Margarita Sanchez-Beato

List of Publications by Year
in descending order

104 papers	4,372 citations	81900 39 h-index	114465 63 g-index
104 all docs	104 docs citations	104 times ranked	5585 citing authors

#	Article	IF	Citations
1	Cell cycle deregulation in B-cell lymphomas. Blood, 2003, 101, 1220-1235.	1.4	329
2	PLCG1 mutations in cutaneous T-cell lymphomas. Blood, 2014, 123, 2034-2043.	1.4	193
3	p53 and bcl-2 expression in high-grade B-cell lymphomas: correlation with survival time. British Journal of Cancer, 1994, 69, 337-341.	6.4	173
4	Structural profiles of TP53 gene mutations predict clinical outcome in diffuse large B-cell lymphoma: an international collaborative study. Blood, 2008, 112, 3088-3098.	1.4	173
5	Analysis of the IgVH somatic mutations in splenic marginal zone lymphoma defines a group of unmutated cases with frequent 7q deletion and adverse clinical course. Blood, 2002, 99, 1299-1304.	1.4	158
6	7q31-32 Allelic Loss Is a Frequent Finding in Splenic Marginal Zone Lymphoma. American Journal of Pathology, 1999, 154, 1583-1589.	3.8	154
7	Progression to Large B-Cell Lymphoma in Splenic Marginal Zone Lymphoma. American Journal of Surgical Pathology, 2001, 25, 1268-1276.	3.7	126
8	Cancer induction by restriction of oncogene expression to the stem cell compartment. EMBO Journal, 2009, 28, 8-20.	7.8	125
9	Molecular heterogeneity in MCL defined by the use of specific VH genes and the frequency of somatic mutations. Blood, 2003, 101, 4042-4046.	1.4	121
10	Loss of p16/INK4A Protein Expression in Non-Hodgkin's Lymphomas Is a Frequent Finding Associated with Tumor Progression. American Journal of Pathology, 1998, 153, 887-897.	3.8	111
11	Nodal Marginal Zone Lymphoma: A Heterogeneous Tumor. American Journal of Surgical Pathology, 2003, 27, 762-771.	3.7	106
12	Nodal marginal zone lymphoma: gene expression and miRNA profiling identify diagnostic markers and potential therapeutic targets. Blood, 2012, 119, e9-e21.	1.4	91
13	Variability in the expression of polycomb proteins in different normal and tumoral tissues. A pilot study using tissue microarrays. Modern Pathology, 2006, 19, 684-694.	5.5	83
14	PIM2 inhibition as a rational therapeutic approach in B-cell lymphoma. Blood, 2011, 118, 5517-5527.	1.4	83
15	MicroRNA signatures in B-cell lymphomas. Blood Cancer Journal, 2012, 2, e57-e57.	6.2	79
16	Mantle cell lymphoma: transcriptional regulation by microRNAs. Leukemia, 2010, 24, 1335-1342.	7.2	72
17	Splenic small B-cell lymphoma with predominant red pulp involvement: a diffuse variant of splenic marginal zone lymphoma?. Histopathology, 2002, 40, 22-30.	2.9	70
18	Overall Survival in Aggressive B-Cell Lymphomas Is Dependent on the Accumulation of Alterations in p53, p16, and p27. American Journal of Pathology, 2001, 159, 205-213.	3.8	68

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19	The role of miRNAs in the pathogenesis and diagnosis of B-cell lymphomas. Blood, 2012, 120, 1782-1790.	1.4	68
20	SUZ12 Promotes Human Epithelial Ovarian Cancer by Suppressing Apoptosis via Silencing HRK. Molecular Cancer Research, 2012, 10, 1462-1472.	3.4	66
21	Abnormal PcG protein expression in Hodgkin's lymphoma. Relation with E2F6 and NFÎºB transcription factors. Journal of Pathology, 2004, 204, 528-537.	4.5	63
22	Analysis of Octamer-Binding Transcription Factors Oct2 and Oct1 and their coactivator BOB.1/OBF.1 in Lymphomas. Modern Pathology, 2002, 15, 211-220.	5.5	62
23	Silencing of the p18INK4c gene by promoter hypermethylation in Reed-Sternberg cells in Hodgkin lymphomas. Blood, 2004, 103, 2351-2357.	1.4	60
24	Mutated JAK kinases and deregulated STAT activity are potential therapeutic targets in cutaneous T-cell lymphoma. Haematologica, 2015, 100, e450-e453.	3.5	59
25	Oxidative Phosphorylation Induces De Novo Expression of the MHC Class I in Tumor Cells through the ERK5 Pathway. Journal of Immunology, 2010, 185, 3498-3503.	0.8	58
26	Polycomb proteins in hematologic malignancies. Blood, 2010, 116, 5465-5475.	1.4	56
27	p21WAF1/CIP1 AND MDM2 EXPRESSION IN NON-HODGKIN'S LYMPHOMA AND THEIR RELATIONSHIP TO p53 STATUS: A p53+, MDM2â^', p21â^' IMMUNOPHENOTYPE ASSOCIATED WITH MISSENSE p53 MUTATIONS. , 1997, 181, 51-61.		55
28	p14ARF nuclear overexpression in aggressive B-cell lymphomas is a sensor of malfunction of the common tumor suppressor pathways. Blood, 2002, 99, 1411-1418.	1.4	53
29	The RHOA G17V gene mutation occurs frequently in peripheral T-cell lymphoma and is associated with a characteristic molecular signature. Blood, 2014, 123, 2893-2894.	1.4	53
30	NIK Controls Classical and Alternative NF-ÎºB Activation and Is Necessary for the Survival of Human T-cell Lymphoma Cells. Clinical Cancer Research, 2013, 19, 2319-2330.	7.0	52
31	B-cell lymphoma mutations: improving diagnostics and enabling targeted therapies. Haematologica, 2014, 99, 222-231.	3.5	52
32	Retinoblastoma (rb) gene product expression in lymphomas. Correlation with Ki67 growth fraction. Journal of Pathology, 1993, 169, 405-412.	4.5	51
33	Transcriptional signature of Ecteinascidin 743 (Yondelis, Trabectedin) in human sarcoma cells explanted from chemo-naÃ¯ve patients. Molecular Cancer Therapeutics, 2005, 4, 814-823.	4.1	50
34	Epstein-Barr virus microRNAs repress BCL6 expression in diffuse large B-cell lymphoma. Leukemia, 2012, 26, 180-183.	7.2	50
35	A Short Mutational Hot Spot in the First Intron of BCL-6 Is Associated with Increased BCL-6 Expression and with Longer Overall Survival in Large B-Cell Lymphomas. American Journal of Pathology, 2002, 160, 1371-1380.	3.8	47
36	TCL1A expression delineates biological and clinical variability in B-cell lymphoma. Modern Pathology, 2009, 22, 206-215.	5.5	46

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37	Splenic marginal zone lymphoma: comprehensive analysis of gene expression and miRNA profiling. Modern Pathology, 2013, 26, 889-901.	5.5	45
38	Action and resistance of monoclonal CD20 antibodies therapy in B-cell Non-Hodgkin Lymphomas. Cancer Treatment Reviews, 2015, 41, 680-689.	7.7	43
39	Deregulated Expression of the Polycomb-Group Protein SUZ12 Target Genes Characterizes Mantle Cell Lymphoma. American Journal of Pathology, 2010, 177, 930-942.	3.8	41
40	p27KIP1 is abnormally expressed in Diffuse Large B-Cell Lymphomas and is associated with an adverse clinical outcome. British Journal of Cancer, 1999, 80, 1427-1434.	6.4	40
41	Epstein-Barr Virus-Latent Membrane Protein 1 Expression Has a Favorable Influence in the Outcome of Patients with Hodgkin's Disease Treated with Chemotherapy. Leukemia and Lymphoma, 2000, 39, 563-572.	1.3	39
42	Extreme sensitivity to YondelisÂ® (Trabectedin, ET-743) in low passaged sarcoma cell lines correlates with mutated p53. Journal of Cellular Biochemistry, 2007, 100, 339-348.	2.6	39
43	New Mutations in Chronic Lymphocytic Leukemia Identified by Target Enrichment and Deep Sequencing. PLoS ONE, 2012, 7, e38158.	2.5	38
44	Recurrent presence of the PLCG1 S345F mutation in nodal peripheral T-cell lymphomas. Haematologica, 2015, 100, e25-e27.	3.5	37
45	Mouse cDNA microarray analysis uncovers Slug targets in mouse embryonic fibroblasts. Genomics, 2006, 87, 113-118.	2.9	34
46	Proliferation centers in chronic lymphocytic leukemia: the niche where NF-ÎºB activation takes place. Leukemia, 2010, 24, 872-876.	7.2	34
47	Simultaneous inhibition of pan-phosphatidylinositol-3-kinases and MEK as a potential therapeutic strategy in peripheral T-cell lymphomas. Haematologica, 2013, 98, 57-64.	3.5	33
48	Analysis of the mutational landscape of classic Hodgkin lymphoma identifies disease heterogeneity and potential therapeutic targets. Oncotarget, 2017, 8, 111386-111395.	1.8	33
49	Unraveling transformation of follicular lymphoma to diffuse large B-cell lymphoma. PLoS ONE, 2019, 14, e0212813.	2.5	31
50	Overlap at the molecular and immunohistochemical levels between angioimmunoblastic T-cell lymphoma and a subgroup of peripheral T-cell lymphomas without specific morphological features. Oncotarget, 2018, 9, 16124-16133.	1.8	30
51	Molecular heterogeneity of splenic marginal zone lymphomas: analysis of mutations in the 5â€² non-coding region of the bcl-6 gene. Leukemia, 2001, 15, 628-634.	7.2	29
52	Unique Phenotypic Profile of Monocytoid B Cells. American Journal of Pathology, 2001, 158, 1363-1369.	3.8	27
53	NFÎºB expression is a feature of both activated B-cell-like and germinal center B-cell-like subtypes of diffuse large B-cell lymphoma. Modern Pathology, 2014, 27, 1331-1337.	5.5	27
54	Circulating myeloid-derived suppressor cells and regulatory T cells as immunological biomarkers in refractory/relapsed diffuse large B-cell lymphoma: translational results from the R2-GDP-GOTEL trial. , 2021, 9, e002323.		26

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55	Proposal and validation of a method to classify genetic subtypes of diffuse large B cell lymphoma. Scientific Reports, 2021, 11, 1886.	3.3	25
56	Peripheral T-cell lymphoma: molecular profiling recognizes subclasses and identifies prognostic markers. Blood Advances, 2021, 5, 5588-5598.	5.2	24
57	MDM2 AND p21WAF1/CIP1, WILD-TYPE p53-INDUCED PROTEINS, ARE REGULARLY EXPRESSED BY STERNBERG-REED CELLS IN HODGKIN'S DISEASE. , 1996, 180, 58-64.		23
58	Analysis of the frequency of microsatellite instability and p53 gene mutation in splenic marginal zone and MALT lymphomas. Journal of Clinical Pathology, 1998, 51, 262-267.	1.9	23
59	Genomic analyses of microdissected Hodgkin and Reed-Sternberg cells: mutations in epigenetic regulators and p53 are frequent in refractory classic Hodgkin lymphoma. Blood Cancer Journal, 2019, 9, 34.	6.2	23
60	Mutational profile of primary breast diffuse large B-cell lymphoma. Oncotarget, 2017, 8, 102888-102897.	1.8	22
61	Hodgkin's lymphoma cells express alternatively spliced forms of HDM2 with multiple effects on cell cycle control. Oncogene, 2006, 25, 2565-2574.	5.9	21
62	Chronic lymphocytic leukemia cells in lymph nodes show frequent NOTCH1 activation. Haematologica, 2015, 100, e200-e203.	3.5	21
63	Transcriptomal profiling of the cellular response to DNA damage mediated by Slug (Snai2). British Journal of Cancer, 2008, 98, 480-488.	6.4	18
64	PIM Kinases as Potential Therapeutic Targets in a Subset of Peripheral T Cell Lymphoma Cases. PLoS ONE, 2014, 9, e112148.	2.5	18
65	Expression of p21WAF1/CIP1 in fetal and adult tissues: simultaneous analysis with Ki67 and p53.. Journal of Clinical Pathology, 1997, 50, 645-653.	2.0	17
66	Development of a Real-Time Reverse Transcription Polymerase Chain Reaction Assay for c-myc Expression That Allows the Identification of a Subset of c-myc+ Diffuse Large B-Cell Lymphoma. Laboratory Investigation, 2003, 83, 143-152.	3.7	17
67	Mutations in the <scp>JAK</scp>/<scp>STAT</scp> pathway genes and activation of the pathway, a relevant finding in nodal Peripheral Tâ€cell lymphoma. British Journal of Haematology, 2018, 183, 497-501.	2.5	17
68	Nucleolar p14ARF Overexpression in Reed-Sternberg Cells in Hodgkin's Lymphoma. American Journal of Pathology, 2002, 160, 569-578.	3.8	16
69	Anomalous retinoblastoma protein expression in Sternberg-Reed cells in Hodgkin's disease: a comparative study with p53 and Ki67 expression. British Journal of Cancer, 1996, 74, 1056-1062.	6.4	15
70	An A91V SNP in the Perforin Gene Is Frequently Found in NK/T-Cell Lymphomas. PLoS ONE, 2014, 9, e91521.	2.5	13
71	Concordance between circulating tumor cells and clinical status during follow-up in anaplastic lymphoma kinase (ALK) non-small-cell lung cancer patients. Oncotarget, 2017, 8, 59408-59416.	1.8	12
72	Somatic hypermutation signature in B-cell low-grade lymphomas. Haematologica, 2008, 93, 1186-1194.	3.5	11

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73	Functional signatures identified in B-cell non-Hodgkin lymphoma profiles. Leukemia and Lymphoma, 2009, 50, 1699-1708.	1.3	10
74	HDAC inhibitors induce cell cycle arrest, activate the apoptotic extrinsic pathway and synergize with a novel PIM inhibitor in Hodgkin lymphomaâ€derived cell lines. British Journal of Haematology, 2011, 152, 352-356.	2.5	10
75	New drugs and targeted treatments in Hodgkinâ€™s lymphoma. Cancer Treatment Reviews, 2014, 40, 457-464.	7.7	10
76	Transformed follicular lymphoma in the rituximab era: A report from theSpanishLymphomaOncologyGroup. Hematological Oncology, 2019, 37, 143-150.	1.7	9
77	BiallelicATMalterations detected at diagnosis identify a subset of treatment-naÃ¯ve chronic lymphocytic leukemia patients with reduced overall survival similar to patients with p53 deletion. Leukemia and Lymphoma, 2017, 58, 859-865.	1.3	8
78	Clonal dynamics monitoring during clinical evolution in chronic lymphocytic leukaemia. Scientific Reports, 2019, 9, 975.	3.3	8
79	An Overview on Diffuse Large B-Cell Lymphoma Models: Towards a Functional Genomics Approach. Cancers, 2021, 13, 2893.	3.7	6
80	Does the presence of hepatitis virus B and C influence the evolution of diffuse large B-cell lymphoma?. Leukemia and Lymphoma, 2015, 56, 1686-1690.	1.3	5
81	Activity and safety of topical pimecrolimus in patients with early stage mycosis fungoides (PimTo-MF): a single-arm, multicentre, phase 2 trial. Lancet Haematology,the, 2022, 9, e425-e433.	4.6	5
82	Lenalidomide plus R-GDP (R2-GDP) in Relapsed/Refractory Diffuse Large B-Cell Lymphoma: Final Results of the R2-GDP-GOTEL Trial and Immune Biomarker Subanalysis. Clinical Cancer Research, 2022, 28, 3658-3668.	7.0	5
83	Molecular basis of targeted therapy in T/NK-cell lymphoma/leukemia: A comprehensive genomic and immunohistochemical analysis of a panel of 33 cell lines. PLoS ONE, 2017, 12, e0177524.	2.5	4
84	PD-1 loss and T-cell exhaustion in CTCL tumoral T cells. Blood, 2021, 138, 1201-1203.	1.4	4
85	Two distinct molecular subtypes of chronic lymphocytic leukemia give new insights on the pathogenesis of the disease and identify novel therapeutic targets. Leukemia and Lymphoma, 2016, 57, 134-142.	1.3	3
86	MDM2 AND p21WAF1CIP1, WILDâ€TYPE p53â€INDUCED PROTEINS, ARE REGULARLY EXPRESSED BY STERNBERGâ€“REED CELLS IN HODGKIN'S DISEASE. Journal of Pathology, 1996, 180, 58-64.	4.5	2
87	Branched clonal evolution: nodal follicular lymphoma and primary diffuse large B-cell lymphoma of the central nervous system. Haematologica, 2019, 104, e326-e329.	3.5	1
88	Genomic mutation profile in progressive chronic lymphocytic leukemia patients prior to first-line chemoimmunotherapy with FCR and rituximab maintenance (REM). PLoS ONE, 2021, 16, e0257353.	2.5	1
89	Characterization of Subclonal Changes Along Progression in Multiple Myeloma.. Blood, 2012, 120, 2924-2924.	1.4	1
90	Abstract 51: Activating PLCG1 mutations in cutaneous T-cell lymphomas.. , 2013, , .		1

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91	An integrated prognostic model for diffuse large Bâ€cell lymphoma treated with immunochemotherapy. EJHaem, 2022, 3, 722-733.	1.0	1
92	Sequential Gene Expression Analysis During the Early Alloreactive Phenomena After Allogeneic BMT Identifies Gene Sets and Pathways Differentially Expressed in the Skin and the Blood of BMT Recipients: Implications for the Discovery of Biomarkers of Cutaneous GVHD That Are Relevant to the Target Organ. Biology of Blood and Marrow Transplantation, 2011, 17, S324.	2.0	0
93	NIK and the Alternative NF-Î²B Pathway in Human Lymphomas.. Blood, 2009, 114, 3943-3943.	1.4	0
94	PI3KCA and PIM Inhibitors in Peripheral T-Cell Lymphomas. Blood, 2010, 116, 4917-4917.	1.4	0
95	Pharmacological Inhibition of PIM Kinases In Chronic Lymphocytic Leukemia Cases with Unfavorable Prognosis Markers. Blood, 2010, 116, 2468-2468.	1.4	0
96	Targeting the Apoptotic Pathway by TW-37, a Novel Bcl-2 Family Small Molecule Inhibitor, In CLL Primary Samples. Blood, 2010, 116, 2470-2470.	1.4	0
97	MicroRNA Signatures In B-Cell Lymphomas. Blood, 2010, 116, 4155-4155.	1.4	0
98	PIM Kinases Inhibition, a Rational Strategy in Peripheral T-Cell Lymphomas,. Blood, 2011, 118, 3494-3494.	1.4	0
99	PI3K Inhibition As a Potential Therapeutic Strategy in Peripheral T-Cell Lymphomas,. Blood, 2011, 118, 3493-3493.	1.4	0
100	Mutational Status of Splenic Marginal Zone Lymphoma Revealed by Whole Exome Sequencing.. Blood, 2012, 120, 2698-2698.	1.4	0
101	Mutations in PLCG1 Is a Frequent Event in Cutaneous T-Cell Lymphomas. Blood, 2012, 120, 300-300.	1.4	0
102	Tumour Suppressor Genes in Hodgkinâ€™s Disease. , 1995, , 209-222.		0
103	A Role of JAK/STAT Pathway in Cutaneous T-Cell Lymphomas: Exploring Its Effects for Targeted Therapy. Blood, 2014, 124, 4498-4498.	1.4	0
104	Diffuse Large B Cell Lymphoma Genetic Classification By Targeted Sequencing and Associations with Immunochemotherapy-Treated Patients' Clinical Outcome. Blood, 2020, 136, 24-25.	1.4	0