382-96	24.3	237
55	Pathway and network analysis of cancer genomes. *Nature Methods*, **2015**, 12, 615-621	21.6	235
54	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
53	Cancer Genome Interpreter annotates the biological and clinical relevance of tumor alterations. *Genome Medicine*, **2018**, 10, 25	14.4	205
52	Gitools: analysis and visualisation of genomic data using interactive heat-maps. *PLoS ONE*, **2011**, 6, e19541	3.7	201

51   Nucleotide excision repair is impaired by binding of transcription factors to DNA. *Nature*, **2016**, 532, 264-7.   50.4   192

50   A compendium of mutational cancer driver genes. *Nature Reviews Cancer*, **2020**, 20, 555-572   31.3   185

49   OncodriveFML: a general framework to identify coding and non-coding regions with cancer driver mutations. *Genome Biology*, **2016**, 17, 128   18.3   143

48   Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. *Genome Research*, **2014**, 24, 212-26   9.7   143

47   A Pan-cancer Landscape of Interactions between Solid Tumors and Infiltrating Immune Cell Populations. *Clinical Cancer Research*, **2018**, 24, 3717-3728   12.9   136

46   Independent component analysis uncovers the landscape of the bladder tumor transcriptome and reveals insights into luminal and basal subtypes. *Cell Reports*, **2014**, 9, 1235-45   10.6   131

45   Computational approaches to identify functional genetic variants in cancer genomes. *Nature Methods*, **2013**, 10, 723-9   21.6   129

44   The mutational footprints of cancer therapies. *Nature Genetics*, **2019**, 51, 1732-1740   36.3   97

43   Notch signal strength controls cell fate in the haemogenic endothelium. *Nature Communications*, **2015**, 6, 8510   17.4   96

42   Reduced mutation rate in exons due to differential mismatch repair. *Nature Genetics*, **2017**, 49, 1684-1692.   36.3   91

41   IntOGen: integration and data mining of multidimensional oncogenomic data. *Nature Methods*, **2010**, 7, 92-3   21.6   90

40   The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. *Genome Biology*, **2013**, 14, r106   18.3   78

39   Local Determinants of the Mutational Landscape of the Human Genome. *Cell*, **2019**, 177, 101-114   56.2   76

38   PARADIGM-SHIFT predicts the function of mutations in multiple cancers using pathway impact analysis. *Bioinformatics*, **2012**, 28, i640-i646   7.2   74

37   Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation. *Genome Medicine*, **2012**, 4, 89   14.4   73

36   Visualizing multidimensional cancer genomics data. *Genome Medicine*, **2013**, 5, 9   14.4   68

35   Somatic and Germline Mutation Periodicity Follow the Orientation of the DNA Minor Groove around Nucleosomes. *Cell*, **2018**, 175, 1074-1087.e18   56.2   54

34   Comparison of algorithms for the detection of cancer drivers at subgene resolution. *Nature Methods*, **2017**, 14, 782-788   21.6   51

33	Mutational landscape of RNA-binding proteins in human cancers. *RNA Biology*, **2018**, 15, 115-129	4.8	47
32	Increased mitochondrial function downstream from KDM5A histone demethylase rescues differentiation in pRB-deficient cells. *Genes and Development*, **2015**, 29, 1817-34	12.6	44
31	The road ahead in genetics and genomics. *Nature Reviews Genetics*, **2020**, 21, 581-596	30.1	43
30	Identification of Cdca7 as a novel Notch transcriptional target involved in hematopoietic stem cell emergence. *Journal of Experimental Medicine*, **2014**, 211, 2411-23	16.6	38
29	The whole-genome panorama of cancer drivers		38
28	OncodriveROLE classifies cancer driver genes in loss of function and activating mode of action. *Bioinformatics*, **2014**, 30, i549-55	7.2	36
27	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. *Scientific Reports*, **2016**, 6, 24570	4.9	24
26	Pervasive lesion segregation shapes cancer genome evolution. *Nature*, **2020**, 583, 265-270	50.4	20
25	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	3.7	20
24	An intronic microRNA links Rb/E2F and EGFR signaling. *PLoS Genetics*, **2014**, 10, e1004493	6	19
23	jHeatmap: an interactive heatmap viewer for the web. *Bioinformatics*, **2014**, 30, 1757-8	7.2	19
22	NF-**B** directly mediates epigenetic deregulation of common microRNAs in Epstein-Barr virus-mediated transformation of B-cells and in lymphomas. *Nucleic Acids Research*, **2014**, 42, 11025-39	20.1	19
21	Systematic analysis of alterations in the ubiquitin proteolysis system reveals its contribution to driver mutations in cancer.. *Nature Cancer*, **2020**, 1, 122-135	15.4	14
20	Genomic and evolutionary classification of lung cancer in never smokers. *Nature Genetics*, **2021**, 53, 1348-1359	30.3	14
19	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. *European Journal of Cancer*, **2019**, 120, 54-64	7.5	13
18	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers. *Bioinformatics*, **2019**, 35, 4788-4790	7.2	12
17	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
16	In silico saturation mutagenesis of cancer genes. *Nature*, **2021**, 596, 428-432	50.4	12

LIST OF PUBLICATIONS

15	The ubiquity of the insulin superfamily across the eukaryotes detected using a bioinformatics approach. *OMICS A Journal of Integrative Biology*, **2011**, 15, 439-47	3.8	8
14	Cytoplasmic accumulation of NCoR in malignant melanoma: consequences of altered gene repression and prognostic significance. *Oncotarget*, **2015**, 6, 9284-94	3.3	7
13	Cancer Genome Interpreter annotates the biological and clinical relevance of tumor alterations		7
12	The evolution of hematopoietic cells under cancer therapy. *Nature Communications*, **2021**, 12, 4803	17.4	7
11	Circuits of cancer drivers revealed by convergent misregulation of transcription factor targets across tumor types. *Genome Medicine*, **2016**, 8, 6	14.4	6
10	Variable interplay of UV-induced DNA damage and repair at transcription factor binding sites. *Nucleic Acids Research*, **2021**, 49, 891-901	20.1	5
9	The evolution of relapse of adult T cell acute lymphoblastic leukemia. *Genome Biology*, **2020**, 21, 284	18.3	5
8	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline.. *Nature*, **2022**,	50.4	4
7	Discovering the drivers of clonal hematopoiesis		4
6	Are carcinogens direct mutagens?. *Nature Genetics*, **2020**, 52, 1137-1138	36.3	4
5	Rational design of cancer gene panels with OncoPaD. *Genome Medicine*, **2016**, 8, 98	14.4	3
4	The evolution of hematopoietic cells under cancer therapy		3
3	Mutational signatures impact the evolution of anti-EGFR antibody resistance in colorectal cancer. *Nature Ecology and Evolution*, **2021**, 5, 1024-1032	12.3	2
2	Altered oncomodules underlie chromatin regulatory factors driver mutations. *Oncotarget*, **2016**, 7, 30748-59	3.3	1
1	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers		1