

Marcos Gonzalez DÃ-az

List of Publications by Year in descending order

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Version: 2024-02-01

230
papers

20,570
citations

20817

60
h-index

11052

137
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all docs

233
docs citations

233
times ranked

22082
citing authors

#	ARTICLE	IF	CITATIONS
1	Design and standardization of PCR primers and protocols for detection of clonal immunoglobulin and T-cell receptor gene recombinations in suspect lymphoproliferations: Report of the BIOMED-2 Concerted Action BMH4-CT98-3936. <i>Leukemia</i> , 2003, 17, 2257-2317.	7.2	2,788
2	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	27.8	2,114
3	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	27.8	1,364
4	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.	7.2	1,359
5	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	21.4	893
6	Non-coding recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2015, 526, 519-524.	27.8	749
7	Next Generation Flow for highly sensitive and standardized detection of minimal residual disease in multiple myeloma. <i>Leukemia</i> , 2017, 31, 2094-2103.	7.2	486
8	Risk-adapted treatment of acute promyelocytic leukemia with all-trans-retinoic acid and anthracycline monochemotherapy: a multicenter study by the PETHEMA group. <i>Blood</i> , 2003, 103, 1237-1243.	1.4	395
9	Prognostic value of deep sequencing method for minimal residual disease detection in multiple myeloma. <i>Blood</i> , 2014, 123, 3073-3079.	1.4	380
10	Early immunophenotypical evaluation of minimal residual disease in acute myeloid leukemia identifies different patient risk groups and may contribute to postinduction treatment stratification. <i>Blood</i> , 2001, 98, 1746-1751.	1.4	316
11	Causes and prognostic factors of remission induction failure in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and idarubicin. <i>Blood</i> , 2008, 111, 3395-3402.	1.4	303
12	Differentiation syndrome in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline chemotherapy: characteristics, outcome, and prognostic factors. <i>Blood</i> , 2009, 113, 775-783.	1.4	279
13	Peripheral T-cell lymphomas: Initial features, natural history, and prognostic factors in a series of 174 patients diagnosed according to the R.E.A.L. Classification. <i>Annals of Oncology</i> , 1998, 9, 849-855.	1.2	264
14	Clinical impact of clonal and subclonal TP53, SF3B1, BIRC3, NOTCH1, and ATM mutations in chronic lymphocytic leukemia. <i>Blood</i> , 2016, 127, 2122-2130.	1.4	260
15	MYD88 L265P is a marker highly characteristic of, but not restricted to, Waldenström's macroglobulinemia. <i>Leukemia</i> , 2013, 27, 1722-1728.	7.2	238
16	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.	1.4	213
17	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.	7.2	188
18	Increased frequency (12%) of circulating chronic lymphocytic leukemia-like B-cell clones in healthy subjects using a highly sensitive multicolor flow cytometry approach. <i>Blood</i> , 2009, 114, 33-37.	1.4	183

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19	NOTCH1 mutations identify a genetic subgroup of chronic lymphocytic leukemia patients with high risk of transformation and poor outcome. <i>Leukemia</i> , 2013, 27, 1100-1106.	7.2	167
20	Concurrent intensive chemotherapy and imatinib before and after stem cell transplantation in newly diagnosed Philadelphia chromosome-positive acute lymphoblastic leukemia. Final results of the CSTIBES02 trial. <i>Haematologica</i> , 2010, 95, 87-95.	3.5	164
21	Immunoglobulin gene rearrangements and the pathogenesis of multiple myeloma. <i>Blood</i> , 2007, 110, 3112-3121.	1.4	157
22	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.	7.2	155
23	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.	1.4	154
24	Minimal residual disease monitoring in multiple myeloma: a comparison between allelic-specific oligonucleotide real-time quantitative polymerase chain reaction and flow cytometry. <i>Haematologica</i> , 2005, 90, 1365-72.	3.5	135
25	A B-cell epigenetic signature defines three biologic subgroups of chronic lymphocytic leukemia with clinical impact. <i>Leukemia</i> , 2015, 29, 598-605.	7.2	129
26	Treatment With All-trans Retinoic Acid and Anthracycline Monochemotherapy for Children With Acute Promyelocytic Leukemia: A Multicenter Study by the PETHEMA Group. <i>Journal of Clinical Oncology</i> , 2005, 23, 7632-7640.	1.6	126
27	Outcome of patients with acute promyelocytic leukemia failing to front-line treatment with all-trans retinoic acid and anthracycline-based chemotherapy (PETHEMA protocols LPA96 and LPA99): benefit of an early intervention. <i>Leukemia</i> , 2007, 21, 446-452.	7.2	124
28	Molecular heterogeneity in MCL defined by the use of specific VH genes and the frequency of somatic mutations. <i>Blood</i> , 2003, 101, 4042-4046.	1.4	121
29	Fludarabine, Cyclophosphamide, and Mitoxantrone as Initial Therapy of Chronic Lymphocytic Leukemia: High Response Rate and Disease Eradication. <i>Clinical Cancer Research</i> , 2008, 14, 155-161.	7.0	117
30	Rituximab, Fludarabine, Cyclophosphamide, and Mitoxantrone: A New, Highly Active Chemoimmunotherapy Regimen for Chronic Lymphocytic Leukemia. <i>Journal of Clinical Oncology</i> , 2009, 27, 4578-4584.	1.6	116
31	Clinical significance of CD56 expression in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline-based regimens. <i>Blood</i> , 2011, 117, 1799-1805.	1.4	112
32	Surface marker analysis in acute myeloid leukaemia and correlation with FAB classification. <i>British Journal of Haematology</i> , 1986, 64, 547-560.	2.5	108
33	TCR β ⁺ /CD4 ⁺ Large Granular Lymphocytosis. <i>American Journal of Pathology</i> , 2003, 163, 763-771.	3.8	104
34	Antithrombin Cambridge II (A384S): an underestimated genetic risk factor for venous thrombosis. <i>Blood</i> , 2007, 109, 4258-4263.	1.4	104
35	Chimerism and minimal residual disease monitoring after reduced intensity conditioning (RIC) allogeneic transplantation. <i>Leukemia</i> , 2002, 16, 1423-1431.	7.2	103
36	Incidence and clinicobiologic characteristics of leukemic B-cell chronic lymphoproliferative disorders with more than one B-cell clone. <i>Blood</i> , 2003, 102, 2994-3002.	1.4	101

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37	SNP-based mapping arrays reveal high genomic complexity in monoclonal gammopathies, from MGUS to myeloma status. <i>Leukemia</i> , 2012, 26, 2521-2529.	7.2	100
38	Mutations in TLR/MYD88 pathway identify a subset of young chronic lymphocytic leukemia patients with favorable outcome. <i>Blood</i> , 2014, 123, 3790-3796.	1.4	97
39	Adult precursor B-ALL with BCR/ABL gene rearrangements displays a unique immunophenotype based on the pattern of CD10, CD34, CD13 and CD38 expression. <i>Leukemia</i> , 2001, 15, 406-414.	7.2	94
40	Central nervous system involvement at first relapse in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and anthracycline monochemotherapy without intrathecal prophylaxis. <i>Haematologica</i> , 2009, 94, 1242-1249.	3.5	93
41	TCR β ⁺ large granular lymphocyte leukemias reflect the spectrum of normal antigen-selected TCR β ⁺ T-cells. <i>Leukemia</i> , 2006, 20, 505-513.	7.2	86
42	Gene expression profile reveals deregulation of genes with relevant functions in the different subclasses of acute myeloid leukemia. <i>Leukemia</i> , 2005, 19, 402-409.	7.2	85
43	Additional chromosome abnormalities in patients with acute promyelocytic leukemia treated with all-trans retinoic acid and chemotherapy. <i>Haematologica</i> , 2010, 95, 424-431.	3.5	84
44	Impaired expression of DICER, DROSHA, SBDS and some microRNAs in mesenchymal stromal cells from myelodysplastic syndrome patients. <i>Haematologica</i> , 2012, 97, 1218-1224.	3.5	83
45	The EuroChimerism concept for a standardized approach to chimerism analysis after allogeneic stem cell transplantation. <i>Leukemia</i> , 2012, 26, 1821-1828.	7.2	83
46	CTLA-4 polymorphisms and clinical outcome after allogeneic stem cell transplantation from HLA-identical sibling donors. <i>Blood</i> , 2007, 110, 461-467.	1.4	82
47	Chromosome 14q32 translocations involving the immunoglobulin heavy chain locus in chronic lymphocytic leukaemia identify a disease subset with poor prognosis. <i>British Journal of Haematology</i> , 2008, 142, 529-537.	2.5	78
48	Molecular stratification model for prognosis in cytogenetically normal acute myeloid leukemia. <i>Blood</i> , 2009, 114, 148-152.	1.4	78
49	Methylation is an inactivating mechanism of the p16 gene in multiple myeloma associated with high plasma cell proliferation and short survival. <i>British Journal of Haematology</i> , 2002, 118, 1034-1040.	2.5	76
50	Profile of polymorphisms of drug-metabolising enzymes and the risk of therapy-related leukaemia. <i>British Journal of Haematology</i> , 2007, 136, 590-596.	2.5	75
51	Prognostic implications of DNA aneuploidy in 156 untreated multiple myeloma patients. <i>British Journal of Haematology</i> , 1995, 90, 106-112.	2.5	74
52	Characterization of aberrant phenotypes in acute myeloblastic leukemia. <i>Annals of Hematology</i> , 1995, 70, 189-194.	1.8	73
53	Expression of <i>MALT1</i> oncogene in hematopoietic stem/progenitor cells recapitulates the pathogenesis of human lymphoma in mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 10534-10539.	7.1	73
54	Monoclonal TCR β ⁺ 13.1+/CD4+/NKa+/CD8 α ⁺ /dim T-LGL lymphocytosis: evidence for an antigen-driven chronic T-cell stimulation origin. <i>Blood</i> , 2007, 109, 4890-4898.	1.4	72

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55	<scp>CXCR4</scp> expression enhances diffuse large B cell lymphoma dissemination and decreases patient survival. <i>Journal of Pathology</i> , 2015, 235, 445-455.	4.5	71
56	Microvesicles from Mesenchymal Stromal Cells Are Involved in HPC-Microenvironment Crosstalk in Myelodysplastic Patients. <i>PLoS ONE</i> , 2016, 11, e0146722.	2.5	70
57	Analysis of natural killer-associated antigens in peripheral blood and bone marrow of multiple myeloma patients and prognostic implications. <i>British Journal of Haematology</i> , 1996, 93, 81-88.	2.5	69
58	A new method for the analysis of plasma cell DNA content in multiple myeloma samples using a CD38/propidium iodide double staining technique. <i>Cytometry</i> , 1994, 17, 332-339.	1.8	68
59	Blood monitoring of circulating tumor plasma cells by next generation flow in multiple myeloma after therapy. <i>Blood</i> , 2019, 134, 2218-2222.	1.4	66
60	Lymphoid subsets and prognostic factors in multiple myeloma. <i>British Journal of Haematology</i> , 1992, 80, 305-309.	2.5	64
61	Chronic lymphocytic leukemia: a clinical and molecular heterogenous disease. <i>Cancer Genetics</i> , 2013, 206, 49-62.	0.4	63
62	Disparity for the minor histocompatibility antigen HA-1 is associated with an increased risk of acute graft-versus-host disease (GvHD) but it does not affect chronic GvHD incidence, disease-free survival or overall survival after allogeneic human leucocyt. <i>British Journal of Haematology</i> , 2001, 114, 931-936.	2.5	60
63	Comparison of next-generation sequencing (NGS) and next-generation flow (NGF) for minimal residual disease (MRD) assessment in multiple myeloma. <i>Blood Cancer Journal</i> , 2020, 10, 108.	6.2	60
64	A high number of losses in 13q14 chromosome band is associated with a worse outcome and biological differences in patients with B-cell chronic lymphoid leukemia. <i>Haematologica</i> , 2009, 94, 364-371.	3.5	59
65	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.	3.5	59
66	Molecular characterization of heavy chain immunoglobulin gene rearrangements in Waldenstrom's macroglobulinemia and IgM monoclonal gammopathy of undetermined significance. <i>Haematologica</i> , 2007, 92, 635-642.	3.5	57
67	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.	7.2	55
68	Rituximab maintenance after first-line therapy with rituximab, fludarabine, cyclophosphamide, and mitoxantrone (R-FCM) for chronic lymphocytic leukemia. <i>Blood</i> , 2013, 122, 3951-3959.	1.4	55
69	3Immunophenotype and DNA cell content in multiple myeloma. <i>Best Practice and Research: Clinical Haematology</i> , 1995, 8, 735-759.	1.1	54
70	Pamidronate induces bone formation in patients with smouldering or indolent myeloma, with no significant anti-tumour effect. <i>British Journal of Haematology</i> , 2002, 118, 239-242.	2.5	54
71	Expanded cells in monoclonal TCR- $\hat{1}\hat{2}^+$ /CD4+/NKa+/CD8 \hat{a}^+ /+dim T-LGL lymphocytosis recognize hCMV antigens. <i>Blood</i> , 2008, 112, 4609-4616.	1.4	54
72	Early intervention during imatinib therapy in patients with newly diagnosed chronic-phase chronic myeloid leukemia: a study of the Spanish PETHEMA group. <i>Haematologica</i> , 2010, 95, 1317-1324.	3.5	53

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73	Pretreatment characteristics and clinical outcome of acute promyelocytic leukaemia patients according to the <i>PML-RARα</i> isoforms: a study of the PETHEMA group. <i>British Journal of Haematology</i> , 2001, 114, 99-103.	2.5	52
74	Immunological phenotype of neoplasms involving the B cell in the last step of differentiation. <i>British Journal of Haematology</i> , 1986, 62, 75-83.	2.5	51
75	Prognostic factors and classification in multiple myeloma. <i>British Journal of Cancer</i> , 1989, 59, 113-118.	6.4	50
76	Differences in genetic changes between multiple myeloma and plasma cell leukemia demonstrated by comparative genomic hybridization. <i>Leukemia</i> , 2001, 15, 840-845.	7.2	50
77	High FOXO3a expression is associated with a poorer prognosis in AML with normal cytogenetics. <i>Leukemia Research</i> , 2009, 33, 1706-1709.	0.8	49
78	Long FLT3 internal tandem duplications and reduced PML-RAR α expression at diagnosis characterize a high-risk subgroup of acute promyelocytic leukemia patients. <i>Haematologica</i> , 2010, 95, 745-751.	3.5	47
79	Serum lactate dehydrogenase level as a prognostic factor in Hodgkin's disease. <i>British Journal of Cancer</i> , 1993, 68, 1227-1231.	6.4	45
80	Role of MTHFR (677, 1298) haplotype in the risk of developing secondary leukemia after treatment of breast cancer and hematological malignancies. <i>Leukemia</i> , 2007, 21, 1413-1422.	7.2	45
81	Design and application of a 23-gene panel by next-generation sequencing for inherited coagulation bleeding disorders. <i>Haemophilia</i> , 2016, 22, 590-597.	2.1	43
82	Homeobox NKX2-3 promotes marginal-zone lymphomagenesis by activating B-cell receptor signalling and shaping lymphocyte dynamics. <i>Nature Communications</i> , 2016, 7, 11889.	12.8	42
83	Cellular and humoral immunogenicity of the mRNA-1273 SARS-CoV-2 vaccine in patients with hematologic malignancies. <i>Blood Advances</i> , 2022, 6, 774-784.	5.2	42
84	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.	3.5	41
85	Differential stability of control gene and fusion gene transcripts over time may hamper accurate quantification of minimal residual disease – a study within the Europe Against Cancer Program. <i>Leukemia</i> , 2004, 18, 884-886.	7.2	40
86	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.	1.8	40
87	Mutations in the RAS-BRAF-MAPK-ERK pathway define a specific subgroup of patients with adverse clinical features and provide new therapeutic options in chronic lymphocytic leukemia. <i>Haematologica</i> , 2019, 104, 576-586.	3.5	40
88	Siglec-6 is a novel target for CAR T-cell therapy in acute myeloid leukemia. <i>Blood</i> , 2021, 138, 1830-1842.	1.4	40
89	Chronic lymphocytic leukaemia with 17p deletion: a retrospective analysis of prognostic factors and therapy results. <i>British Journal of Haematology</i> , 2012, 157, 67-74.	2.5	39
90	Incomplete DJH rearrangements of the IgH gene are frequent in multiple myeloma patients: immunobiological characteristics and clinical implications. <i>Leukemia</i> , 2003, 17, 1398-1403.	7.2	38

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91	Next-generation sequencing and FISH studies reveal the appearance of gene mutations and chromosomal abnormalities in hematopoietic progenitors in chronic lymphocytic leukemia. <i>Journal of Hematology and Oncology</i> , 2017, 10, 83.	17.0	38
92	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.	1.4	37
93	Molecular Characterization of Chronic Lymphocytic Leukemia Patients with a High Number of Losses in 13q14. <i>PLoS ONE</i> , 2012, 7, e48485.	2.5	37
94	Application of a molecular diagnostic algorithm for haemophilia A and B using next-generation sequencing of entire F8, F9 and VWF genes. <i>Thrombosis and Haemostasis</i> , 2017, 117, 66-74.	3.4	36
95	Lymphoid subsets in acute myeloid leukemias: Increased number of cells with NK phenotype and normal T-cell distribution. <i>Annals of Hematology</i> , 1993, 67, 217-222.	1.8	35
96	Low-count monoclonal B-cell lymphocytosis persists after seven years of follow up and is associated with a poorer outcome. <i>Haematologica</i> , 2018, 103, 1198-1208.	3.5	34
97	Immunophenotypic, genomic and clinical characteristics of blast crisis of chronic myelogenous leukaemia. <i>British Journal of Haematology</i> , 1991, 79, 408-414.	2.5	33
98	Does microgranular variant morphology of acute promyelocytic leukemia independently predict a less favorable outcome compared with classical M3 APL? A joint study of the North American Intergroup and the PETHEMA Group. <i>Blood</i> , 2010, 116, 5650-5659.	1.4	33
99	Genomic complexity and IGHV mutational status are key predictors of outcome of chronic lymphocytic leukemia patients with TP53 disruption. <i>Haematologica</i> , 2014, 99, e231-e234.	3.5	33
100	Common Infectious Agents and Monoclonal B-Cell Lymphocytosis: A Cross-Sectional Epidemiological Study among Healthy Adults. <i>PLoS ONE</i> , 2012, 7, e52808.	2.5	32
101	Array comparative genomic hybridization identifies genetic regions associated with outcome in aggressive diffuse large B-cell lymphomas. <i>Cancer</i> , 2009, 115, 3728-3737.	4.1	31
102	Molecular Characterization of Immunoglobulin Gene Rearrangements in Diffuse Large B-Cell Lymphoma. <i>American Journal of Pathology</i> , 2012, 181, 1879-1888.	3.8	31
103	Impact of measurable residual disease by decentralized flow cytometry: a PETHEMA real-world study in 1076 patients with acute myeloid leukemia. <i>Leukemia</i> , 2021, 35, 2358-2370.	7.2	31
104	p16/INK4a gene inactivation by hypermethylation is associated with aggressive variants of monoclonal gammopathies. <i>The Hematology Journal</i> , 2001, 2, 146-149.	1.4	30
105	Characterization of a reference material for BCR-ABL (M-BCR) mRNA quantitation by real-time amplification assays: towards new standards for gene expression measurements. <i>Leukemia</i> , 2007, 21, 1481-1487.	7.2	29
106	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.	2.5	29
107	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.	3.5	29
108	Karyotypic complexity rather than chromosome 8 abnormalities aggravates the outcome of chronic lymphocytic leukemia patients with TP53 aberrations. <i>Oncotarget</i> , 2016, 7, 80916-80924.	1.8	29

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109	Minimal residual disease evaluation by flow cytometry is a complementary tool to cytogenetics for treatment decisions in acute myeloid leukaemia. <i>Leukemia Research</i> , 2016, 40, 1-9.	0.8	29
110	B-cell chronic lymphocytic leukaemia: Prognostic value of the immunophenotype and the clinico-haematological features. <i>American Journal of Hematology</i> , 1989, 31, 26-31.	4.1	28
111	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.	1.2	28
112	The number of tumor infiltrating T-cell subsets in lymph nodes from patients with Hodgkin lymphoma is associated with the outcome after first line ABVD therapy. <i>Leukemia and Lymphoma</i> , 2017, 58, 1144-1152.	1.3	28
113	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.	7.2	27
114	Combined Patterns of IGHV Repertoire and Cytogenetic/Molecular Alterations in Monoclonal B Lymphocytosis versus Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2013, 8, e67751.	2.5	27
115	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.	3.5	27
116	A high proportion of cells carrying trisomy 12 is associated with a worse outcome in patients with chronic lymphocytic leukemia. <i>Hematological Oncology</i> , 2016, 34, 84-92.	1.7	26
117	Life expectancy of follicular lymphoma patients in complete response at 30 months is similar to that of the Spanish general population. <i>British Journal of Haematology</i> , 2019, 185, 480-491.	2.5	26
118	Impact of BCR/ABL gene expression on the proliferative rate of different subpopulations of haematopoietic cells in chronic myeloid leukaemia. <i>British Journal of Haematology</i> , 2006, 135, 43-51.	2.5	25
119	A novel predictive approach for GVHD after allogeneic SCT based on clinical variables and cytokine gene polymorphisms. <i>Blood Advances</i> , 2018, 2, 1719-1737.	5.2	25
120	T-cell subpopulations in patients with monoclonal gammopathies: Essential monoclonal gammopathy, multiple myeloma, and Waldenstrom macroglobulinemia. <i>American Journal of Hematology</i> , 1985, 20, 267-273.	4.1	24
121	Gene rearrangement in acute non-lymphoblastic leukaemia: correlation with morphological and immunophenotypic characteristics of blast cells. <i>British Journal of Haematology</i> , 1995, 89, 104-109.	2.5	24
122	Clinical, biological, and immunophenotypical characteristics of B-cell chronic lymphocytic leukemia with trisomy 12 by fluorescence in situ hybridization. <i>Cytometry</i> , 1995, 22, 217-222.	1.8	24
123	Methylenetetrahydrofolate reductase genotype does not play a role in multiple myeloma pathogenesis. <i>British Journal of Haematology</i> , 2002, 117, 890-892.	2.5	24
124	A Low Frequency of Losses in 11q Chromosome Is Associated with Better Outcome and Lower Rate of Genomic Mutations in Patients with Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2015, 10, e0143073.	2.5	24
125	Richter transformation driven by Epstein-Barr virus reactivation during therapy-related immunosuppression in chronic lymphocytic leukaemia. <i>Journal of Pathology</i> , 2018, 245, 61-73.	4.5	24
126	Biological and clinical significance of dysplastic hematopoiesis in patients with newly diagnosed multiple myeloma. <i>Blood</i> , 2020, 135, 2375-2387.	1.4	24

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127	HLA-DPB1 MISMATCH IN HLA-A-B-DRB1 IDENTICAL SIBLING DONOR STEM CELL TRANSPLANTATION AND ACUTE GRAFT-VERSUS-HOST DISEASE. <i>Transplantation</i> , 2004, 77, 1107-1110.	1.0	23
128	HLA specificities are related to development and prognosis of diffuse large B-cell lymphoma. <i>Blood</i> , 2013, 122, 1448-1454.	1.4	23
129	Circulating clonotypic B cells in multiple myeloma and monoclonal gammopathy of undetermined significance. <i>Haematologica</i> , 2014, 99, 155-162.	3.5	23
130	Detection of chromothripsis-like patterns with a custom array platform for chronic lymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2015, 54, 668-680.	2.8	23
131	Long-term treatment results for acute megakaryoblastic leukaemia patients: a multicentre study. <i>British Journal of Haematology</i> , 1992, 82, 671-675.	2.5	22
132	Association between the proliferative rate of neoplastic B cells, their maturation stage, and underlying cytogenetic abnormalities in B-cell chronic lymphoproliferative disorders: analysis of a series of 432 patients. <i>Blood</i> , 2008, 111, 5130-5141.	1.4	22
133	Clinical practice guidelines for diagnosis, treatment, and follow-up of patients with mantle cell lymphoma. Recommendations from the GEL/TAMO Spanish Cooperative Group. <i>Annals of Hematology</i> , 2013, 92, 1151-1179.	1.8	22
134	Molecular and cytogenetic characterization of expanded B-cell clones from multiclonal versus monoclonal B-cell chronic lymphoproliferative disorders. <i>Haematologica</i> , 2014, 99, 897-907.	3.5	22
135	Mapping of Genetic Abnormalities of Primary Tumours from Metastatic CRC by High-Resolution SNP Arrays. <i>PLoS ONE</i> , 2010, 5, e13752.	2.5	22
136	Combination of interferon and dexamethasone in refractory multiple myeloma. <i>Hematological Oncology</i> , 1990, 8, 185-189.	1.7	20
137	Immunoglobulin lambda isotype gene rearrangements in B cell malignancies. <i>Leukemia</i> , 2001, 15, 121-127.	7.2	20
138	Hairy cell leukemia treated initially with purine analogs: a retrospective study of 107 patients from the Spanish Cooperative Group on Chronic Lymphocytic Leukemia (GELLC). <i>Leukemia and Lymphoma</i> , 2014, 55, 1007-1012.	1.3	20
139	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. <i>Haematologica</i> , 2015, 100, e183-e185.	3.5	20
140	Molecular characteristics and gene segment usage in IGH gene rearrangements in multiple myeloma. <i>Haematologica</i> , 2005, 90, 906-13.	3.5	20
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