Maria C ChillÃ³n

List of Publications by Year
in descending order

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74 papers	3,747 citations	218677 26 h-index	128289 60 g-index
74 all docs	74 docs citations	74 times ranked	5375 citing authors

#	Article	IF	Citations
1	Standardization and quality control studies of â€˜real-timeâ€™ quantitative reverse transcriptase polymerase chain reaction of fusion gene transcripts for residual disease detection in leukemia â€“ A Europe Against Cancer Program. Leukemia, 2003, 17, 2318-2357.	7.2	1,359
2	MYD88 L265P is a marker highly characteristic of, but not restricted to, WaldenstrÃ¶mâ€™s macroglobulinemia. Leukemia, 2013, 27, 1722-1728.	7.2	238
3	Bisphosphonate-related osteonecrosis of the jaw is associated with polymorphisms of the cytochrome P450 CYP2C8 in multiple myeloma: a genome-wide single nucleotide polymorphism analysis. Blood, 2008, 112, 2709-2712.	1.4	213
4	Deregulation of microRNA expression in the different genetic subtypes of multiple myeloma and correlation with gene expression profiling. Leukemia, 2010, 24, 629-637.	7.2	188
5	Critical evaluation of ASO RQ-PCR for minimal residual disease evaluation in multiple myeloma. A comparative analysis with flow cytometry. Leukemia, 2014, 28, 391-397.	7.2	155
6	Risk-adapted treatment of acute promyelocytic leukemia with all-trans retinoic acid and anthracycline monochemotherapy: long-term outcome of the LPA 99 multicenter study by the PETHEMA Group. Blood, 2008, 112, 3130-3134.	1.4	154
7	Molecular stratification model for prognosis in cytogenetically normal acute myeloid leukemia. Blood, 2009, 114, 148-152.	1.4	78
8	Using quantification of the PML-RARÂ transcript to stratify the risk of relapse in patients with acute promyelocytic leukemia. Haematologica, 2007, 92, 315-322.	3.5	77
9	Prognostic value of FLT3 mutations in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline monochemotherapy. Haematologica, 2011, 96, 1470-1477.	3.5	59
10	De novo methylation of tumor suppressor gene p16/INK4a is a frequent finding in multiple myeloma patients at diagnosis. Leukemia, 2000, 14, 183-187.	7.2	56
11	Patterns of BCR/ABL gene rearrangements by interphase fluorescence in situ hybridization (FISH) in BCR/ABL+ leukemias: incidence and underlying genetic abnormalities. Leukemia, 2003, 17, 1124-1129.	7.2	56
12	Prognostic significance of FLT3 mutational status and expression levels in MLL-AF4+ and MLL-germline acute lymphoblastic leukemia. Leukemia, 2012, 26, 2360-2366.	7.2	55
13	High FOXO3a expression is associated with a poorer prognosis in AML with normal cytogenetics. Leukemia Research, 2009, 33, 1706-1709.	0.8	49
14	Long FLT3 internal tandem duplications and reduced PML-RARÂ expression at diagnosis characterize a high-risk subgroup of acute promyelocytic leukemia patients. Haematologica, 2010, 95, 745-751.	3.5	47
15	The relevance of preferentially expressed antigen of melanoma (PRAME) as a marker of disease activity and prognosis in acute promyelocytic leukemia. Haematologica, 2008, 93, 1797-1805.	3.5	41
16	BAALC is an important predictor of refractoriness to chemotherapy and poor survival in intermediate-risk acute myeloid leukemia (AML). Annals of Hematology, 2010, 89, 453-458.	1.8	40
17	FLT3-activating mutations are associated with poor prognostic features in AML at diagnosis but they are not an independent prognostic factor. The Hematology Journal, 2004, 5, 239-246.	1.4	37
18	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBPÎ±. Leukemia, 2016, 30, 674-682.	7.2	36

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19	Molecular Characterization of Immunoglobulin Gene Rearrangements in Diffuse Large B-Cell Lymphoma. American Journal of Pathology, 2012, 181, 1879-1888.	3.8	31
20	From WaldenstrÃ¶mâ€™s macroglobulinemia to aggressive diffuse large B-cell lymphoma: a whole-exome analysis of abnormalities leading to transformation. Blood Cancer Journal, 2017, 7, e591-e591.	6.2	31
21	Low expression of ZHX2, but not RCBTB2 or RAN, is associated with poor outcome in multiple myeloma. British Journal of Haematology, 2008, 141, 212-215.	2.5	29
22	Upregulation of Dicer is more frequent in monoclonal gammopathies of undetermined significance than in multiple myeloma patients and is associated with longer survival in symptomatic myeloma patients. Haematologica, 2011, 96, 468-471.	3.5	29
23	Detection of MYD88 L265P Mutation by Real-Time Allele-Specific Oligonucleotide Polymerase Chain Reaction. Applied Immunohistochemistry and Molecular Morphology, 2014, 22, 768-773.	1.2	28
24	Deletions and rearrangements of cyclin-dependent kinase 4 inhibitor gene p16 are associated with poor prognosis in B cell non-Hodgkinâ€™s lymphomas. Leukemia, 1997, 11, 1915-1920.	7.2	27
25	Incomplete DJH rearrangements as a novel tumor target for minimal residual disease quantitation in multiple myeloma using real-time PCR. Leukemia, 2003, 17, 1051-1057.	7.2	27
26	Flow cytometric immunobead assay for fast and easy detection of PMLâ€“RARA fusion proteins for the diagnosis of acute promyelocytic leukemia. Leukemia, 2012, 26, 1976-1985.	7.2	27
27	Ligand-independent FLT3 activation does not cooperate with MLL-AF4 to immortalize/transform cord blood CD34+ cells. Leukemia, 2014, 28, 666-674.	7.2	27
28	Panobinostat as part of induction and maintenance for elderly patients with newly diagnosed acute myeloid leukemia: phase Ib/II panobidara study. Haematologica, 2015, 100, 1294-1300.	3.5	27
29	The cryptic IRF2BP2-RARA fusion transforms hematopoietic stem/progenitor cells and induces retinoid-sensitive acute promyelocytic leukemia. Leukemia, 2017, 31, 747-751.	7.2	24
30	HLA specificities are related to development and prognosis of diffuse large B-cell lymphoma. Blood, 2013, 122, 1448-1454.	1.4	23
31	A Next-Generation Sequencing Strategy for Evaluating the Most Common Genetic Abnormalities in Multiple Myeloma. Journal of Molecular Diagnostics, 2017, 19, 99-106.	2.8	22
32	Prediction of peripheral neuropathy in multiple myeloma patients receiving bortezomib and thalidomide: a genetic study based on a single nucleotide polymorphism array. Hematological Oncology, 2017, 35, 746-751.	1.7	22
33	Mapping of Genetic Abnormalities of Primary Tumours from Metastatic CRC by High-Resolution SNP Arrays. PLoS ONE, 2010, 5, e13752.	2.5	22
34	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. Haematologica, 2015, 100, e183-e185.	3.5	20
35	Molecular characteristics and gene segment usage in IGH gene rearrangements in multiple myeloma. Haematologica, 2005, 90, 906-13.	3.5	20
36	Two new 3?PML Breakpoints in t(15;17)(q22;q21)-positive acute promyelocytic leukemia. , 2000, 27, 35-43.		19

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37	High-resolution copy number analysis of paired normal-tumor samples from diffuse large B cell lymphoma. Annals of Hematology, 2016, 95, 253-262.	1.8	19
38	Unraveling the heterogeneity of IgM monoclonal gammopathies: a gene mutational and gene expression study. Annals of Hematology, 2018, 97, 475-484.	1.8	19
39	The detection of contaminating clonal cells in apheresis products is related to response and outcome in multiple myeloma undergoing autologous peripheral blood stem cell transplantation. Leukemia, 2000, 14, 1493-1499.	7.2	18
40	The use of CD138 positively selected marrow samples increases the applicability of minimal residual disease assessment by PCR in patients with multiple myeloma. Annals of Hematology, 2013, 92, 97-100.	1.8	18
41	The predominant myeloma clone at diagnosis, CDR3 defined, is constantly detectable across all stages of disease evolution. Leukemia, 2015, 29, 1435-1437.	7.2	17
42	Molecular profiling of immunoglobulin heavy-chain gene rearrangements unveils new potential prognostic markers for multiple myeloma patients. Blood Cancer Journal, 2020, 10, 14.	6.2	16
43	Kappa deleting element as an alternative molecular target for minimal residual disease assessment by realâ€time quantitative <scp>PCR</scp> in patients with multiple myeloma. European Journal of Haematology, 2012, 89, 328-335.	2.2	15
44	Networking for advanced molecular diagnosis in acute myeloid leukemia patients is possible: the PETHEMA NGS-AML project. Haematologica, 2021, 106, 3079-3089.	3.5	15
45	Gene scanning of VDJH-amplified segments is a clinically relevant technique to detect contaminating tumor cells in the apheresis products of multiple myeloma patients undergoing autologous peripheral blood stem cell transplantation. Bone Marrow Transplantation, 2001, 28, 665-672.	2.4	14
46	Frequency of HLAâ€A, â€B and â€DRB1 specificities and haplotypic associations in the population of Castilla y LeÃ³n (northwestâ€central Spain). Tissue Antigens, 2011, 78, 249-255.	1.0	14
47	Liquid biopsy: a nonâ€invasive approach for Hodgkin lymphoma genotyping. British Journal of Haematology, 2021, 195, 542-551.	2.5	14
48	MYD88 Mutations: Transforming the Landscape of IgM Monoclonal Gammopathies. International Journal of Molecular Sciences, 2022, 23, 5570.	4.1	14
49	Simultaneous analysis of the expression of 14 genes with individual prognostic value in myelodysplastic syndrome patients at diagnosis: WT1 detection in peripheral blood adversely affects survival. Annals of Hematology, 2012, 91, 1887-1895.	1.8	12
50	Do endothelial cells belong to the primitive stem leukemic clone in CML? Role of extracellular vesicles. Leukemia Research, 2015, 39, 921-924.	0.8	12
51	Clinical significance of complex karyotype at diagnosis in pediatric and adult patients with de novo acute promyelocytic leukemia treated with ATRA and chemotherapy. Leukemia and Lymphoma, 2019, 60, 1146-1155.	1.3	12
52	Identification of relapseâ€associated gene mutations by nextâ€generation sequencing in lowâ€risk acute myeloid leukaemia patients. British Journal of Haematology, 2020, 189, 718-730.	2.5	12
53	Immunoglobulin gene rearrangement IGHV3-48 is a predictive marker of histological transformation into aggressive lymphoma in follicular lymphomas. Blood Cancer Journal, 2019, 9, 52.	6.2	11
54	A New Next-Generation Sequencing Strategy for the Simultaneous Analysis of Mutations and Chromosomal Rearrangements at DNA Level in Acute Myeloid Leukemia Patients. Journal of Molecular Diagnostics, 2020, 22, 60-71.	2.8	11

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55	Basophil-lineage commitment in acute promyelocytic leukemia predicts for severe bleeding after starting therapy. Modern Pathology, 2018, 31, 1318-1331.	5.5	9
56	An analysis of the impact of CD56 expression in de novo acute promyelocytic leukemia patients treated with upfront all-trans retinoic acid and anthracycline-based regimens. Leukemia and Lymphoma, 2019, 60, 1030-1035.	1.3	9
57	Involvement of primary mesenchymal precursors and hematopoietic bone marrow cells from chronic myeloid leukemia patients by BCRâ€ABL1 fusion gene. American Journal of Hematology, 2014, 89, 288-294.	4.1	8
58	Focal Adhesion Genes Refine the Intermediate-Risk Cytogenetic Classification of Acute Myeloid Leukemia. Cancers, 2018, 10, 436.	3.7	8
59	Evaluating gene expression profiling by quantitative polymerase chain reaction to develop a clinically feasible test for outcome prediction in multiple myeloma. British Journal of Haematology, 2013, 163, 223-234.	2.5	7
60	Status of methylation of p16 gene in multiple myeloma: a comparative study of three methods for its detection. Clinical Biochemistry, 2000, 33, 415-418.	1.9	5
61	Risk of placentaâ€mediated pregnancy complications or pregnancyâ€related <scp>VTE</scp> in <scp>VTE</scp>â€asymptomatic families of probands with <scp>VTE</scp> and heterozygosity for factor V <scp>L</scp>eiden or <scp>G</scp>20210 prothrombin mutation. European Journal of Haematology, 2012, 89, 250-255.	2.2	5
62	Quantitative PCR: an alternative approach to detect common copy number alterations in multiple myeloma. Annals of Hematology, 2017, 96, 1699-1705.	1.8	5
63	NEDD9, an independent good prognostic factor in intermediate-risk acute myeloid leukemia patients. Oncotarget, 2017, 8, 76003-76014.	1.8	5
64	Clinical and Prognostic Value of Discrepancies in Microsatellite DNA Regions Between Recipient and Donor in Human Leukocyte Antigen-Identical Allogeneic Transplantation Setting. Transplantation, 2008, 86, 983-990.	1.0	4
65	Wilms Tumor 1 gene expression levels improve risk stratification in <scp>AML</scp> patients. Results of a multicentre study within the Spanish Group for Molecular Biology in Haematology. British Journal of Haematology, 2018, 181, 542-546.	2.5	4
66	HLA specificities are associated with prognosis in IGHV-mutated CLL-like high-count monoclonal B cell lymphocytosis. PLoS ONE, 2017, 12, e0172978.	2.5	4
67	The presence of DRB1*01 allele in multiple myeloma patients is associated with an indolent disease. Tissue Antigens, 2008, 71, 548-551.	1.0	3
68	Genetic complexity impacts the clinical outcome of follicular lymphoma patients. Blood Cancer Journal, 2021, 11, 11.	6.2	3
69	The novel <scp>HLAâ€DQB1</scp>*06:03:27 allele characterised by sequenceâ€based typing in a European bone marrow donor. Hla, 2021, 98, 498-500.	0.6	3
70	Two new 3â€² PML Breakpoints in t(15;17)(q22;q21)â€positive acute promyelocytic leukemia. Genes Chromosomes and Cancer, 2000, 27, 35-43.	2.8	3
71	Identification of the novel HLAâ€A*23:01:01:27 allele in an acute myeloid patient and related donor. Hla, 2022, 100, 62-64.	0.6	3
72	Exportinâ€1 E571K mutation is a common finding in patients with classical Hodgkin lymphoma. Hematological Oncology, 2019, 37, 215-218.	1.7	2

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73	Allele and haplotype frequencies of HLA-A, -B, -C, -DRB1, -DQB1 and -DQA1 in Castile and Leon region from North West of Spain. Human Immunology, 2021, 82, 549-550.	2.4	1
74	Management of mixed acute rejection driven by a de novo donor-specific complement-binding anti-DQB1*03:01 antibody and intraepithelial CD8 T-cells in a kidney recipient: a case report. British Journal of Biomedical Science, 2021, 78, 244-247.	1.3	0