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List of Publications by Year in descending order

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Version: 2024-02-01

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	Identification of the novel <i>HLA*23:01:01:27</i> allele in an acute myeloid patient and related donor. <i>Hla</i> , 2022, 100, 62-64.	0.6	3
2	MYD88 Mutations: Transforming the Landscape of IgM Monoclonal Gammopathies. <i>International Journal of Molecular Sciences</i> , 2022, 23, 5570.	4.1	14
3	Genetic complexity impacts the clinical outcome of follicular lymphoma patients. <i>Blood Cancer Journal</i> , 2021, 11, 11.	6.2	3
4	The novel <i>HLA-DQB1*06:03:27</i> allele characterised by sequence-based typing in a European bone marrow donor. <i>Hla</i> , 2021, 98, 498-500.	0.6	3
5	Liquid biopsy: a non-invasive approach for Hodgkin lymphoma genotyping. <i>British Journal of Haematology</i> , 2021, 195, 542-551.	2.5	14
6	Allele and haplotype frequencies of HLA-A, -B, -C, -DRB1, -DQB1 and -DQA1 in Castile and Leon region from North West of Spain. <i>Human Immunology</i> , 2021, 82, 549-550.	2.4	1
7	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. <i>British Journal of Biomedical Science</i> , 2021, 78, 244-247.	1.3	0
8	Networking for advanced molecular diagnosis in acute myeloid leukemia patients is possible: the PETHEMA NGS-AML project. <i>Haematologica</i> , 2021, 106, 3079-3089.	3.5	15
9	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.	2.8	11
10	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.	2.5	12
11	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.	6.2	16
12	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.	6.2	11
13	Clinical significance of complex karyotype at diagnosis in pediatric and adult patients with <i>de novo</i> acute promyelocytic leukemia treated with ATRA and chemotherapy. <i>Leukemia and Lymphoma</i> , 2019, 60, 1146-1155.	1.3	12
14	Exportin1 E571K mutation is a common finding in patients with classical Hodgkin lymphoma. <i>Hematological Oncology</i> , 2019, 37, 215-218.	1.7	2
15	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.	1.3	9
16	Unraveling the heterogeneity of IgM monoclonal gammopathies: a gene mutational and gene expression study. <i>Annals of Hematology</i> , 2018, 97, 475-484.	1.8	19
17	Basophil-lineage commitment in acute promyelocytic leukemia predicts for severe bleeding after starting therapy. <i>Modern Pathology</i> , 2018, 31, 1318-1331.	5.5	9
18	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.	2.5	4

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19	Focal Adhesion Genes Refine the Intermediate-Risk Cytogenetic Classification of Acute Myeloid Leukemia. <i>Cancers</i> , 2018, 10, 436.	3.7	8
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.	6.2	31
21	Quantitative PCR: an alternative approach to detect common copy number alterations in multiple myeloma. <i>Annals of Hematology</i> , 2017, 96, 1699-1705.	1.8	5
22	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.	2.8	22
23	The cryptic IRF2BP2-RARA fusion transforms hematopoietic stem/progenitor cells and induces retinoid-sensitive acute promyelocytic leukemia. <i>Leukemia</i> , 2017, 31, 747-751.	7.2	24
24	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.	1.7	22
25	HLA specificities are associated with prognosis in IGHV-mutated CLL-like high-count monoclonal B cell lymphocytosis. <i>PLoS ONE</i> , 2017, 12, e0172978.	2.5	4
26	<i>NEDD9</i> , an independent good prognostic factor in intermediate-risk acute myeloid leukemia patients. <i>Oncotarget</i> , 2017, 8, 76003-76014.	1.8	5
27	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.	1.8	19
28	Reprogramming human B cells into induced pluripotent stem cells and its enhancement by C/EBP β . <i>Leukemia</i> , 2016, 30, 674-682.	7.2	36
29	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
30	CIP2A high expression is a poor prognostic factor in normal karyotype acute myeloid leukemia. <i>Haematologica</i> , 2015, 100, e183-e185.	3.5	20
31	Do endothelial cells belong to the primitive stem leukemic clone in CML? Role of extracellular vesicles. <i>Leukemia Research</i> , 2015, 39, 921-924.	0.8	12
32	The predominant myeloma clone at diagnosis, CDR3 defined, is constantly detectable across all stages of disease evolution. <i>Leukemia</i> , 2015, 29, 1435-1437.	7.2	17
33	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
34	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
35	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.	4.1	8
36	Ligand-independent FLT3 activation does not cooperate with MLL-AF4 to immortalize/transform cord blood CD34+ cells. <i>Leukemia</i> , 2014, 28, 666-674.	7.2	27

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37	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.	1.8	18
38	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
39	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.	2.5	7
40	HLA specificities are related to development and prognosis of diffuse large B-cell lymphoma. <i>Blood</i> , 2013, 122, 1448-1454.	1.4	23
41	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.	2.2	15
42	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.	1.8	12
43	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.	7.2	27
44	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
45	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
46	Risk of placenta-mediated pregnancy complications or pregnancy-related VTE in asymptomatic families of probands with VTE and heterozygosity for factor V Leiden or G20210 prothrombin mutation. <i>European Journal of Haematology</i> , 2012, 89, 250-255.	2.2	5
47	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
48	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
49	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
50	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
51	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
52	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
53	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
54	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

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55	Molecular stratification model for prognosis in cytogenetically normal acute myeloid leukemia. <i>Blood</i> , 2009, 114, 148-152.	1.4	78
56	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
57	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
58	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
59	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
60	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
61	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.	1.0	4
62	Using quantification of the PML-RAR α transcript to stratify the risk of relapse in patients with acute promyelocytic leukemia. <i>Haematologica</i> , 2007, 92, 315-322.	3.5	77
63	Molecular characteristics and gene segment usage in IGH gene rearrangements in multiple myeloma. <i>Haematologica</i> , 2005, 90, 906-13.	3.5	20
64	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
65	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
66	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.	7.2	56
67	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
68	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.	2.4	14
69	Two new 3'PML Breakpoints in t(15;17)(q22;q21)-positive acute promyelocytic leukemia. , 2000, 27, 35-43.		19
70	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.	7.2	56
71	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.	7.2	18
72	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.	1.9	5

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73	Two new 3' PML Breakpoints in t(15;17)(q22;q21)-positive acute promyelocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2000, 27, 35-43.	2.8	3
74	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.	7.2	27