## LluÃ-s HernÃ;ndez

List of Publications by Year in descending order

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44 papers 5,317 citations

172443 29 h-index 302107 39 g-index

44 all docs

44 docs citations

44 times ranked 7773 citing authors

#	Article	IF	CITATIONS
1	The receptor of the colony-stimulating factor-1 (CSF-1R) is a novel prognostic factor and therapeutic target in follicular lymphoma. Leukemia, 2021, 35, 2635-2649.	7.2	32
2	ENDOG Impacts on Tumor Cell Proliferation and Tumor Prognosis in the Context of PI3K/PTEN Pathway Status. Cancers, 2021, 13, 3803.	3.7	3
3	Differential expression of long nonâ€coding <scp>RNA</scp> s are related to proliferation and histological diversity in follicular lymphomas. British Journal of Haematology, 2019, 184, 373-383.	2.5	12
4	Expression of the transcribed ultraconserved region 70 and the related long nonâ€coding <scp>RNA AC</scp> 092652.2â€202 has prognostic value in Chronic Lymphocytic Leukaemia. British Journal of Haematology, 2019, 184, 1045-1050.	2.5	10
5	SOXC and MiR17â€92 gene expression profiling defines two subgroups with different clinical outcome in mantle cell lymphoma. Genes Chromosomes and Cancer, 2016, 55, 531-540.	2.8	18
6	The MYC <i>/miR-17-92</i> axis in lymphoproliferative disorders: A common pathway with therapeutic potential. Oncotarget, 2015, 6, 19381-19392.	1.8	51
7	microRNA Expression Profiles Identify Subtypes of Mantle Cell Lymphoma with Different Clinicobiological Characteristics. Clinical Cancer Research, 2013, 19, 3121-3129.	7.0	35
8	Landscape of somatic mutations and clonal evolution in mantle cell lymphoma. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 18250-18255.	7.1	488
9	SOX11 regulates PAX5 expression and blocks terminal B-cell differentiation in aggressive mantle cell lymphoma. Blood, 2013, 121, 2175-2185.	1.4	129
10	Epigenomic analysis detects widespread gene-body DNA hypomethylation in chronic lymphocytic leukemia. Nature Genetics, 2012, 44, 1236-1242.	21.4	525
11	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. Nature, 2011, 475, 101-105.	27.8	1,364
12	Molecular Pathogenesis of Mantle Cell Lymphoma: New Perspectives and Challenges With Clinical Implications. Seminars in Hematology, 2011, 48, 155-165.	3.4	16
13	Identification of Methylated Genes Associated with Aggressive Clinicopathological Features in Mantle Cell Lymphoma. PLoS ONE, 2011, 6, e19736.	2.5	32
14	Epigenetic Activation of SOX11 in Lymphoid Neoplasms by Histone Modifications. PLoS ONE, 2011, 6, e21382.	2.5	38
15	MicroRNA profiles of t(14;18)–negative follicular lymphoma support a late germinal center B-cell phenotype. Blood, 2011, 118, 5550-5558.	1.4	77
16	Genomic and Gene Expression Profiling Defines Indolent Forms of Mantle Cell Lymphoma. Cancer Research, 2010, 70, 1408-1418.	0.9	429
17	MicroRNA Expression, Chromosomal Alterations, and Immunoglobulin Variable Heavy Chain Hypermutations in Mantle Cell Lymphomas. Cancer Research, 2009, 69, 7071-7078.	0.9	78
18	EML4-ALK Rearrangement in Non-Small Cell Lung Cancer and Non-Tumor Lung Tissues. American Journal of Pathology, 2009, 174, 661-670.	3.8	301

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19	Activation of the Endoplasmic Reticulum Stress-Associated Transcription Factor X Box-Binding Protein-1 Occurs in a Subset of Normal Germinal-Center B Cells and in Aggressive B-Cell Lymphomas with Prognostic Implications. American Journal of Pathology, 2009, 174, 2337-2346.	3.8	32
20	Uniparental disomies, homozygous deletions, amplifications, and target genes in mantle cell lymphoma revealed by integrative high-resolution whole-genome profiling. Blood, 2009, 113, 3059-3069.	1.4	162
21	Increased messenger ribonucleic acid expression of the cyclin-dependent kinase inhibitor p27Kip1 in cleavage-stage human embryos exhibiting developmental arrest. Fertility and Sterility, 2008, 89, 1557-1562.	1.0	4
22	Five-Gene Model to Predict Survival in Mantle-Cell Lymphoma Using Frozen or Formalin-Fixed, Paraffin-Embedded Tissue. Journal of Clinical Oncology, 2008, 26, 4966-4972.	1.6	101
23	Increased MDM2 expression is associated with inferior survival in mantle cell lymphoma, but not related to the MDM2 SNP309. Haematologica, 2007, 92, 574-575.	3.5	30
24	Genomic imbalances and patterns of karyotypic variability in mantle-cell lymphoma cell lines. Leukemia Research, 2006, 30, 923-934.	0.8	45
25	Analysis of Aurora-A and hMPS1 mitotic kinases in mantle cell lymphoma. International Journal of Cancer, 2006, 118, 357-363.	5.1	28
26	Checkpoint kinase 1 (CHK1) protein and mRNA expression is downregulated in aggressive variants of human lymphoid neoplasms. Leukemia, 2005, 19, 112-117.	7.2	42
27	CDK4 and MDM2 Gene Alterations Mainly Occur in Highly Proliferative and Aggressive Mantle Cell Lymphomas with Wild-type INK4a/ARF Locus. Cancer Research, 2005, 65, 2199-2206.	0.9	93
28	Identification of Anaplastic Lymphoma Kinase Variant Translocations Using 5'RACE., 2005, 115, 295-314.		1
29	Alterations of Cell Cycle-Regulatory Genes in Prostate Cancer. Pathobiology, 2002, 70, 1-10.	3.8	36
30	ATM gene inactivation in mantle cell lymphoma mainly occurs by truncating mutations and missense mutations involving the phosphatidylinositol-3 kinase domain and is associated with increasing numbers of chromosomal imbalances. Blood, 2002, 99, 238-244.	1.4	151
31	CHK2-decreased protein expression and infrequent genetic alterations mainly occur in aggressive types of non-Hodgkin lymphomas. Blood, 2002, 100, 4602-4608.	1.4	67
32	Diversity of Genomic Breakpoints in TFG-ALK Translocations in Anaplastic Large Cell Lymphomas. American Journal of Pathology, 2002, 160, 1487-1494.	3.8	102
33	Molecular Characterization of a New ALK Translocation Involving Moesin (MSN-ALK) in Anaplastic Large Cell Lymphoma. Laboratory Investigation, 2001, 81, 419-426.	3.7	158
34	Differential Expression of cdc25 Cell-Cycle–Activating Phosphatases in Human Colorectal Carcinoma. Laboratory Investigation, 2001, 81, 465-473.	3.7	74
35	cdc25a and the splicing variant cdc25b2, but not cdc25B1, -B3 or -C, are over-expressed in aggressive human non-Hodgkin's lymphomas. , 2000, 89, 148-152.		56
36	INK4a/ARFLocus Alterations in Human Non-Hodgkin's Lymphomas Mainly Occur in Tumors with Wild-Type p53 Gene. American Journal of Pathology, 2000, 156, 1987-1996.	3.8	83

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37	Disregulation of p16MTS1/CDK4I protein and mRNA expression is associated with gene alterations in squamous-cell carcinoma of the larynx., 1999, 81, 705-711.		19
38	Expression of potentially oncogenic HHV-8 genes in an EBV-negative primary effusion lymphoma occurring in an HIV-seronegative patient., 1999, 189, 288-293.		44
39	Ki-ras gene mutations and absence ofp53 gene mutations in spontaneous and urethane-induced early lung lesions in CBA/J mice. Molecular Carcinogenesis, 1998, 21, 251-260.	2.7	33
40	Deletions and Loss of Expression of P16INK4a and P21Waf1 Genes Are Associated With Aggressive Variants of Mantle Cell Lymphomas. Blood, 1997, 89, 272-280.	1.4	219
41	p16MTS1/CDK4I mutations and concomitant loss of heterozygosity at 9p21-23 are frequent events in squamous cell carcinoma of the larynx. Oncogene, 1997, 15, 1445-1453.	5.9	45
42	p21WAF1/Cip1 expression is associated with cell differentiation but not with p53 mutations in squamous cell carcinomas of the larynx., 1997, 183, 156-163.		44
43	p21WAF1Cip1 expression is associated with cell differentiation but not with p53 mutations in squamous cell carcinomas of the larynx. Journal of Pathology, 1997, 183, 156-163.	4.5	1
44	Deletions and Loss of Expression of P16INK4a and P21Waf1 Genes Are Associated With Aggressive Variants of Mantle Cell Lymphomas. Blood, 1997, 89, 272-280.	1.4	9