

Luca Agnelli

List of Publications by Year in descending order

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135
papers

4,764
citations

61857

43
h-index

102304

66
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136
all docs

136
docs citations

136
times ranked

7184
citing authors

#	ARTICLE	IF	CITATIONS
1	Editorial: Genomics of Lymphoproliferative Disease. <i>Frontiers in Oncology</i> , 2021, 11, 660016.	1.3	0
2	Human pluripotent stem cells identify molecular targets of trisomy 12 in chronic lymphocytic leukemia patients. <i>Cell Reports</i> , 2021, 34, 108845.	2.9	3
3	Bioinformatics Pipeline to Analyze lncRNA Arrays. <i>Methods in Molecular Biology</i> , 2021, 2348, 45-53.	0.4	1
4	PSMB4 and PSMD4 Are Correlated with 1q21 Amplification in CD138 + Plasma Cells: New Potential Druggable Targets in Myeloma Patients. <i>Blood</i> , 2021, 138, 2657-2657.	0.6	0
5	Long non-coding RNA NEAT1 targeting impairs the DNA repair machinery and triggers anti-tumor activity in multiple myeloma. <i>Leukemia</i> , 2020, 34, 234-244.	3.3	80
6	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. <i>Genetics in Medicine</i> , 2020, 22, 35-43.	1.1	12
7	Myeloma Cells Deplete Bone Marrow Glutamine and Inhibit Osteoblast Differentiation Limiting Asparagine Availability. <i>Cancers</i> , 2020, 12, 3267.	1.7	22
8	Revealing the Impact of Structural Variants in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020, 1, 258-273.	2.6	81
9	NEAT1 Long Isoform Is Highly Expressed in Chronic Lymphocytic Leukemia Irrespectively of Cytogenetic Groups or Clinical Outcome. <i>Non-coding RNA</i> , 2020, 6, 11.	1.3	11
10	Tracing CLL-biased stereotyped immunoglobulin gene rearrangements in normal B cell subsets using a high-throughput immunogenetic approach. <i>Molecular Medicine</i> , 2020, 26, 25.	1.9	17
11	The new small tyrosine kinase inhibitor ARQ531 targets acute myeloid leukemia cells by disrupting multiple tumor-addicted programs. <i>Haematologica</i> , 2020, 105, 2420-2431.	1.7	12
12	Expression Pattern and Biological Significance of the lncRNA ST3GAL6-AS1 in Multiple Myeloma. <i>Cancers</i> , 2020, 12, 782.	1.7	6
13	The transcriptomic profile of CD138 ⁺ cells from patients with early progression from smoldering to active multiple myeloma remains substantially unchanged. <i>Haematologica</i> , 2019, 104, e465-e469.	1.7	8
14	Integration of transcriptional and mutational data simplifies the stratification of peripheral Tâ€cell lymphoma. <i>American Journal of Hematology</i> , 2019, 94, 628-634.	2.0	16
15	Expanding the repertoire of miRNAs and miRNA-offset RNAs expressed in multiple myeloma by small RNA deep sequencing. <i>Blood Cancer Journal</i> , 2019, 9, 21.	2.8	10
16	Long non-coding RNA NEAT1 shows high expression unrelated to molecular features and clinical outcome in multiple myeloma. <i>Haematologica</i> , 2019, 104, e72-e76.	1.7	27
17	Drugging the lncRNA MALAT1 via LNA gapmer ASO inhibits gene expression of proteasome subunits and triggers anti-multiple myeloma activity. <i>Leukemia</i> , 2018, 32, 1948-1957.	3.3	179
18	Long Non-Coding RNAs in Multiple Myeloma. <i>Genes</i> , 2018, 9, 69.	1.0	22

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19	A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. Scientific Reports, 2018, 8, 6557.	1.6	34
20	Abstract 4071: Investigation of thyroid tumor microenvironment by immunohistochemical and bioinformatic analyses. , 2018, , .		0
21	<i>IL21R</i> expressing CD14 ⁺ CD16 ⁺ monocytes expand in multiple myeloma patients leading to increased osteoclasts. Haematologica, 2017, 102, 773-784.	1.7	36
22	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
23	In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. Genes, 2016, 7, 107.	1.0	17
24	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. Oncotarget, 2016, 7, 14814-14830.	0.8	79
25	Dependence on glutamine uptake and glutamine addiction characterize myeloma cells: a new attractive target. Blood, 2016, 128, 667-679.	0.6	128
26	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
27	Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. Blood, 2016, 127, 221-232.	0.6	97
28	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
29	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
30	miR-451a is underexpressed and targets AKT/mTOR pathway in papillary thyroid carcinoma. Oncotarget, 2016, 7, 12731-12747.	0.8	77
31	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
32	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
33	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
34	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
35	Molecular spectrum of <i>BRAF</i> , <i>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
36	A compendium of <i>DIS3</i> mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	0.8	40

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37	Next-generation sequencing in multiple myeloma: insights into the molecular heterogeneity of the disease. <i>International Journal of Hematologic Oncology</i> , 2014, 3, 367-376.	0.7	2
38	Distinct patterns of global promoter methylation in early stage chronic lymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 264-273.	1.5	10
39	Lenalidomide and low-dose dexamethasone for newly diagnosed primary plasma cell leukemia. <i>Leukemia</i> , 2014, 28, 222-225.	3.3	77
40	High-throughput sequencing for the identification of NOTCH1 mutations in early stage chronic lymphocytic leukaemia: biological and clinical implications. <i>British Journal of Haematology</i> , 2014, 165, 629-639.	1.2	52
41	Rescue of Hippo coactivator YAP1 triggers DNA damage-induced apoptosis in hematological cancers. <i>Nature Medicine</i> , 2014, 20, 599-606.	15.2	250
42	Relevance of telomere/telomerase system impairment in early stage chronic lymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2014, 53, 612-621.	1.5	38
43	microRNAome Expression in Chronic Lymphocytic Leukemia: Comparison with Normal B-cell Subsets and Correlations with Prognostic and Clinical Parameters. <i>Clinical Cancer Research</i> , 2014, 20, 4141-4153.	3.2	52
44	Ammonium Production and Glutamine-Addiction of Myeloma Cells: New Attractive Targets in Multiple Myeloma. <i>Blood</i> , 2014, 124, 2067-2067.	0.6	2
45	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. <i>Blood</i> , 2014, 124, 28-28.	0.6	0
46	Identification of a New Subclass of ALK Negative Anaplastic Large Cell Lymphoma Expressing Aberrant Levels of ERBB4 Transcripts. <i>Blood</i> , 2014, 124, 1679-1679.	0.6	0
47	Molecular profiling of multiple myeloma: from gene expression analysis to next-generation sequencing. <i>Expert Opinion on Biological Therapy</i> , 2013, 13, S55-S68.	1.4	20
48	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. <i>Experimental Hematology</i> , 2013, 41, 387-397.e1.	0.2	65
49	Small nucleolar RNAs as new biomarkers in chronic lymphocytic leukemia. <i>BMC Medical Genomics</i> , 2013, 6, 27.	0.7	73
50	Genome-wide analysis of primary plasma cell leukemia identifies recurrent imbalances associated with changes in transcriptional profiles. <i>American Journal of Hematology</i> , 2013, 88, 16-23.	2.0	60
51	Chromosome 2p gain in monoclonal B-cell lymphocytosis and in early stage chronic lymphocytic leukemia. <i>American Journal of Hematology</i> , 2013, 88, 24-31.	2.0	27
52	B-cell receptor configuration and adverse cytogenetics are associated with autoimmune hemolytic anemia in chronic lymphocytic leukemia. <i>American Journal of Hematology</i> , 2013, 88, 32-36.	2.0	36
53	Hypoxia-inducible factor (HIF)-1 α suppression in myeloma cells blocks tumoral growth in vivo inhibiting angiogenesis and bone destruction. <i>Leukemia</i> , 2013, 27, 1697-1706.	3.3	104
54	Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , 2013, 162, 348-359.	1.2	53

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55	Clinical Monoclonal B Lymphocytosis versus Rai 0 Chronic Lymphocytic Leukemia: A Comparison of Cellular, Cytogenetic, Molecular, and Clinical Features. <i>Clinical Cancer Research</i> , 2013, 19, 5890-5900.	3.2	60
56	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. <i>Leukemia</i> , 2013, 27, 451-463.	3.3	48
57	Transcriptional Characterization of a Prospective Series of Primary Plasma Cell Leukemia Revealed Signatures Associated with Tumor Progression and Poorer Outcome. <i>Clinical Cancer Research</i> , 2013, 19, 3247-3258.	3.2	50
58	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. <i>Clinical Cancer Research</i> , 2013, 19, 3130-3142.	3.2	86
59	The Genomics of Multiple Myeloma and Its Relevance in the Molecular Classification and Risk Stratification of the Disease. , 2013, , 543-570.		0
60	High-Throughput Sequencing For The Identification Of NOTCH1 mutations In Early Stage Chronic Lymphocytic Leukemia: Biological and Clinical Implications. <i>Blood</i> , 2013, 122, 1622-1622.	0.6	0
61	MicroRNAs in the Pathobiology of Multiple Myeloma. <i>Current Cancer Drug Targets</i> , 2012, 12, 823-837.	0.8	44
62	Identification of a 3-gene model as a powerful diagnostic tool for the recognition of ALK-negative anaplastic large-cell lymphoma. <i>Blood</i> , 2012, 120, 1274-1281.	0.6	101
63	The expression pattern of small nucleolar and small Cajal body-specific RNAs characterizes distinct molecular subtypes of multiple myeloma. <i>Blood Cancer Journal</i> , 2012, 2, e96-e96.	2.8	70
64	Increased osteocyte death in multiple myeloma patients: role in myeloma-induced osteoclast formation. <i>Leukemia</i> , 2012, 26, 1391-1401.	3.3	116
65	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-cell Receptors. <i>Clinical Cancer Research</i> , 2012, 18, 1870-1878.	3.2	33
66	Analysis of Transcriptome, Mirnome and Genomic Profiles in Association with Clinical Outcome in a Prospective Series of Primary Plasma Cell Leukemia. <i>Blood</i> , 2012, 120, 3938-3938.	0.6	1
67	Abstract 4575: Three-gene diagnostic classifier for ALK negative ALCL. , 2012, , .		0
68	B-Cell Receptor Configuration and Adverse Cytogenetics Are Associated with Autoimmune Hemolytic Anemia in Chronic Lymphocytic Leukemia. <i>Blood</i> , 2012, 120, 1780-1780.	0.6	0
69	Hypoxia-Inducible Factor (HIF)-1a Is A Therapeutic Target in Myeloma-Induced Angiogenesis and Bone Destruction in Vivo.. <i>Blood</i> , 2012, 120, 2947-2947.	0.6	0
70	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. <i>Blood</i> , 2012, 120, 1811-1811.	0.6	0
71	Improved Risk Stratification in Myeloma Using Microrna-Based Classifier. <i>Blood</i> , 2012, 120, 932-932.	0.6	1
72	The Expression Pattern of Small Nucleolar and Small Cajal Body-Specific RNAs Characterizes Distinct Molecular Subtypes of Multiple Myeloma. <i>Blood</i> , 2012, 120, 3955-3955.	0.6	0

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73	1.2 Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of CLL. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2011, 11, S141-S142.	0.2	0
74	3.20 Stereotyped B-Cell Receptor is Associated with Immune Thrombocytopenia in CLL. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2011, 11, S209-S211.	0.2	0
75	Relevance of Stereotyped B-Cell Receptors in the Context of the Molecular, Cytogenetic and Clinical Features of Chronic Lymphocytic Leukemia. <i>PLoS ONE</i> , 2011, 6, e24313.	1.1	36
76	HOXB7 expression by myeloma cells regulates their pro-angiogenic properties in multiple myeloma patients. <i>Leukemia</i> , 2011, 25, 527-537.	3.3	39
77	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. <i>Experimental Hematology</i> , 2011, 39, 55-65.	0.2	7
78	Overexpression of HOXB7 and homeobox genes characterizes multiple myeloma patients lacking the major primary immunoglobulin heavy chain locus translocations. <i>American Journal of Hematology</i> , 2011, 86, E64-E66.	2.0	9
79	Biological and clinical relevance of quantitative global methylation of repetitive DNA sequences in chronic lymphocytic leukemia. <i>Epigenetics</i> , 2011, 6, 188-194.	1.3	58
80	The Reconstruction of Transcriptional Networks Reveals Critical Genes with Implications for Clinical Outcome of Multiple Myeloma. <i>Clinical Cancer Research</i> , 2011, 17, 7402-7412.	3.2	65
81	Hypoxia-Inducible Factor (HIF)-1 α Is a Therapeutic Target in Myeloma-Induced Angiogenesis. <i>Blood</i> , 2011, 118, 3927-3927.	0.6	2
82	Evidence of Distinct Tumour-Propagating Cell Populations with Different Properties in Primary Human Hepatocellular Carcinoma. <i>PLoS ONE</i> , 2011, 6, e21369.	1.1	56
83	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. <i>PLoS ONE</i> , 2011, 6, e23854.	1.1	37
84	Abstract 1229: Prognostic significance of telomere length in B-chronic lymphocytic leukemia patients in early stage disease. , 2011, , .		0
85	Prognostic Significance of Telomere Length in Chronic Lymphocytic Leukemia Patients in Early Stage Disease,. <i>Blood</i> , 2011, 118, 3890-3890.	0.6	7
86	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,. <i>Blood</i> , 2011, 118, 3928-3928.	0.6	0
87	Immune Thrombocytopenia in Patients with Chronic Lymphocytic Leukemia Is Associated with Stereotyped B-Cell Receptors. <i>Blood</i> , 2011, 118, 2847-2847.	0.6	0
88	Genome-Wide Analysis of Primary Plasma-Cell Leukemia Identifies Recurrent Imbalances Associated with Transcriptional Profile Alterations. <i>Blood</i> , 2011, 118, 2878-2878.	0.6	3
89	Distinct transcriptional profiles characterize bone microenvironment mesenchymal cells rather than osteoblasts in relationship with multiple myeloma bone disease. <i>Experimental Hematology</i> , 2010, 38, 141-153.	0.2	57
90	Bone osteoblastic and mesenchymal stromal cells lack primarily tumoral features in multiple myeloma patients. <i>Leukemia</i> , 2010, 24, 1368-1370.	3.3	8

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91	Integrative Genomics Analyses Reveal Molecularly Distinct Subgroups of B-Cell Chronic Lymphocytic Leukemia Patients with 13q14 Deletion. <i>Clinical Cancer Research</i> , 2010, 16, 5641-5653.	3.2	52
92	Gene Expression Profiling Uncovers Molecular Classifiers for the Recognition of Anaplastic Large-Cell Lymphoma Within Peripheral T-Cell Neoplasms. <i>Journal of Clinical Oncology</i> , 2010, 28, 1583-1590.	0.8	152
93	In Vitro and In Vivo Evidences of Osteocyte Involvement In Myeloma-Induced Osteolysis. <i>Blood</i> , 2010, 116, 131-131.	0.6	2
94	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. <i>Blood</i> , 2010, 116, 448-448.	0.6	1
95	Abstract 181: Biological and clinical relevance of quantitative global methylation in repetitive DNA sequences in B-cell chronic lymphocytic leukemia. , 2010, , .		0
96	Abstract 2161: Network-based inference of ALK oncogenic signaling in T-cell lymphoproliferative disorders. , 2010, , .		0
97	Integrative Genomic Analysis of Primary Plasma Cell Leukemia Revealed Strong Gene and MicroRNA Dosage Effect. <i>Blood</i> , 2010, 116, 4040-4040.	0.6	0
98	Analysis of Stereotyped IGHV Distribution In a Series of 1133 Chronic Lymphocytic Leukemia Patients: The Experience of a Multicenter Italian Study Group. <i>Blood</i> , 2010, 116, 2423-2423.	0.6	0
99	Identification of primary MAFB target genes in multiple myeloma. <i>Experimental Hematology</i> , 2009, 37, 78-86.	0.2	45
100	Integrative high-resolution microarray analysis of human myeloma cell lines reveals deregulated miRNA expression associated with allelic imbalances and gene expression profiles. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 521-531.	1.5	60
101	A SNP microarray and FISH-based procedure to detect allelic imbalances in multiple myeloma: An integrated genomics approach reveals a wide gene dosage effect. <i>Genes Chromosomes and Cancer</i> , 2009, 48, 603-614.	1.5	134
102	Identification of microRNA expression patterns and definition of a microRNA/mRNA regulatory network in distinct molecular groups of multiple myeloma. <i>Blood</i> , 2009, 114, e20-e26.	0.6	224
103	Identification of MicroRNA Expression Patterns and Definition of a MicroRNAs/mRNA Regulatory Network in Distinct Molecular Groups of Multiple Myeloma.. <i>Blood</i> , 2009, 114, 2824-2824.	0.6	1
104	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
105	Are the Myeloma Bone Microenvironment Cells Tumoral or Not?.. <i>Blood</i> , 2009, 114, 1816-1816.	0.6	0
106	HOXB7 Is Critically Involved in Multiple Myeloma-Induced Angiogenic Switch.. <i>Blood</i> , 2009, 114, 125-125.	0.6	0
107	An integrative genomic approach reveals coordinated expression of intronic miR-335, miR-342, and miR-561 with deregulated host genes in multiple myeloma. <i>BMC Medical Genomics</i> , 2008, 1, 37.	0.7	104
108	Molecular and transcriptional characterization of 17p loss in B-cell chronic lymphocytic leukemia. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 781-793.	1.5	59

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109	Immunoreactivity for cyclin D1 is a reliable marker of gene aberration in plasma cell myeloma but does not specify patients prognosis. <i>Leukemia Research</i> , 2008, 32, 1628-1632.	0.4	1
110	Genome-Wide DNA Copy Number Analysis by SNP Arrays of B-Cell Chronic Lymphocytic Leukemia: Correlation with Known Biological and Molecular Prognostic Markers.. <i>Blood</i> , 2008, 112, 1061-1061.	0.6	0
111	Integrative Genomic Approach Identifies Deregulated MicroRNAs in Human Myeloma Cell Lines.. <i>Blood</i> , 2008, 112, 1684-1684.	0.6	0
112	HOXB7 Overexpression in Mesenchymal Cells Stimulates the Production of Pro-Angiogenic Molecules: Potential Role in Multiple Myeloma Associated Angiogenesis. <i>Blood</i> , 2008, 112, 2743-2743.	0.6	0
113	Bone Microenvironment Cells Show a Different Pattern of Gene Expression Profiling in Relationship with the Presence of Osteolytic Bone Lesions in Multiple Myeloma Patients. <i>Blood</i> , 2008, 112, 2740-2740.	0.6	0
114	Integrative genomic analysis reveals distinct transcriptional and genetic features associated with chromosome 13 deletion in multiple myeloma. <i>Haematologica</i> , 2007, 92, 56-65.	1.7	34
115	Relevance of Ras gene mutations in the context of the molecular heterogeneity of multiple myeloma. <i>Hematological Oncology</i> , 2007, 25, 6-10.	0.8	8
116	Molecular characterization of human multiple myeloma cell lines by integrative genomics: Insights into the biology of the disease. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 226-238.	1.5	62
117	Molecular and transcriptional characterization of the novel 17p11.2â€p12 amplicon in multiple myeloma. <i>Genes Chromosomes and Cancer</i> , 2007, 46, 1109-1118.	1.5	20
118	Transcriptional features of multiple myeloma patients with chromosome 1q gain. <i>Leukemia</i> , 2007, 21, 1113-1116.	3.3	45
119	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. <i>British Journal of Haematology</i> , 2007, 136, 565-573.	1.2	66
120	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.. <i>Blood</i> , 2007, 110, 3513-3513.	0.6	0
121	Effect of Dioxin (TCDD) on Gene Transcription of Human CD34+ Hematopoietic Cells.. <i>Blood</i> , 2007, 110, 4033-4033.	0.6	0
122	Molecular and Transcriptional Characterization of the Novel 17p11.2-p12 Chromosome Amplification in Multiple Myeloma.. <i>Blood</i> , 2007, 110, 2486-2486.	0.6	0
123	Genome-Wide Analysis of DNA Copy Number in Multiple Myeloma Using High-Density SNP Arrays Reveals Clustering Patterns with Distinct Transcriptional Profiles.. <i>Blood</i> , 2007, 110, 2482-2482.	0.6	0
124	The prevalence and clinical implications of c-kit expression in plasma cell myeloma. <i>Histopathology</i> , 2006, 48, 529-535.	1.6	14
125	Functional validation of the anaplastic lymphoma kinase signature identifies CEBPB and Bcl2A1 as critical target genes. <i>Journal of Clinical Investigation</i> , 2006, 116, 3171-3182.	3.9	139
126	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.. <i>Blood</i> , 2006, 108, 3437-3437.	0.6	0

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127	Identification of Specific Transcriptional Patterns Associated with Hyperdiploidy in Multiple Myeloma.. Blood, 2006, 108, 3412-3412.	0.6	0
128	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
129	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
130	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
131	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
132	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
133	Different Gene Expression Profiles of CD133+ Cells from Cord Blood and Mobilized Peripheral Blood.. Blood, 2005, 106, 4210-4210.	0.6	1
134	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
135	Characterization of Oncogene Dysregulation in Multiple Myeloma by Combined FISH and DNA Microarray Analyses.. Blood, 2004, 104, 4844-4844.	0.6	0