Ignacio Varela

List of Publications by Year
in descending order

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84 papers	27,210 citations	57758 44 h-index	58581 82 g-index
89 all docs	89 docs citations	89 times ranked	38497 citing authors

#	Article	IF	Citations
1	PLCÎ³1/PKCÎ¸ Downstream Signaling Controls Cutaneous T-Cell Lymphoma Development and Progression. Journal of Investigative Dermatology, 2022, 142, 1391-1400.e15.	0.7	5
2	Role of SWI/SNF chromatin remodeling genes in lung cancer development. Biochemical Society Transactions, 2022, 50, 1143-1150.	3.4	6
3	HDAC7 is a major contributor in the pathogenesis of infant t(4;11) proB acute lymphoblastic leukemia. Leukemia, 2021, 35, 2086-2091.	7.2	8
4	ARID2 deficiency promotes tumor progression and is associated with higher sensitivity to chemotherapy in lung cancer. Oncogene, 2021, 40, 2923-2935.	5.9	22
5	Integrative methylome-transcriptome analysis unravels cancer cell vulnerabilities in infant MLL-rearranged B cell acute lymphoblastic leukemia. Journal of Clinical Investigation, 2021, 131, .	8.2	14
6	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.	3.4	10
7	Tumor Functional Heterogeneity Unraveled by scRNA-seq Technologies. Trends in Cancer, 2020, 6, 13-19.	7.4	130
8	Analysis pipelines for cancer genome sequencing in mice. Nature Protocols, 2020, 15, 266-315.	12.0	25
9	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.	1.4	5
10	Bone Marrow Clonogenic Myeloid Progenitors from NPM1-Mutated AML Patients Do Not Harbor the NPM1 Mutation: Implication for the Cell-Of-Origin of NPM1+ AML. Genes, 2020, 11, 73.	2.4	2
11	Discovery of a CD10-negative B-progenitor in human fetal life identifies unique ontogeny-related developmental programs. Blood, 2019, 134, 1059-1071.	1.4	62
12	Natural history and cell of origin of TCF3-ZNF384 and PTPN11 mutations in monozygotic twins with concordant BCP-ALL. Blood, 2019, 134, 900-905.	1.4	25
13	Enhanced hemato-endothelial specification during human embryonic differentiation through developmental cooperation between AF4-MLL and MLL-AF4 fusions. Haematologica, 2019, 104, 1189-1201.	3.5	15
14	Unraveling the cellular origin and clinical prognostic markers of infant B-cell acute lymphoblastic leukemia using genome-wide analysis. Haematologica, 2019, 104, 1176-1188.	3.5	76
15	CD133-directed CAR T-cells for MLL leukemia: on-target, off-tumor myeloablative toxicity. Leukemia, 2019, 33, 2090-2125.	7.2	30
16	Evolutionary routes and KRAS dosage define pancreatic cancer phenotypes. Nature, 2018, 554, 62-68.	27.8	328
17	Clonal haematopoiesis is not prevalent in survivors of childhood cancer. British Journal of Haematology, 2018, 181, 537-539.	2.5	12
18	Somatic Mutations Reveal Lineage Relationships and Age-Related Mutagenesis in Human Hematopoiesis. Cell Reports, 2018, 25, 2308-2316.e4.	6.4	170

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19	Applied diagnostics in liver cancer. Efficient combinations of sorafenib with targeted inhibitors blocking AKT/mTOR. Oncotarget, 2018, 9, 30869-30882.	1.8	9
20	UTX-mediated enhancer and chromatin remodeling suppresses myeloid leukemogenesis through noncatalytic inverse regulation of ETS and GATA programs. Nature Genetics, 2018, 50, 883-894.	21.4	117
21	Evaluation of Toll-like-receptor gene family variants as prognostic biomarkers in rheumatoid arthritis. Immunology Letters, 2017, 187, 35-40.	2.5	7
22	Molecular synergy underlies the co-occurrence patterns and phenotype of NPM1-mutant acute myeloid leukemia. Blood, 2017, 130, 1911-1922.	1.4	63
23	Rapid parallel acquisition of somatic mutations after <scp>NPM</scp>1 in acute myeloid leukaemia evolution. British Journal of Haematology, 2017, 176, 825-829.	2.5	3
24	Shared Oncogenic Pathways Implicated in Both Virus-Positive and UV-Induced Merkel Cell Carcinomas. Journal of Investigative Dermatology, 2017, 137, 197-206.	0.7	78
25	JAK2 V617F hematopoietic clones are present several years prior to MPN diagnosis and follow different expansion kinetics. Blood Advances, 2017, 1, 968-971.	5.2	42
26	Intratumoral heterogeneity and clonal evolution in blood malignancies and solid tumors. Oncotarget, 2017, 8, 66742-66746.	1.8	12
27	Analysis of the mutational landscape of classic Hodgkin lymphoma identifies disease heterogeneity and potential therapeutic targets. Oncotarget, 2017, 8, 111386-111395.	1.8	33
28	Multiplexed pancreatic genome engineering and cancer induction by transfection-based CRISPR/Cas9 delivery in mice. Nature Communications, 2016, 7, 10770.	12.8	145
29	Development and validation of a comprehensive genomic diagnostic tool for myeloid malignancies. Blood, 2016, 128, e1-e9.	1.4	49
30	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.	3.5	35
31	Identification of a germline F692L drug resistance variant in cis with Flt3-internal tandem duplication in knock-in mice. Haematologica, 2016, 101, e328-e331.	3.5	5
32	Development Refractoriness of MLL-Rearranged Human B Cell Acute Leukemias to Reprogramming into Pluripotency. Stem Cell Reports, 2016, 7, 602-618.	4.8	38
33	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, 2478-2489.	0.9	37
34	Leukemia-Associated Somatic Mutations Drive Distinct Patterns of Age-Related Clonal Hemopoiesis. Cell Reports, 2015, 10, 1239-1245.	6.4	443
35	Colorectal Adenomas Contain Multiple Somatic Mutations That Do Not Coincide with Synchronous Adenocarcinoma Specimens. PLoS ONE, 2015, 10, e0119946.	2.5	11
36	Recurrent chromosomal gains and heterogeneous driver mutations characterise papillary renal cancer evolution. Nature Communications, 2015, 6, 6336.	12.8	100

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37	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, 13982-13987.	7.1	172
38	The E3 ligase RNF43 inhibits Wnt signaling downstream of mutated Î²-catenin by sequestering TCF4 to the nuclear membrane. Science Signaling, 2015, 8, ra90.	3.6	67
39	A Truncated Variant of ASCC1, a Novel Inhibitor of NF-ÎºB, Is Associated with Disease Severity in Patients with Rheumatoid Arthritis. Journal of Immunology, 2015, 195, 5415-5420.	0.8	17
40	A conditional piggyBac transposition system for genetic screening in mice identifies oncogenic networks in pancreatic cancer. Nature Genetics, 2015, 47, 47-56.	21.4	77
41	Characterization of gene mutations and copy number changes in acute myeloid leukemia using a rapid target enrichment protocol. Haematologica, 2015, 100, 214-222.	3.5	43
42	Individualized strategies to target specific mechanisms of disease in malignant melanoma patients displaying unique mutational signatures. Oncotarget, 2015, 6, 25452-25465.	1.8	3
43	A novel mutation in ADAMTS13 of a child with Upshaw-Schulman Syndrome. Thrombosis and Haemostasis, 2014, 112, 1065-1068.	3.4	3
44	Sin3b Interacts with Myc and Decreases Myc Levels. Journal of Biological Chemistry, 2014, 289, 22221-22236.	3.4	29
45	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.	9.6	101
46	Development of synchronous VHL syndrome tumors reveals contingencies and constraints to tumor evolution. Genome Biology, 2014, 15, 433.	8.8	69
47	Genomic architecture and evolution of clear cell renal cell carcinomas defined by multiregion sequencing. Nature Genetics, 2014, 46, 225-233.	21.4	1,103
48	A next-generation dual-recombinase system for time- and host-specific targeting of pancreatic cancer. Nature Medicine, 2014, 20, 1340-1347.	30.7	188
49	Spatial and temporal diversity in genomic instability processes defines lung cancer evolution. Science, 2014, 346, 251-256.	12.6	962
50	Whole-exome sequencing in splenic marginal zone lymphoma reveals mutations in genes involved in marginal zone differentiation. Leukemia, 2014, 28, 1334-1340.	7.2	115
51	PLCG1 mutations in cutaneous T-cell lymphomas. Blood, 2014, 123, 2034-2043.	1.4	193
52	Abstract 983: Intratumor heterogeneity in non-small cell lung cancer inferred by multi-region exome sequencing. , 2014, , .		0
53	A Genetic Progression Model of BrafV600E-Induced Intestinal Tumorigenesis Reveals Targets for Therapeutic Intervention. Cancer Cell, 2013, 24, 15-29.	16.8	183
54	Inflammatory and immune response genes have significantly altered expression in schizophrenia. Molecular Psychiatry, 2013, 18, 1056-1057.	7.9	49

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55	Detailed molecular characterisation of acute myeloid leukaemia with a normal karyotype using targeted DNA capture. Leukemia, 2013, 27, 1820-1825.	7.2	29
56	Whole exome sequencing of adenoid cystic carcinoma. Journal of Clinical Investigation, 2013, 123, 2965-2968.	8.2	233
57	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	27.8	1,535
58	Intratumor Heterogeneity and Branched Evolution Revealed by Multiregion Sequencing. New England Journal of Medicine, 2012, 366, 883-892.	27.0	6,769
59	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	28.9	1,673
60	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	28.9	1,249
61	Mutational Status of Splenic Marginal Zone Lymphoma Revealed by Whole Exome Sequencing.. Blood, 2012, 120, 2698-2698.	1.4	0
62	Mutations in PLCG1 Is a Frequent Event in Cutaneous T-Cell Lymphomas. Blood, 2012, 120, 300-300.	1.4	0
63	Characterization of Subclonal Changes Along Progression in Multiple Myeloma.. Blood, 2012, 120, 2924-2924.	1.4	1
64	Targeted gene correction of Î±1-antitrypsin deficiency in induced pluripotent stem cells. Nature, 2011, 478, 391-394.	27.8	635
65	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	28.9	2,020
66	Aging and chronic DNA damage response activate a regulatory pathway involving miR-29 and p53. EMBO Journal, 2011, 30, 2219-2232.	7.8	216
67	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	27.8	1,127
68	Splicing-Directed Therapy in a New Mouse Model of Human Accelerated Aging. Science Translational Medicine, 2011, 3, 106ra107.	12.4	334
69	Nuclear envelope alterations generate an agingâ€like epigenetic pattern in mice deficient in Zmpste24 metalloprotease. Aging Cell, 2010, 9, 947-957.	6.7	50
70	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	27.8	972
71	A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196.	27.8	1,519
72	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. Nature, 2010, 467, 1109-1113.	27.8	1,200

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73	Somatic structural rearrangements in genetically engineered mouse mammary tumors. Genome Biology, 2010, 11, R100.	9.6	24
74	Complex landscapes of somatic rearrangement in human breast cancer genomes. Nature, 2009, 462, 1005-1010.	27.8	776
75	Combined treatment with statins and aminobisphosphonates extends longevity in a mouse model of human premature aging. Nature Medicine, 2008, 14, 767-772.	30.7	355
76	Microcephalia with mandibular and dental dysplasia in adult Zmpste24â€deficient mice. Journal of Anatomy, 2008, 213, 509-519.	1.5	14
77	Nuclear envelope defects cause stem cell dysfunction in premature-aging mice. Journal of Cell Biology, 2008, 181, 27-35.	5.2	160
78	Premature aging in mice activates a systemic metabolic response involving autophagy induction. Human Molecular Genetics, 2008, 17, 2196-2211.	2.9	141
79	Nuclear envelope defects cause stem cell dysfunction in premature-aging mice. Journal of Experimental Medicine, 2008, 205, i10-i10.	8.5	0
80	Human progeroid syndromes, aging and cancer: new genetic and epigenetic insights into old questions. Cellular and Molecular Life Sciences, 2007, 64, 155-170.	5.4	77
81	Accelerated ageing in mice deficient in Zmpste24 protease is linked to p53 signalling activation. Nature, 2005, 437, 564-568.	27.8	438
82	From Immature Lamin to Premature Aging: Molecular Pathways and Therapeutic Opportunities. Cell Cycle, 2005, 4, 1732-1735.	2.6	31
83	AtFACE-2, a functional Prenylated Protein Protease from Arabidopsis thaliana Related to Mammalian Ras-converting Enzymes. Journal of Biological Chemistry, 2003, 278, 42091-42097.	3.4	46
84	Identification, functional expression and enzymic analysis of two distinct CaaX proteases from Caenorhabditis elegans. Biochemical Journal, 2003, 370, 1047-1054.	3.7	28