

# Maria C ChillÃ³n

## List of Publications by Year in descending order

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74  
papers

3,747  
citations

249298

26  
h-index

145109

60  
g-index

74  
all docs

74  
docs citations

74  
times ranked

5757  
citing authors

#	ARTICLE	IF	CITATIONS
1	Standardization and quality control studies of "real-time" quantitative reverse transcriptase polymerase chain reaction of fusion gene transcripts for residual disease detection in leukemia " A Europe Against Cancer Program. <i>Leukemia</i> , 2003, 17, 2318-2357.	3.3	1,359
2	MYD88 L265P is a marker highly characteristic of, but not restricted to, Waldenström's macroglobulinemia. <i>Leukemia</i> , 2013, 27, 1722-1728.	3.3	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. <i>Blood</i> , 2008, 112, 2709-2712.	0.6	213
4	Deregulation of microRNA expression in the different genetic subtypes of multiple myeloma and correlation with gene expression profiling. <i>Leukemia</i> , 2010, 24, 629-637.	3.3	188
5	Critical evaluation of ASO RQ-PCR for minimal residual disease evaluation in multiple myeloma. A comparative analysis with flow cytometry. <i>Leukemia</i> , 2014, 28, 391-397.	3.3	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. <i>Blood</i> , 2008, 112, 3130-3134.	0.6	154
7	Molecular stratification model for prognosis in cytogenetically normal acute myeloid leukemia. <i>Blood</i> , 2009, 114, 148-152.	0.6	78
8	Using quantification of the PML-RAR $\alpha$ transcript to stratify the risk of relapse in patients with acute promyelocytic leukemia. <i>Haematologica</i> , 2007, 92, 315-322.	1.7	77
9	Prognostic value of FLT3 mutations in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline monochemotherapy. <i>Haematologica</i> , 2011, 96, 1470-1477.	1.7	59
10	De novo methylation of tumor suppressor gene p16/INK4a is a frequent finding in multiple myeloma patients at diagnosis. <i>Leukemia</i> , 2000, 14, 183-187.	3.3	56
11	Patterns of BCR/ABL gene rearrangements by interphase fluorescence in situ hybridization (FISH) in BCR/ABL+ leukemias: incidence and underlying genetic abnormalities. <i>Leukemia</i> , 2003, 17, 1124-1129.	3.3	56
12	Prognostic significance of FLT3 mutational status and expression levels in MLL-AF4+ and MLL-germline acute lymphoblastic leukemia. <i>Leukemia</i> , 2012, 26, 2360-2366.	3.3	55
13	High FOXO3a expression is associated with a poorer prognosis in AML with normal cytogenetics. <i>Leukemia Research</i> , 2009, 33, 1706-1709.	0.4	49
14	Long FLT3 internal tandem duplications and reduced PML-RAR $\alpha$ expression at diagnosis characterize a high-risk subgroup of acute promyelocytic leukemia patients. <i>Haematologica</i> , 2010, 95, 745-751.	1.7	47
15	The relevance of preferentially expressed antigen of melanoma (PRAME) as a marker of disease activity and prognosis in acute promyelocytic leukemia. <i>Haematologica</i> , 2008, 93, 1797-1805.	1.7	41
16	BAALC is an important predictor of refractoriness to chemotherapy and poor survival in intermediate-risk acute myeloid leukemia (AML). <i>Annals of Hematology</i> , 2010, 89, 453-458.	0.8	40
17	FLT3-activating mutations are associated with poor prognostic features in AML at diagnosis but they are not an independent prognostic factor. <i>The Hematology Journal</i> , 2004, 5, 239-246.	2.0	37
18	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBP $\beta$ . <i>Leukemia</i> , 2016, 30, 674-682.	3.3	36

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19	Molecular Characterization of Immunoglobulin Gene Rearrangements in Diffuse Large B-Cell Lymphoma. <i>American Journal of Pathology</i> , 2012, 181, 1879-1888.	1.9	31
20	From Waldenström's macroglobulinemia to aggressive diffuse large B-cell lymphoma: a whole-exome analysis of abnormalities leading to transformation. <i>Blood Cancer Journal</i> , 2017, 7, e591-e591.	2.8	31
21	Low expression of ZHX2, but not RCBTB2 or RAN, is associated with poor outcome in multiple myeloma. <i>British Journal of Haematology</i> , 2008, 141, 212-215.	1.2	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. <i>Haematologica</i> , 2011, 96, 468-471.	1.7	29
23	Detection of MYD88 L265P Mutation by Real-Time Allele-Specific Oligonucleotide Polymerase Chain Reaction. <i>Applied Immunohistochemistry and Molecular Morphology</i> , 2014, 22, 768-773.	0.6	28
24	Deletions and rearrangements of cyclin-dependent kinase 4 inhibitor gene p16 are associated with poor prognosis in B cell non-Hodgkin's lymphomas. <i>Leukemia</i> , 1997, 11, 1915-1920.	3.3	27
25	Incomplete DJH rearrangements as a novel tumor target for minimal residual disease quantitation in multiple myeloma using real-time PCR. <i>Leukemia</i> , 2003, 17, 1051-1057.	3.3	27
26	Flow cytometric immunobead assay for fast and easy detection of PML-RARA fusion proteins for the diagnosis of acute promyelocytic leukemia. <i>Leukemia</i> , 2012, 26, 1976-1985.	3.3	27
27	Ligand-independent FLT3 activation does not cooperate with MLL-AF4 to immortalize/transform cord blood CD34+ cells. <i>Leukemia</i> , 2014, 28, 666-674.	3.3	27
28	Panobinostat as part of induction and maintenance for elderly patients with newly diagnosed acute myeloid leukemia: phase Ib/II panobidara study. <i>Haematologica</i> , 2015, 100, 1294-1300.	1.7	27
29	The cryptic IRF2BP2-RARA fusion transforms hematopoietic stem/progenitor cells and induces retinoid-sensitive acute promyelocytic leukemia. <i>Leukemia</i> , 2017, 31, 747-751.	3.3	24
30	HLA specificities are related to development and prognosis of diffuse large B-cell lymphoma. <i>Blood</i> , 2013, 122, 1448-1454.	0.6	23
31	A Next-Generation Sequencing Strategy for Evaluating the Most Common Genetic Abnormalities in Multiple Myeloma. <i>Journal of Molecular Diagnostics</i> , 2017, 19, 99-106.	1.2	22
32	Prediction of peripheral neuropathy in multiple myeloma patients receiving bortezomib and thalidomide: a genetic study based on a single nucleotide polymorphism array. <i>Hematological Oncology</i> , 2017, 35, 746-751.	0.8	22
33	Mapping of Genetic Abnormalities of Primary Tumours from Metastatic CRC by High-Resolution SNP Arrays. <i>PLoS ONE</i> , 2010, 5, e13752.	1.1	22
34	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. <i>Haematologica</i> , 2015, 100, e183-e185.	1.7	20
35	Molecular characteristics and gene segment usage in IGH gene rearrangements in multiple myeloma. <i>Haematologica</i> , 2005, 90, 906-13.	1.7	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. <i>Annals of Hematology</i> , 2016, 95, 253-262.	0.8	19
38	Unraveling the heterogeneity of IgM monoclonal gammopathies: a gene mutational and gene expression study. <i>Annals of Hematology</i> , 2018, 97, 475-484.	0.8	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. <i>Leukemia</i> , 2000, 14, 1493-1499.	3.3	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. <i>Annals of Hematology</i> , 2013, 92, 97-100.	0.8	18
41	The predominant myeloma clone at diagnosis, CDR3 defined, is constantly detectable across all stages of disease evolution. <i>Leukemia</i> , 2015, 29, 1435-1437.	3.3	17
42	Molecular profiling of immunoglobulin heavy-chain gene rearrangements unveils new potential prognostic markers for multiple myeloma patients. <i>Blood Cancer Journal</i> , 2020, 10, 14.	2.8	16
43	Kappa deleting element as an alternative molecular target for minimal residual disease assessment by real-time quantitative PCR in patients with multiple myeloma. <i>European Journal of Haematology</i> , 2012, 89, 328-335.	1.1	15
44	Networking for advanced molecular diagnosis in acute myeloid leukemia patients is possible: the PETHEMA NGS-AML project. <i>Haematologica</i> , 2021, 106, 3079-3089.	1.7	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. <i>Bone Marrow Transplantation</i> , 2001, 28, 665-672.	1.3	14
46	Frequency of HLA-A, -B and -DRB1 specificities and haplotypic associations in the population of Castilla y León (northwest-central Spain). <i>Tissue Antigens</i> , 2011, 78, 249-255.	1.0	14
47	Liquid biopsy: a non-invasive approach for Hodgkin lymphoma genotyping. <i>British Journal of Haematology</i> , 2021, 195, 542-551.	1.2	14
48	MYD88 Mutations: Transforming the Landscape of IgM Monoclonal Gammopathies. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5570.	1.8	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. <i>Annals of Hematology</i> , 2012, 91, 1887-1895.	0.8	12
50	Do endothelial cells belong to the primitive stem leukemic clone in CML? Role of extracellular vesicles. <i>Leukemia Research</i> , 2015, 39, 921-924.	0.4	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. <i>Leukemia and Lymphoma</i> , 2019, 60, 1146-1155.	0.6	12
52	Identification of relapse-associated gene mutations by next-generation sequencing in low-risk acute myeloid leukaemia patients. <i>British Journal of Haematology</i> , 2020, 189, 718-730.	1.2	12
53	Immunoglobulin gene rearrangement IGHV3-48 is a predictive marker of histological transformation into aggressive lymphoma in follicular lymphomas. <i>Blood Cancer Journal</i> , 2019, 9, 52.	2.8	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. <i>Journal of Molecular Diagnostics</i> , 2020, 22, 60-71.	1.2	11

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55	Basophil-lineage commitment in acute promyelocytic leukemia predicts for severe bleeding after starting therapy. <i>Modern Pathology</i> , 2018, 31, 1318-1331.	2.9	9
56	An analysis of the impact of CD56 expression in <i>de novo</i> acute promyelocytic leukemia patients treated with upfront all-trans retinoic acid and anthracycline-based regimens. <i>Leukemia and Lymphoma</i> , 2019, 60, 1030-1035.	0.6	9
57	Involvement of primary mesenchymal precursors and hematopoietic bone marrow cells from chronic myeloid leukemia patients by <i>BCR-ABL1</i> fusion gene. <i>American Journal of Hematology</i> , 2014, 89, 288-294.	2.0	8
58	Focal Adhesion Genes Refine the Intermediate-Risk Cytogenetic Classification of Acute Myeloid Leukemia. <i>Cancers</i> , 2018, 10, 436.	1.7	8
59	Evaluating gene expression profiling by quantitative polymerase chain reaction to develop a clinically feasible test for outcome prediction in multiple myeloma. <i>British Journal of Haematology</i> , 2013, 163, 223-234.	1.2	7
60	Status of methylation of p16 gene in multiple myeloma: a comparative study of three methods for its detection. <i>Clinical Biochemistry</i> , 2000, 33, 415-418.	0.8	5
61	Risk of placenta-mediated pregnancy complications or pregnancy-related <i>VTE</i> in asymptomatic families of probands with <i>VTE</i> and heterozygosity for factor V <i>L</i> or <i>G</i> 20210 prothrombin mutation. <i>European Journal of Haematology</i> , 2012, 89, 250-255.	1.1	5
62	Quantitative PCR: an alternative approach to detect common copy number alterations in multiple myeloma. <i>Annals of Hematology</i> , 2017, 96, 1699-1705.	0.8	5
63	<i>NEDD9</i> , an independent good prognostic factor in intermediate-risk acute myeloid leukemia patients. <i>Oncotarget</i> , 2017, 8, 76003-76014.	0.8	5
64	Clinical and Prognostic Value of Discrepancies in Microsatellite DNA Regions Between Recipient and Donor in Human Leukocyte Antigen-Identical Allogeneic Transplantation Setting. <i>Transplantation</i> , 2008, 86, 983-990.	0.5	4
65	Wilms Tumor 1 gene expression levels improve risk stratification in <i>AML</i> patients. Results of a multicentre study within the Spanish Group for Molecular Biology in Haematology. <i>British Journal of Haematology</i> , 2018, 181, 542-546.	1.2	4
66	HLA specificities are associated with prognosis in IGHV-mutated CLL-like high-count monoclonal B cell lymphocytosis. <i>PLoS ONE</i> , 2017, 12, e0172978.	1.1	4
67	The presence of DRB1*01 allele in multiple myeloma patients is associated with an indolent disease. <i>Tissue Antigens</i> , 2008, 71, 548-551.	1.0	3
68	Genetic complexity impacts the clinical outcome of follicular lymphoma patients. <i>Blood Cancer Journal</i> , 2021, 11, 11.	2.8	3
69	The novel <i>HLA-DQB1</i> *06:03:27 allele characterised by sequence-based typing in a European bone marrow donor. <i>Hla</i> , 2021, 98, 498-500.	0.4	3
70	Two new PML Breakpoints in t(15;17)(q22;q21)-positive acute promyelocytic leukemia. , 2000, 27, 35.		3
71	Identification of the novel <i>HLA-A*23:01:01:27</i> allele in an acute myeloid patient and related donor. <i>Hla</i> , 2022, 100, 62-64.	0.4	3
72	Exportin1 E571K mutation is a common finding in patients with classical Hodgkin lymphoma. <i>Hematological Oncology</i> , 2019, 37, 215-218.	0.8	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.	1.2	1
74	Management of mixed acute rejection driven by a <i>de novo</i> 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.	1.2	0