Luca Agnelli

List of Publications by Year in descending order

135 papers	4,764 citations	61857 43 h-index	102304 66 g-index
136 all docs	136 docs citations	136 times ranked	7184 citing authors

#	Article	IF	Citations
1	Rescue of Hippo coactivator YAP1 triggers DNA damage–induced apoptosis in hematological cancers. Nature Medicine, 2014, 20, 599-606.	15.2	250
2	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. Blood, 2009, 114, e20-e26.	0.6	224
3	Drugging the lncRNA MALAT1 via LNA gapmeR ASO inhibits gene expression of proteasome subunits and triggers anti-multiple myeloma activity. Leukemia, 2018, 32, 1948-1957.	3.3	179
4	Gene Expression Profiling Uncovers Molecular Classifiers for the Recognition of Anaplastic Large-Cell Lymphoma Within Peripheral T-Cell Neoplasms. Journal of Clinical Oncology, 2010, 28, 1583-1590.	0.8	152
5	Functional validation of the anaplastic lymphoma kinase signature identifies CEBPB and Bcl2A1 as critical target genes. Journal of Clinical Investigation, 2006, 116, 3171-3182.	3.9	139
6	A SNP microarray and FISH–based procedure to detect allelic imbalances in multiple myeloma: An integrated genomics approach reveals a wide gene dosage effect. Genes Chromosomes and Cancer, 2009, 48, 603-614.	1.5	134
7	Dependence on glutamine uptake and glutamine addiction characterize myeloma cells: a new attractive target. Blood, 2016, 128, 667-679.	0.6	128
8	Molecular Classification of Multiple Myeloma: A Distinct Transcriptional Profile Characterizes Patients Expressing CCND1 and Negative for 14q32 Translocations. Journal of Clinical Oncology, 2005, 23, 7296-7306.	0.8	123
9	Gene expression profiling of plasma cell dyscrasias reveals molecular patterns associated with distinct IGH translocations in multiple myeloma. Oncogene, 2005, 24, 2461-2473.	2.6	118
10	Increased osteocyte death in multiple myeloma patients: role in myeloma-induced osteoclast formation. Leukemia, 2012, 26, 1391-1401.	3.3	116
11	An integrative genomic approach reveals coordinated expression of intronic miR-335, miR-342, and miR-561 with deregulated host genes in multiple myeloma. BMC Medical Genomics, 2008, 1, 37.	0.7	104
12	Hypoxia-inducible factor (HIF)-1α suppression in myeloma cells blocks tumoral growth in vivo inhibiting angiogenesis and bone destruction. Leukemia, 2013, 27, 1697-1706.	3.3	104
13	Identification of a 3-gene model as a powerful diagnostic tool for the recognition of ALK-negative anaplastic large-cell lymphoma. Blood, 2012, 120, 1274-1281.	0.6	101
14	Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. Blood, 2016, 127, 221-232.	0.6	97
15	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. Clinical Cancer Research, 2013, 19, 3130-3142.	3.2	86
16	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	2.6	81
17	Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. Leukemia, 2020, 34, 234-244.	3.3	80
18	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. Oncotarget, 2016, 7, 14814-14830.	0.8	79

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19	Lenalidomide and low-dose dexamethasone for newly diagnosed primary plasma cell leukemia. Leukemia, 2014, 28, 222-225.	3.3	77
20	miR-451a is underexpressed and targets AKT/mTOR pathway in papillary thyroid carcinoma. Oncotarget, 2016, 7, 12731-12747.	0.8	77
21	Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. BMC Medical Genomics, 2013, 6, 27.	0.7	73
22	The expression pattern of small nucleolar and small Cajal body-specific RNAs characterizes distinct molecular subtypes of multiple myeloma. Blood Cancer Journal, 2012, 2, e96-e96.	2.8	70
23	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. British Journal of Haematology, 2007, 136, 565-573.	1.2	66
24	The Reconstruction of Transcriptional Networks Reveals Critical Genes with Implications for Clinical Outcome of Multiple Myeloma. Clinical Cancer Research, 2011, 17, 7402-7412.	3.2	65
25	Immunomodulatory drugs lenalidomide and pomalidomide inhibit multiple myeloma-induced osteoclast formation and the RANKL/OPG ratio in the myeloma microenvironment targeting the expression of adhesion molecules. Experimental Hematology, 2013, 41, 387-397.e1.	0.2	65
26	Molecular spectrum of <i>BRAF, NRAS</i> and <i>KRAS</i> gene mutations in plasma cell dyscrasias: implication for MEK-ERK pathway activation. Oncotarget, 2015, 6, 24205-24217.	0.8	65
27	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. Genes Chromosomes and Cancer, 2007, 46, 226-238.	1.5	62
28	Integrative high‐resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. Genes Chromosomes and Cancer, 2009, 48, 521-531.	1.5	60
29	Genome‐wide analysis of primary plasma cell leukemia identifies recurrent imbalances associated with changes in transcriptional profiles. American Journal of Hematology, 2013, 88, 16-23.	2.0	60
30	Clinical Monoclonal B Lymphocytosis versus Rai 0 Chronic Lymphocytic Leukemia: A Comparison of Cellular, Cytogenetic, Molecular, and Clinical Features. Clinical Cancer Research, 2013, 19, 5890-5900.	3.2	60
31	Molecular and transcriptional characterization of 17p loss in B‐cell chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2008, 47, 781-793.	1.5	59
32	Biological and clinical relevance of quantitative global methylation of repetitive DNA sequences in chronic lymphocytic leukemia. Epigenetics, 2011, 6, 188-194.	1.3	58
33	Distinct transcriptional profiles characterize bone microenvironment mesenchymal cells rather than osteoblasts in relationship with multiple myeloma bone disease. Experimental Hematology, 2010, 38, 141-153.	0.2	57
34	Evidence of Distinct Tumour-Propagating Cell Populations with Different Properties in Primary Human Hepatocellular Carcinoma. PLoS ONE, 2011, 6, e21369.	1.1	56
35	Improved risk stratification in myeloma using a micro<scp>RNA</scp>‐based classifier. British Journal of Haematology, 2013, 162, 348-359.	1.2	53
36	Integrative Genomics Analyses Reveal Molecularly Distinct Subgroups of B-Cell Chronic Lymphocytic Leukemia Patients with 13q14 Deletion. Clinical Cancer Research, 2010, 16, 5641-5653.	3.2	52

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37	High‐throughput sequencing for the identification of *NOTCH1* mutations in early stage chronic lymphocytic leukaemia: biological and clinical implications. British Journal of Haematology, 2014, 165, 629-639.	1.2	52
38	microRNAome Expression in Chronic Lymphocytic Leukemia: Comparison with Normal B-cell Subsets and Correlations with Prognostic and Clinical Parameters. Clinical Cancer Research, 2014, 20, 4141-4153.	3.2	52
39	Transcriptional Characterization of a Prospective Series of Primary Plasma Cell Leukemia Revealed Signatures Associated with Tumor Progression and Poorer Outcome. Clinical Cancer Research, 2013, 19, 3247-3258.	3.2	50
40	Characterization of oncogene dysregulation in multiple myeloma by combined FISH and DNA microarray analyses. Genes Chromosomes and Cancer, 2005, 42, 117-127.	1.5	49
41	Myeloma cells inhibit non-canonical wnt co-receptor ror2 expression in human bone marrow osteoprogenitor cells: effect of wnt5a/ror2 pathway activation on the osteogenic differentiation impairment induced by myeloma cells. Leukemia, 2013, 27, 451-463.	3.3	48
42	lncRNA profiling in early-stage chronic lymphocytic leukemia identifies transcriptional fingerprints with relevance in clinical outcome. Blood Cancer Journal, 2016, 6, e468-e468.	2.8	47
43	Transcriptional features of multiple myeloma patients with chromosome 1q gain. Leukemia, 2007, 21, 1113-1116.	3.3	45
44	Identification of primary MAFB target genes in multiple myeloma. Experimental Hematology, 2009, 37, 78-86.	0.2	45
45	MicroRNAs in the Pathobiology of Multiple Myeloma. Current Cancer Drug Targets, 2012, 12, 823-837.	0.8	44
46	Disentangling the microRNA regulatory *milieu* in multiple myeloma: integrative genomics analysis outlines mixed miRNA-TF circuits and pathway-derived networks modulated in t(4;14) patients. Oncotarget, 2016, 7, 2367-2378.	0.8	41
47	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. Oncotarget, 2015, 6, 19132-19147.	0.8	41
48	A compendium of *DIS3* mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	0.8	40
49	HOXB7 expression by myeloma cells regulates their pro-angiogenic properties in multiple myeloma patients. Leukemia, 2011, 25, 527-537.	3.3	39
50	Relevance of telomere/telomerase system impairment in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 612-621.	1.5	38
51	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. PLoS ONE, 2011, 6, e23854.	1.1	37
52	Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of Chronic Lymphocytic Leukemia. PLoS ONE, 2011, 6, e24313.	1.1	36
53	B‐cell receptor configuration and adverse cytogenetics are associated with autoimmune hemolytic anemia in chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 32-36.	2.0	36
54	*IL21R* expressing CD14+ CD16+ monocytes expand in multiple myeloma patients leading to increased osteoclasts. Haematologica, 2017, 102, 773-784.	1.7	36

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55	Integrative genomic analysis reveals distinct transcriptional and genetic features associated with chromosome 13 deletion in multiple myeloma. Haematologica, 2007, 92, 56-65.	1.7	34
56	A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. Scientific Reports, 2018, 8, 6557.	1.6	34
57	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-cell Receptors. Clinical Cancer Research, 2012, 18, 1870-1878.	3.2	33
58	Galectin-1 suppression delineates a new strategy to inhibit myeloma-induced angiogenesis and tumoral growth in vivo. Leukemia, 2016, 30, 2351-2363.	3.3	29
59	Chromosome 2p gain in monoclonal B–cell lymphocytosis and in early stage chronic lymphocytic leukemia. American Journal of Hematology, 2013, 88, 24-31.	2.0	27
60	Long non-coding RNA NEAT1 shows high expression unrelated to molecular features and clinical outcome in multiple myeloma. Haematologica, 2019, 104, e72-e76.	1.7	27
61	Transcription repression activity is associated with the type I isoform of the MMSET gene involved in t(4;14) in multiple myeloma. British Journal of Haematology, 2005, 131, 214-218.	1.2	24
62	Molecular Classification and Pharmacogenetics of Primary Plasma Cell Leukemia: An Initial Approach toward Precision Medicine. International Journal of Molecular Sciences, 2015, 16, 17514-17534.	1.8	23
63	Association between gene and miRNA expression profiles and stereotyped subset #4 B-cell receptor in chronic lymphocytic leukemia. Leukemia and Lymphoma, 2015, 56, 3150-3158.	0.6	23
64	Long Non-Coding RNAs in Multiple Myeloma. Genes, 2018, 9, 69.	1.0	22
65	Myeloma Cells Deplete Bone Marrow Glutamine and Inhibit Osteoblast Differentiation Limiting Asparagine Availability. Cancers, 2020, 12, 3267.	1.7	22
66	Molecular and transcriptional characterization of the novel 17p11.2–p12 amplicon in multiple myeloma. Genes Chromosomes and Cancer, 2007, 46, 1109-1118.	1.5	20
67	Molecular profiling of multiple myeloma: from gene expression analysis to next-generation sequencing. Expert Opinion on Biological Therapy, 2013, 13, S55-S68.	1.4	20
68	In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. Genes, 2016, 7, 107.	1.0	17
69	Tracing CLL-biased stereotyped immunoglobulin gene rearrangements in normal B cell subsets using a high-throughput immunogenetic approach. Molecular Medicine, 2020, 26, 25.	1.9	17
70	Integration of transcriptional and mutational data simplifies the stratification of peripheral T–cell lymphoma. American Journal of Hematology, 2019, 94, 628-634.	2.0	16
71	Insulin Growth Factor 1 Receptor Expression Is Associated with NOTCH1 Mutation, Trisomy 12 and Aggressive Clinical Course in Chronic Lymphocytic Leukaemia. PLoS ONE, 2015, 10, e0118801.	1.1	15
72	The prevalence and clinical implications of c-kit expression in plasma cell myeloma. Histopathology, 2006, 48, 529-535.	1.6	14

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73	Targeted resequencing of FECH locus reveals that a novel deep intronic pathogenic variant and eQTLs may cause erythropoietic protoporphyria (EPP) through a methylation-dependent mechanism. Genetics in Medicine, 2020, 22, 35-43.	1.1	12
74	The new small tyrosine kinase inhibitor ARQ531 targets acute myeloid leukemia cells by disrupting multiple tumor-addicted programs. Haematologica, 2020, 105, 2420-2431.	1.7	12
75	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. Non-coding RNA, 2020, 6, 11.	1.3	11
76	Distinct patterns of global promoter methylation in early stage chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2014, 53, 264-273.	1.5	10
77	Expanding the repertoire of miRNAs and miRNA-offset RNAs expressed in multiple myeloma by small RNA deep sequencing. Blood Cancer Journal, 2019, 9, 21.	2.8	10
78	Overexpression of HOXB7 and homeobox genes characterizes multiple myeloma patients lacking the major primary immunoglobulin heavy chain locus translocations. American Journal of Hematology, 2011, 86, E64-E66.	2.0	9
79	Relevance ofRas gene mutations in the context of the molecular heterogeneity of multiple myeloma. Hematological Oncology, 2007, 25, 6-10.	0.8	8
80	Bone osteoblastic and mesenchymal stromal cells lack primarily tumoral features in multiple myeloma patients. Leukemia, 2010, 24, 1368-1370.	3.3	8
81	The transcriptomic profile of CD138$^+$ cells from patients with early progression from smoldering to active multiple myeloma remains substantially unchanged. Haematologica, 2019, 104, e465-e469.	1.7	8
82	The proapoptotic effect of zoledronic acid is independent of either the bone microenvironment or the intrinsic resistance to bortezomib of myeloma cells and is enhanced by the combination with arsenic trioxide. Experimental Hematology, 2011, 39, 55-65.	0.2	7
83	Prognostic Significance of Telomere Length in Chronic Lymphocytic Leukemia Patients in Early Stage Disease,. Blood, 2011, 118, 3890-3890.	0.6	7
84	Expression Pattern and Biological Significance of the lncRNA ST3GAL6-AS1 in Multiple Myeloma. Cancers, 2020, 12, 782.	1.7	6
85	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
86	Human pluripotent stem cells identify molecular targets of trisomy 12 in chronic lymphocytic leukemia patients. Cell Reports, 2021, 34, 108845.	2.9	3
87	Genome-Wide Analysis of Primary Plasma-Cell Leukemia Identifies Recurrent Imbalances Associated with Transcriptional Profile Alterations. Blood, 2011, 118, 2878-2878.	0.6	3
88	Next-generation sequencing in multiple myeloma: insights into the molecular heterogeneity of the disease. International Journal of Hematologic Oncology, 2014, 3, 367-376.	0.7	2
89	In Vitro and In Vivo Evidences of Osteocyte Involvement In Myeloma-Induced Osteolysis. Blood, 2010, 116, 131-131.	0.6	2
90	Hypoxia-Inducible Factor (HIF)-1Î± Is a Therapeutic Target in Myeloma-Induced Angiogenesis. Blood, 2011, 118, 3927-3927.	0.6	2

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91	Ammonium Production and Glutamine-Addiction of Myeloma Cells: New Attractive Targets in Multiple Myeloma. Blood, 2014, 124, 2067-2067.	0.6	2
92	Peripheral T-Cell Lymphomas Not Otherwise Specified: Potential Novel Molecular Entities Based on Both Tumor and Microenvironment Cellular Components. Blood, 2016, 128, 4098-4098.	0.6	2
93	Immunoreactivity for cyclin D1 is a reliable marker of gene aberration in plasma cell myeloma but does not specify patients prognosis. Leukemia Research, 2008, 32, 1628-1632.	0.4	1
94	Bioinformatics Pipeline to Analyze lncRNA Arrays. Methods in Molecular Biology, 2021, 2348, 45-53.	0.4	1
95	Identification of MicroRNA Expression Patterns and Definition of a MicroRNAs/mRNA Regulatory Network in Distinct Molecular Groups of Multiple Myeloma.. Blood, 2009, 114, 2824-2824.	0.6	1
96	The Immunomodulatory Drugs Lenalidomide and Pomalidomide Inhibit Multiple Myeloma-Induced Osteoclast Formation and RANKL/OPG Ratio In Myeloma Microenvironment Targeting the Expression of Adhesion Molecules. Blood, 2010, 116, 448-448.	0.6	1
97	Analysis of Transcriptome, Mirnome and Genomic Profiles in Association with Clinical Outcome in a Prospective Series of Primary Plasma Cell Leukemia. Blood, 2012, 120, 3938-3938.	0.6	1
98	Different Gene Expression Profiles of CD133+ Cells from Cord Blood and Mobilized Peripheral Blood.. Blood, 2005, 106, 4210-4210.	0.6	1
99	Improved Risk Stratification in Myeloma Using Microrna-Based Classifier. Blood, 2012, 120, 932-932.	0.6	1
100	1.2 Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of CLL. Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S141-S142.	0.2	0
101	3.20 Stereotyped B-Cell Receptor is Associated with Immune Thrombocytopenia in CLL. Clinical Lymphoma, Myeloma and Leukemia, 2011, 11, S209-S211.	0.2	0
102	Editorial: Genomics of Lymphoproliferative Disease. Frontiers in Oncology, 2021, 11, 660016.	1.3	0
103	Gene Expression Profiling of Plasma Cell Dyscrasias: The Role of IGH Translocations in the Heterogeneity of Multiple Myeloma.. Blood, 2004, 104, 4845-4845.	0.6	0
104	Characterization of Oncogene Dysregulation in Multiple Myeloma by Combined FISH and DNA Microarray Analyses.. Blood, 2004, 104, 4844-4844.	0.6	0
105	DKK-1 and sFRP-3 Expression by Myeloma Cell and Bone Marrow Plasma Levels in Multiple Myeloma and MGUS Patients: Potential Relationship with Bone Status.. Blood, 2006, 108, 3437-3437.	0.6	0
106	Identification of Specific Transcriptional Patterns Associated with Hyperdiploidy in Multiple Myeloma.. Blood, 2006, 108, 3412-3412.	0.6	0
107	Mesenchymal and Osteoblastic Cells Isolated from Multiple Myeloma Patients Reveal a Different Behavior, Phenotype and Gene Expression Profiling in Relationship with the Presence of Osteolytic Bone Lesions.. Blood, 2006, 108, 3511-3511.	0.6	0
108	Gene Expression Profiling of Isolated Mesenchymal and Osteoblastic Cells Exhibits a Different Pattern of Expression in Multiple Myeloma Patients as Compared to Healthy Subjects: Potential Relationship with the Presence of Bone Lesions.. Blood, 2007, 110, 3513-3513.	0.6	0

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109	Effect of Dioxin (TCDD) on Gene Transcription of Human CD34+ Hematopoietic Cells.. Blood, 2007, 110, 4033-4033.	0.6	0
110	Molecular and Transcriptional Characterization of the Novel 17p11.2-p12 Chromosome Amplification in Multiple Myeloma.. Blood, 2007, 110, 2486-2486.	0.6	0
111	Genome-Wide Analysis of DNA Copy Number in Multiple Myeloma Using High-Density SNP Arrays Reveals Clustering Patterns with Distinct Transcriptional Profiles.. Blood, 2007, 110, 2482-2482.	0.6	0
112	Genome-Wide DNA Copy Number Analysis by SNP Arrays of B-Cell Chronic Lymphocytic Leukemia: Correlation with Known Biological and Molecular Prognostic Markers.. Blood, 2008, 112, 1061-1061.	0.6	0
113	Integrative Genomic Approach Identifies Deregulated MicroRNAs in Human Myeloma Cell Lines.. Blood, 2008, 112, 1684-1684.	0.6	0
114	HOXB7 Overexpression in Mesenchymal Cells Stimulates the Production of Pro-Angiogenic Molecules: Potential Role in Multiple Myeloma Associated Angiogenesis. Blood, 2008, 112, 2743-2743.	0.6	0
115	Bone Microenvironment Cells Show a Different Pattern of Gene Expression Profiling in Relationship with the Presence of Osteolytic Bone Lesions in Multiple Myeloma Patients. Blood, 2008, 112, 2740-2740.	0.6	0
116	Are the Myeloma Bone Microevironment Cells Tumoral or Not?.. Blood, 2009, 114, 1816-1816.	0.6	0
117	HOXB7 Is Critically Involved in Multiple Myeloma-Induced Angiogenic Switch.. Blood, 2009, 114, 125-125.	0.6	0
118	Abstract 181: Biological and clinical relevance of quantitative global methylation in repetitive DNA sequences in B-cell chronic lymphocytic leukemia. , 2010, , .		0
119	Abstract 2161: Network-based inference of ALK oncogenic signaling in T-cell lymphoproliferative disorders. , 2010, , .		0
120	Integrative Genomic Analysis of Primary Plasma Cell Leukemia Revealed Strong Gene and MicroRNA Dosage Effect. Blood, 2010, 116, 4040-4040.	0.6	0
121	Analysis of Stereotyped IGHV Distribution In a Series of 1133 Chronic Lymphocytic Leukemia Patients: The Experience of a Multicenter Italian Study Group. Blood, 2010, 116, 2423-2423.	0.6	0
122	Abstract 1229: Prognostic significance of telomere length in B-chronic lymphocytic leukemia patients in early stage disease. , 2011, , .		0
123	The Activation of Wnt5a-Mediated Non Canonical Wnt Signaling in Human Bone Marrow Osteoprogenitor Cells Increases Osteoblastogenesis and Counterbalances the Inhibitory Effect of Myeloma Cells on Ror2/FZD5 Expression,. Blood, 2011, 118, 3928-3928.	0.6	0
124	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. Blood, 2011, 118, 2847-2847.	0.6	0
125	Abstract 4575: Three-gene diagnostic classifier for ALK negative ALCL. , 2012, , .		0
126	B-Cell Receptor Configuration and Adverse Cytogenetics Are Associated with Autoimmune Hemolytic Anemia in Chronic Lymphocytic Leukemia. Blood, 2012, 120, 1780-1780.	0.6	0

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127	Hypoxia-Inducible Factor (HIF)-1a Is A Therapeutic Target in Myeloma-Induced Angiogenesis and Bone Destruction in Vivo.. Blood, 2012, 120, 2947-2947.	0.6	0
128	Trascriptome Analysis of Bone Marrow CD14+ Monocytes Revealed Differential Expression Profiles in Symptomatic Multiple Myeloma (MM) Compared to Smoldering MM and Monoclonal Gammopathy of Undetermined Significance. Blood, 2012, 120, 1811-1811.	0.6	0
129	The Expression Pattern of Small Nucleolar and Small Cajal Body-Specific RNAs Characterizes Distinct Molecular Subtypes of Multiple Myeloma. Blood, 2012, 120, 3955-3955.	0.6	0
130	The Genomics of Multiple Myeloma and Its Relevance in the Molecular Classification and Risk Stratification of the Disease. , 2013, , 543-570.		0
131	High-Throughput Sequencing For The Identification Of NOTCH1 mutations In Early Stage Chronic Lymphocytic Leukemia: Biological and Clinical Implications. Blood, 2013, 122, 1622-1622.	0.6	0
132	Overexpression of Pro-Osteoclastogenic Cytokine Receptors and Chemokines By Bone Marrow CD14+ Monocytes of Multiple Myeloma (MM) Patients As Compared to Smoldering MM (SMM) and Monoclonal Gammopathy of Uncertain Significance (MGUS): Role of Interleukin(IL)-21 Receptor/IL-21 Axis in MM-Induced Osteoclastogenesis. Blood, 2014, 124, 28-28.	0.6	0
133	Identification of a New Subclass of ALK Negative Anaplastic Large Cell Lymphoma Expressing Aberrant Levels of ERBB4 Transcripts. Blood, 2014, 124, 1679-1679.	0.6	0
134	Abstract 4071: Investigation of thyroid tumor microenvironment by immunohistochemical and bioinformatic analyses. , 2018, , .		0
135	PSMB4 and PSMD4 Are Correlated with 1q21 Amplification in CD138 + Plasma Cells: New Potential Druggable Targets in Myeloma Patients. Blood, 2021, 138, 2657-2657.	0.6	0