Lorenzo Melchor

List of Publications by Year
in descending order

39 papers	2,762 citations	257357 24 h-index	330025 37 g-index
42 all docs	42 docs citations	42 times ranked	4661 citing authors

#	Article	IF	Citations
1	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. Journal of Clinical Oncology, 2015, 33, 3911-3920.	0.8	463
2	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Nature Communications, 2015, 6, 6997.	5.8	261
3	Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. Leukemia, 2014, 28, 384-390.	3.3	252
4	Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. Blood, 2012, 120, 1077-1086.	0.6	231
5	Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. Leukemia, 2014, 28, 1705-1715.	3.3	207
6	Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. Blood, 2013, 122, 219-226.	0.6	147
7	The complex genetic landscape of familial breast cancer. Human Genetics, 2013, 132, 845-863.	1.8	125
8	The impact of intra-clonal heterogeneity on the treatment of multiple myeloma. British Journal of Haematology, 2014, 165, 441-454.	1.2	91
9	Wnt and Neuregulin1/ErbB signalling extends 3D culture of hormone responsive mammary organoids. Nature Communications, 2016, 7, 13207.	5.8	88
10	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794.	3.2	81
11	Comprehensive characterization of the DNA amplification at 13q34 in human breast cancer reveals TFDP1 and CUL4A as likely candidate target genes. Breast Cancer Research, 2009, 11, R86.	2.2	75
12	Distinct genomic aberration patterns are found in familial breast cancer associated with different immunohistochemical subtypes. Oncogene, 2008, 27, 3165-3175.	2.6	74
13	Serum free immunoglobulin light chain evaluation as a marker of impact from intraclonal heterogeneity on myeloma outcome. Blood, 2014, 123, 3414-3419.	0.6	68
14	Clonal evolution in myeloma: the impact of maintenance lenalidomide and depth of response on the genetics and sub-clonal structure of relapsed disease in uniformly treated newly diagnosed patients. Haematologica, 2019, 104, 1440-1450.	1.7	67
15	Coexistent hyperdiploidy does not abrogate poor prognosis in myeloma with adverse cytogenetics and may precede IGH translocations. Blood, 2015, 125, 831-840.	0.6	57
16	A predictor based on the somatic genomic changes of the BRCA1/BRCA2 breast cancer tumors identifies the non-BRCA1/BRCA2 tumors with BRCA1 promoter hypermethylation. Clinical Cancer Research, 2005, 11, 1146-53.	3.2	51
17	Immunohistochemical classification of non-BRCA1/2 tumors identifies different groups that demonstrate the heterogeneity of BRCAX families. Modern Pathology, 2007, 20, 1298-1306.	2.9	48
18	Identification of cellular and genetic drivers of breast cancer heterogeneity in genetically engineered mouse tumour models. Journal of Pathology, 2014, 233, 124-137.	2.1	47

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19	An integrative hypothesis about the origin and development of sporadic and familial breast cancer subtypes. Carcinogenesis, 2008, 29, 1475-1482.	1.3	45
20	Analysis of myelodysplastic syndromes with complex karyotypes by high-resolution comparative genomic hybridization and subtelomeric CGH array. Genes Chromosomes and Cancer, 2005, 42, 287-298.	1.5	40
21	A haplotype containing thep53polymorphisms Ins16bp and Arg72Pro modifies cancer risk inBRCA2mutation carriers. Human Mutation, 2006, 27, 242-248.	1.1	35
22	Gene amplification of the transcription factor DP1 and CTNND1 in human lung cancer. Journal of Pathology, 2010, 222, 89-98.	2.1	33
23	Estrogen Receptor Status Could Modulate the Genomic Pattern in Familial and Sporadic Breast Cancer. Clinical Cancer Research, 2007, 13, 7305-7313.	3.2	31
24	Genomic analysis of the 8p11-12 amplicon in familial breast cancer. International Journal of Cancer, 2007, 120, 714-717.	2.3	30
25	The Accumulation of Specific Amplifications Characterizes Two Different Genomic Pathways of Evolution of Familial Breast Tumors. Clinical Cancer Research, 2005, 11, 8577-8584.	3.2	16
26	About the origin and development of hereditary conventional renal cell carcinoma in a four-generation t(3;8)(p14.1;q24.23) family. European Journal of Human Genetics, 2005, 13, 570-578.	1.4	15
27	Biology and Treatment of Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S65-S70.	0.2	15
28	Wholeâ€exome <scp>DNA</scp> sequence analysis of Brca2â€•and Trp53â€deficient mouse mammary gland tumours. Journal of Pathology, 2015, 236, 186-200.	2.1	14
29	Highway to heaven: mammary gland development and differentiation. Breast Cancer Research, 2008, 10, 305.	2.2	6
30	Understanding the cytological diploidization mechanism of polyploid wild wheats. Cytogenetic and Genome Research, 2005, 109, 205-209.	0.6	5
31	Cumulative advantages and social capabilities in scientific mobility in the Health Sciences: The Spanish case. PLoS ONE, 2017, 12, e0173204.	1.1	5
32	Reproductive history determines Erb b 2 locus amplification, WNT signalling and tumour phenotype in a murine breast cancer model. DMM Disease Models and Mechanisms, 2021, 14, .	1.2	3
33	The impact of long-term lenalidomide exposure on the cellular composition of bone marrow. Leukemia and Lymphoma, 2014, 55, 2665-2668.	0.6	2
34	The Spectrum of Epigenetic Mutations in Myeloma and Their Clinical Impact. Blood, 2014, 124, 2194-2194.	0.6	2
35	Co-Existent Hyperdiploidy Does Not Abrogate The Poor Prognosis Associated With Adverse Cytogenetics In Myeloma. Blood, 2013, 122, 529-529.	0.6	1
36	Mutational Patterns and Copy Number Changes at Diagnosis Are a Powerful Tool to Predict Outcome: Result of the Sequencing Study of 463 Newly Diagnosed Myeloma Trial Patients. Blood, 2014, 124, 637-637.	0.6	1

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37	Discovery Of Genome Wide Epigenetic Programming In t(4;14) Multiple Myeloma and In The Progression From Myeloma To Plasma Cell Leukemia Via Methyl Binding Domain Protein Capture and Sequencing. Blood, 2013, 122, 599-599.	0.6	0
38	Single-Cell Genetic Analysis Reveals The Genetic Composition Of Founder Clones, Phylogenetic Patterns Of Branching and Parallel Evolution, and Clonal Fluctuations Following Patient Treatment In Multiple Myeloma. Blood, 2013, 122, 398-398.	0.6	0
39	The Extent of Intra-Clonal Genetic Diversity within the Myeloma Clone Is a Predictive Biomarker of Progression and Outcome after Treatment. Blood, 2014, 124, 640-640.	0.6	0