Ignacio Varela

List of Publications by Year in Descending Order

82 papers	21,940 citations	42 h-index	89 g-index
89 ext. papers	25,289 ext. citations	17.4 avg, IF	5.48 L-index

#	Paper	IF	Citations
82	HDAC7 is a major contributor in the pathogenesis of infant t(4;11) proB acute lymphoblastic leukemia. *Leukemia*, **2021**, 35, 2086-2091	10.7	2
81	ARID2 deficiency promotes tumor progression and is associated with higher sensitivity to chemotherapy in lung cancer. *Oncogene*, **2021**, 40, 2923-2935	9.2	4
80	Integrative methylome-transcriptome analysis unravels cancer cell vulnerabilities in infant MLL-rearranged B cell acute lymphoblastic leukemia. *Journal of Clinical Investigation*, **2021**, 131,	15.9	1
79	Shared D-J rearrangements reveal cell of origin of TCF3-ZNF384 and PTPN11 mutations in monozygotic twins with concordant BCP-ALL. *Blood*, **2020**, 136, 1108-1111	2.2	3
78	Bone Marrow Clonogenic Myeloid Progenitors from -Mutated AML Patients Do Not Harbor the Mutation: Implication for the Cell-Of-Origin of AML. *Genes*, **2020**, 11,	4.2	1
77	The MNT transcription factor autoregulates its expression and supports proliferation in MYC-associated factor X (MAX)-deficient cells. *Journal of Biological Chemistry*, **2020**, 295, 2001-2017	5.4	3
76	Tumor Functional Heterogeneity Unraveled by scRNA-seq Technologies. *Trends in Cancer*, **2020**, 6, 13-19	12.5	54
75	Analysis pipelines for cancer genome sequencing in mice. *Nature Protocols*, **2020**, 15, 266-315	18.8	12
74	Enhanced hemato-endothelial specification during human embryonic differentiation through developmental cooperation between and fusions. *Haematologica*, **2019**, 104, 1189-1201	6.6	12
73	Unraveling the cellular origin and clinical prognostic markers of infant B-cell acute lymphoblastic leukemia using genome-wide analysis. *Haematologica*, **2019**, 104, 1176-1188	6.6	44
72	Discovery of a CD10-negative B-progenitor in human fetal life identifies unique ontogeny-related developmental programs. *Blood*, **2019**, 134, 1059-1071	2.2	28
71	Natural history and cell of origin of - and mutations in monozygotic twins with concordant BCP-ALL. *Blood*, **2019**, 134, 900-905	2.2	16
70	CD133-directed CAR T-cells for MLL leukemia: on-target, off-tumor myeloablative toxicity. *Leukemia*, **2019**, 33, 2090-2125	10.7	16
69	Evolutionary routes and KRAS dosage define pancreatic cancer phenotypes. *Nature*, **2018**, 554, 62-68	50.4	192
68	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. *Nature Genetics*, **2018**, 50, 883-894	36.3	73
67	Clonal haematopoiesis is not prevalent in survivors of childhood cancer. *British Journal of Haematology*, **2018**, 181, 537-539	4.5	6
66	Somatic Mutations Reveal Lineage Relationships and Age-Related Mutagenesis in Human Hematopoiesis. *Cell Reports*, **2018**, 25, 2308-2316.e4	10.6	97

65	Applied diagnostics in liver cancer. Efficient combinations of sorafenib with targeted inhibitors blocking AKT/mTOR. *Oncotarget*, **2018**, 9, 30869-30882	3.3	8
64	Evaluation of Toll-like-receptor gene family variants as prognostic biomarkers in rheumatoid arthritis. *Immunology Letters*, **2017**, 187, 35-40	4.1	6
63	Molecular synergy underlies the co-occurrence patterns and phenotype of -mutant acute myeloid leukemia. *Blood*, **2017**, 130, 1911-1922	2.2	42
62	Rapid parallel acquisition of somatic mutations after NPM1 in acute myeloid leukaemia evolution. *British Journal of Haematology*, **2017**, 176, 825-829	4.5	3
61	Shared Oncogenic Pathways Implicated in Both Virus-Positive and UV-Induced Merkel Cell Carcinomas. *Journal of Investigative Dermatology*, **2017**, 137, 197-206	4.3	55
60	V617F hematopoietic clones are present several years prior to MPN diagnosis and follow different expansion kinetics. *Blood Advances*, **2017**, 1, 968-971	7.8	21
59	Intratumoral heterogeneity and clonal evolution in blood malignancies and solid tumors. *Oncotarget*, **2017**, 8, 66742-66746	3.3	10
58	Analysis of the mutational landscape of classic Hodgkin lymphoma identifies disease heterogeneity and potential therapeutic targets. *Oncotarget*, **2017**, 8, 111386-111395	3.3	16
57	Identification of a germline F692L drug resistance variant in cis with Flt3-internal tandem duplication in knock-in mice. *Haematologica*, **2016**, 101, e328-31	6.6	4
56	Development Refractoriness of MLL-Rearranged Human B Cell Acute Leukemias to Reprogramming into Pluripotency. *Stem Cell Reports*, **2016**, 7, 602-618	8	29
55	Activated KRAS Cooperates with MLL-AF4 to Promote Extramedullary Engraftment and Migration of Cord Blood CD34+ HSPC But Is Insufficient to Initiate Leukemia. *Cancer Research*, **2016**, 76, 2478-89	10.1	33
54	Multiplexed pancreatic genome engineering and cancer induction by transfection-based CRISPR/Cas9 delivery in mice. *Nature Communications*, **2016**, 7, 10770	17.4	110
53	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. *Blood*, **2016**, 128, e1-9	2.2	36
52	A functional variant of TLR10 modifies the activity of NFkB and may help predict a worse prognosis in patients with rheumatoid arthritis. *Arthritis Research and Therapy*, **2016**, 18, 221	5.7	24
51	Recurrent chromosomal gains and heterogeneous driver mutations characterise papillary renal cancer evolution. *Nature Communications*, **2015**, 6, 6336	17.4	85
50	CRISPR/Cas9 somatic multiplex-mutagenesis for high-throughput functional cancer genomics in mice. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 13982-7	11.5	135
49	The E3 ligase RNF43 inhibits Wnt signaling downstream of mutated Ecatenin by sequestering TCF4 to the nuclear membrane. *Science Signaling*, **2015**, 8, ra90	8.8	53
48	The Life History of 21 Breast Cancers. *Cell*, **2015**, 162, 924	56.2	7

47	A Truncated Variant of ASCC1, a Novel Inhibitor of NF-B, Is Associated with Disease Severity in Patients with Rheumatoid Arthritis. *Journal of Immunology*, **2015**, 195, 5415-20	5.3	15
46	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. *Nature Genetics*, **2015**, 47, 47-56	36.3	59
45	Characterization of gene mutations and copy number changes in acute myeloid leukemia using a rapid target enrichment protocol. *Haematologica*, **2015**, 100, 214-22	6.6	38
44	Leukemia-associated somatic mutations drive distinct patterns of age-related clonal hemopoiesis. *Cell Reports*, **2015**, 10, 1239-45	10.6	343
43	Colorectal adenomas contain multiple somatic mutations that do not coincide with synchronous adenocarcinoma specimens. *PLoS ONE*, **2015**, 10, e0119946	3.7	7
42	Individualized strategies to target specific mechanisms of disease in malignant melanoma patients displaying unique mutational signatures. *Oncotarget*, **2015**, 6, 25452-65	3.3	3
41	A next-generation dual-recombinase system for time- and host-specific targeting of pancreatic cancer. *Nature Medicine*, **2014**, 20, 1340-1347	50.5	149
40	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. *Science*, **2014**, 346, 251-6	33.3	752
39	Whole-exome sequencing in splenic marginal zone lymphoma reveals mutations in genes involved in marginal zone differentiation. *Leukemia*, **2014**, 28, 1334-40	10.7	90
38	PLCG1 mutations in cutaneous T-cell lymphomas. *Blood*, **2014**, 123, 2034-43	2.2	150
37	A novel mutation in ADAMTS13 of a child with Upshaw-Schulman Syndrome. *Thrombosis and Haemostasis*, **2014**, 112, 1065-8	7	3
36	Sin3b interacts with Myc and decreases Myc levels. *Journal of Biological Chemistry*, **2014**, 289, 22221-36	5.4	21
35	An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge. *Genome Biology*, **2014**, 15, R53	18.3	86
34	Development of synchronous VHL syndrome tumors reveals contingencies and constraints to tumor evolution. *Genome Biology*, **2014**, 15, 433	18.3	53
33	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. *Nature Genetics*, **2014**, 46, 225-233	36.3	866
32	A genetic progression model of Braf(V600E)-induced intestinal tumorigenesis reveals targets for therapeutic intervention. *Cancer Cell*, **2013**, 24, 15-29	24.3	146
31	Inflammatory and immune response genes have significantly altered expression in schizophrenia. *Molecular Psychiatry*, **2013**, 18, 1056-7	15.1	42
30	Detailed molecular characterisation of acute myeloid leukaemia with a normal karyotype using targeted DNA capture. *Leukemia*, **2013**, 27, 1820-5	10.7	26

29	Whole exome sequencing of adenoid cystic carcinoma. *Journal of Clinical Investigation*, **2013**, 123, 2965-8	15.9	188
28	The landscape of cancer genes and mutational processes in breast cancer. *Nature*, **2012**, 486, 400-4	50.4	1264
27	Intratumor heterogeneity and branched evolution revealed by multiregion sequencing. *New England Journal of Medicine*, **2012**, 366, 883-892	59.2	5559
26	Mutational processes molding the genomes of 21 breast cancers. *Cell*, **2012**, 149, 979-93	56.2	1279
25	The life history of 21 breast cancers. *Cell*, **2012**, 149, 994-1007	56.2	979
24	Mutational Status of Splenic Marginal Zone Lymphoma Revealed by Whole Exome Sequencing.. *Blood*, **2012**, 120, 2698-2698	2.2	
23	Mutations in PLCG1 Is a Frequent Event in Cutaneous T-Cell Lymphomas. *Blood*, **2012**, 120, 300-300	2.2	
22	Characterization of Subclonal Changes Along Progression in Multiple Myeloma.. *Blood*, **2012**, 120, 2924-2924	2.2	0
21	Targeted gene correction of α1-antitrypsin deficiency in induced pluripotent stem cells. *Nature*, **2011**, 478, 391-4	50.4	557
20	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. *Cell*, **2011**, 144, 27-40	56.2	1628
19	Aging and chronic DNA damage response activate a regulatory pathway involving miR-29 and p53. *EMBO Journal*, **2011**, 30, 2219-32	13	182
18	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. *Nature*, **2011**, 469, 539-42	50.4	943
17	Splicing-directed therapy in a new mouse model of human accelerated aging. *Science Translational Medicine*, **2011**, 3, 106ra107	17.5	240
16	Nuclear envelope alterations generate an aging-like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. *Aging Cell*, **2010**, 9, 947-57	9.9	44
15	A small-cell lung cancer genome with complex signatures of tobacco exposure. *Nature*, **2010**, 463, 184-90	50.4	852
14	A comprehensive catalogue of somatic mutations from a human cancer genome. *Nature*, **2010**, 463, 191-6	50.4	1303
13	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. *Nature*, **2010**, 467, 1109-13	50.4	1013
12	Somatic structural rearrangements in genetically engineered mouse mammary tumors. *Genome Biology*, **2010**, 11, R100	18.3	22

11	Complex landscapes of somatic rearrangement in human breast cancer genomes. *Nature*, **2009**, 462, 1005-10	50.4	684
10	Combined treatment with statins and aminobisphosphonates extends longevity in a mouse model of human premature aging. *Nature Medicine*, **2008**, 14, 767-72	50.5	300
9	Microcephalia with mandibular and dental dysplasia in adult Zmpste24-deficient mice. *Journal of Anatomy*, **2008**, 213, 509-19	2.9	12
8	Nuclear envelope defects cause stem cell dysfunction in premature-aging mice. *Journal of Cell Biology*, **2008**, 181, 27-35	7.3	145
7	Premature aging in mice activates a systemic metabolic response involving autophagy induction. *Human Molecular Genetics*, **2008**, 17, 2196-211	5.6	123
6	Nuclear envelope defects cause stem cell dysfunction in premature-aging mice. *Journal of Experimental Medicine*, **2008**, 205, i10-i10	16.6	
5	Human progeroid syndromes, aging and cancer: new genetic and epigenetic insights into old questions. *Cellular and Molecular Life Sciences*, **2007**, 64, 155-70	10.3	71
4	Accelerated ageing in mice deficient in Zmpste24 protease is linked to p53 signalling activation. *Nature*, **2005**, 437, 564-8	50.4	362
3	From immature lamin to premature aging: molecular pathways and therapeutic opportunities. *Cell Cycle*, **2005**, 4, 1732-5	4.7	30
2	AtFACE-2, a functional prenylated protein protease from Arabidopsis thaliana related to mammalian Ras-converting enzymes. *Journal of Biological Chemistry*, **2003**, 278, 42091-7	5.4	42
1	Identification, functional expression and enzymic analysis of two distinct CaaX proteases from Caenorhabditis elegans. *Biochemical Journal*, **2003**, 370, 1047-54	3.8	25