

Abel Gonzalez-Perez

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

68

papers

10,861

citations

39

h-index

80

g-index

80

ext. papers

15,075

ext. citations

22.7

avg, IF

6.19

L-index

#	Paper	IF	Citations
68	Signatures of TOP1 transcription-associated mutagenesis in cancer and germline.. <i>Nature</i> , 2022 ,	50.4	4
67	Variable interplay of UV-induced DNA damage and repair at transcription factor binding sites. <i>Nucleic Acids Research</i> , 2021 , 49, 891-901	20.1	5
66	Mutational signatures impact the evolution of anti-EGFR antibody resistance in colorectal cancer. <i>Nature Ecology and Evolution</i> , 2021 , 5, 1024-1032	12.3	2
65	In silico saturation mutagenesis of cancer genes. <i>Nature</i> , 2021 , 596, 428-432	50.4	12
64	The evolution of hematopoietic cells under cancer therapy. <i>Nature Communications</i> , 2021 , 12, 4803	17.4	7
63	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021 , 53, 1348-1359	36.59	14
62	Pervasive lesion segregation shapes cancer genome evolution. <i>Nature</i> , 2020 , 583, 265-270	50.4	20
61	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020 , 578, 94-101	50.4	849
60	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020 , 578, 102-111	50.4	220
59	Systematic analysis of alterations in the ubiquitin proteolysis system reveals its contribution to driver mutations in cancer.. <i>Nature Cancer</i> , 2020 , 1, 122-135	15.4	14
58	The evolution of relapse of adult T cell acute lymphoblastic leukemia. <i>Genome Biology</i> , 2020 , 21, 284	18.3	5
57	A compendium of mutational cancer driver genes. <i>Nature Reviews Cancer</i> , 2020 , 20, 555-572	31.3	185
56	Are carcinogens direct mutagens?. <i>Nature Genetics</i> , 2020 , 52, 1137-1138	36.3	4
55	The road ahead in genetics and genomics. <i>Nature Reviews Genetics</i> , 2020 , 21, 581-596	30.1	43
54	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. <i>European Journal of Cancer</i> , 2019 , 120, 54-64	7.5	13
53	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers. <i>Bioinformatics</i> , 2019 , 35, 4788-4790	7.2	12
52	Local Determinants of the Mutational Landscape of the Human Genome. <i>Cell</i> , 2019 , 177, 101-114	56.2	76

51	The mutational footprints of cancer therapies. <i>Nature Genetics</i> , 2019 , 51, 1732-1740	36.3	97
50	A Pan-cancer Landscape of Interactions between Solid Tumors and Infiltrating Immune Cell Populations. <i>Clinical Cancer Research</i> , 2018 , 24, 3717-3728	12.9	136
49	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18	56.2	854
48	Cancer Genome Interpreter annotates the biological and clinical relevance of tumor alterations. <i>Genome Medicine</i> , 2018 , 10, 25	14.4	205
47	Mutational landscape of RNA-binding proteins in human cancers. <i>RNA Biology</i> , 2018 , 15, 115-129	4.8	47
46	Somatic and Germline Mutation Periodicity Follow the Orientation of the DNA Minor Groove around Nucleosomes. <i>Cell</i> , 2018 , 175, 1074-1087.e18	56.2	54
45	Whole-genome landscapes of major melanoma subtypes. <i>Nature</i> , 2017 , 545, 175-180	50.4	662
44	Comparison of algorithms for the detection of cancer drivers at subgene resolution. <i>Nature Methods</i> , 2017 , 14, 782-788	21.6	51
43	Reduced mutation rate in exons due to differential mismatch repair. <i>Nature Genetics</i> , 2017 , 49, 1684-1693	36.3	91
42	Rational design of cancer gene panels with OncoPaD. <i>Genome Medicine</i> , 2016 , 8, 98	14.4	3
41	Circuits of cancer drivers revealed by convergent misregulation of transcription factor targets across tumor types. <i>Genome Medicine</i> , 2016 , 8, 6	14.4	6
40	OncodriveFML: a general framework to identify coding and non-coding regions with cancer driver mutations. <i>Genome Biology</i> , 2016 , 17, 128	18.3	143
39	Altered oncomodules underlie chromatin regulatory factors driver mutations. <i>Oncotarget</i> , 2016 , 7, 30748-59	9.9	1
38	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016 , 166, 740-754	56.2	892
37	Uncovering disease mechanisms through network biology in the era of Next Generation Sequencing. <i>Scientific Reports</i> , 2016 , 6, 24570	4.9	24
36	Nucleotide excision repair is impaired by binding of transcription factors to DNA. <i>Nature</i> , 2016 , 532, 264-70	50.4	192
35	In silico prescription of anticancer drugs to cohorts of 28 tumor types reveals targeting opportunities. <i>Cancer Cell</i> , 2015 , 27, 382-96	24.3	237
34	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015 , 526, 519-24	50.4	565

33	Pathway and network analysis of cancer genomes. <i>Nature Methods</i> , 2015 , 12, 615-621	21.6	235
32	Notch signal strength controls cell fate in the haemogenic endothelium. <i>Nature Communications</i> , 2015 , 6, 8510	17.4	96
31	Increased mitochondrial function downstream from KDM5A histone demethylase rescues differentiation in pRB-deficient cells. <i>Genes and Development</i> , 2015 , 29, 1817-34	12.6	44
30	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. <i>Nature Genetics</i> , 2015 , 47, 106-14	36.3	547
29	Cytoplasmic accumulation of NCoR in malignant melanoma: consequences of altered gene repression and prognostic significance. <i>Oncotarget</i> , 2015 , 6, 9284-94	3.3	7
28	Transcriptome characterization by RNA sequencing identifies a major molecular and clinical subdivision in chronic lymphocytic leukemia. <i>Genome Research</i> , 2014 , 24, 212-26	9.7	143
27	Identification of Cdca7 as a novel Notch transcriptional target involved in hematopoietic stem cell emergence. <i>Journal of Experimental Medicine</i> , 2014 , 211, 2411-23	16.6	38
26	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944	56.2	935
25	An intronic microRNA links Rb/E2F and EGFR signaling. <i>PLoS Genetics</i> , 2014 , 10, e1004493	6	19
24	Independent component analysis uncovers the landscape of the bladder tumor transcriptome and reveals insights into luminal and basal subtypes. <i>Cell Reports</i> , 2014 , 9, 1235-45	10.6	131
23	OncodriveROLE classifies cancer driver genes in loss of function and activating mode of action. <i>Bioinformatics</i> , 2014 , 30, i549-55	7.2	36
22	jHeatmap: an interactive heatmap viewer for the web. <i>Bioinformatics</i> , 2014 , 30, 1757-8	7.2	19
21	NF- κ B directly mediates epigenetic deregulation of common microRNAs in Epstein-Barr virus-mediated transformation of B-cells and in lymphomas. <i>Nucleic Acids Research</i> , 2014 , 42, 11025-39	20.1	19
20	Computational approaches to identify functional genetic variants in cancer genomes. <i>Nature Methods</i> , 2013 , 10, 723-9	21.6	129
19	OncodriveCLUST: exploiting the positional clustering of somatic mutations to identify cancer genes. <i>Bioinformatics</i> , 2013 , 29, 2238-44	7.2	276
18	Visualizing multidimensional cancer genomics data. <i>Genome Medicine</i> , 2013 , 5, 9	14.4	68
17	Comprehensive identification of mutational cancer driver genes across 12 tumor types. <i>Scientific Reports</i> , 2013 , 3, 2650	4.9	350
16	The mutational landscape of chromatin regulatory factors across 4,623 tumor samples. <i>Genome Biology</i> , 2013 , 14, r106	18.3	78

15	IntOGen-mutations identifies cancer drivers across tumor types. <i>Nature Methods</i> , 2013 , 10, 1081-2	21.6	374
14	Oncodrive-CIS: a method to reveal likely driver genes based on the impact of their copy number changes on expression. <i>PLoS ONE</i> , 2013 , 8, e55489	3.7	20
13	Improving the prediction of the functional impact of cancer mutations by baseline tolerance transformation. <i>Genome Medicine</i> , 2012 , 4, 89	14.4	73
12	PARADIGM-SHIFT predicts the function of mutations in multiple cancers using pathway impact analysis. <i>Bioinformatics</i> , 2012 , 28, i640-i646	7.2	74
11	Functional impact bias reveals cancer drivers. <i>Nucleic Acids Research</i> , 2012 , 40, e169	20.1	238
10	Gitools: analysis and visualisation of genomic data using interactive heat-maps. <i>PLoS ONE</i> , 2011 , 6, e19547	3.7	201
9	Improving the assessment of the outcome of nonsynonymous SNVs with a consensus deleteriousness score, Condel. <i>American Journal of Human Genetics</i> , 2011 , 88, 440-9	11	599
8	The ubiquity of the insulin superfamily across the eukaryotes detected using a bioinformatics approach. <i>OMICS A Journal of Integrative Biology</i> , 2011 , 15, 439-47	3.8	8
7	IntOGen: integration and data mining of multidimensional oncogenomic data. <i>Nature Methods</i> , 2010 , 7, 92-3	21.6	90
6	Cancer Genome Interpreter annotates the biological and clinical relevance of tumor alterations		7
5	The whole-genome panorama of cancer drivers		38
4	Discovering the drivers of clonal hematopoiesis		4
3	The evolution of hematopoietic cells under cancer therapy		3
2	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12
1	OncodriveCLUSTL: a sequence-based clustering method to identify cancer drivers		1