List of Publications by Year in descending order

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Κλτιλ Τοροερτι

#	Article	IF	CITATIONS
1	DIS3 mutations in multiple myeloma impact the transcriptional signature and clinical outcome. Haematologica, 2022, 107, 921-932.	1.7	14
2	Impact on thrombotic risk of canonical and atypical CALR mutations in essential thrombocythemia. A single-center cohort study. Thrombosis Research, 2022, 210, 67-69.	0.8	3
3	Halting the FGF/FGFR axis leads to antitumor activity in Waldenström macroglobulinemia by silencing MYD88. Blood, 2021, 137, 2495-2508.	0.6	4
4	Epigenetic Regulation of Mitochondrial Quality Control Genes in Multiple Myeloma: A Sequenom MassARRAY Pilot Investigation on HMCLs. Journal of Clinical Medicine, 2021, 10, 1295.	1.0	5
5	Specific targeting of the KRAS mutational landscape in myeloma as a tool to unveil the elicited antitumor activity. Blood, 2021, 138, 1705-1720.	0.6	10
6	miR-22 Modulates Lenalidomide Activity by Counteracting MYC Addiction in Multiple Myeloma. Cancers, 2021, 13, 4365.	1.7	13
7	Functional Impact of Genomic Complexity on the Transcriptome of Multiple Myeloma. Clinical Cancer Research, 2021, 27, 6479-6490.	3.2	9
8	Transcriptomic Analysis in Multiple Myeloma and Primary Plasma Cell Leukemia with t(11;14) Reveals Different Expression Patterns with Biological Implications in Venetoclax Sensitivity. Cancers, 2021, 13, 4898.	1.7	8
9	Bioinformatics Pipeline to Analyze IncRNA Arrays. Methods in Molecular Biology, 2021, 2348, 45-53.	0.4	1
10	Chronic lymphocytic leukemia cells impair osteoblastogenesis and promote osteoclastogenesis: role of TNFα, IL-6 and IL-11 cytokines. Haematologica, 2021, 106, 2598-2612.	1.7	9
11	Oleil Hydroxytyrosol (HTOL) Exerts Anti-Myeloma Activity by Antagonizing Key Survival Pathways in Malignant Plasma Cells. International Journal of Molecular Sciences, 2021, 22, 11639.	1.8	4
12	Dissecting the Biological Relevance and Clinical Impact of IncRNA MIAT in Multiple Myeloma. Cancers, 2021, 13, 5518.	1.7	0
13	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
14	Cancer Associated Fibroblasts and Senescent Thyroid Cells in the Invasive Front of Thyroid Carcinoma. Cancers, 2020, 12, 112.	1.7	30
15	Amino acid depletion triggered by ÊŸ-asparaginase sensitizes MM cells to carfilzomib by inducing mitochondria ROS-mediated cell death. Blood Advances, 2020, 4, 4312-4326.	2.5	19
16	Exploiting MYC-induced PARPness to target genomic instability in multiple myeloma. Haematologica, 2020, 106, 185-195.	1.7	33
17	COPZ1 depletion in thyroid tumor cells triggers type I IFN response and immunogenic cell death. Cancer Letters, 2020, 476, 106-119.	3.2	7
18	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

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19	Expression Pattern and Biological Significance of the IncRNA ST3GAL6-AS1 in Multiple Myeloma. Cancers, 2020, 12, 782.	1.7	6
20	RNA Regulator of Lipogenesis (RROL) Is a Novel Lncrna Mediating Protein-Protein Interaction at Gene Regulatory Loci Driving Lipogenic Programs in Multiple Myeloma. Blood, 2020, 136, 20-21.	0.6	0
21	Revealing Transcriptome Deregulation upon Genomic Complexity in Multiple Myeloma. Blood, 2020, 136, 3-4.	0.6	0
22	miR-22 suppresses DNA ligase III addiction in multiple myeloma. Leukemia, 2019, 33, 487-498.	3.3	39
23	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
24	A GBM-like V-ATPase signature directs cell-cell tumor signaling and reprogramming via large oncosomes. EBioMedicine, 2019, 41, 225-235.	2.7	25
25	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
26	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
27	IDH2 inhibition enhances proteasome inhibitor responsiveness in hematological malignancies. Blood, 2019, 133, 156-167.	0.6	40
28	PARP1-Mediated Alt-NHEJ Repair Is a Therapeutic Target in Multiple Myeloma. Blood, 2019, 134, 3107-3107.	0.6	0
29	Global methylation patterns in primary plasma cell leukemia. Leukemia Research, 2018, 73, 95-102.	0.4	13
30	A compendium of long non-coding RNAs transcriptional fingerprint in multiple myeloma. Scientific Reports, 2018, 8, 6557.	1.6	34
31	Tryptophan Deprivation Promotes an Adaptive Response and Contributes to Bioenergetics in Multiple Myeloma. Blood, 2018, 132, 4511-4511.	0.6	8
32	Activation of the Non-Canonical Estrogen Receptor Gper As a Novel Therapeutic Strategy Against WaldenstrÃf¶m Macroglobulinemia. Blood, 2018, 132, 1585-1585.	0.6	0
33	<i>IL21R</i> expressing CD14 ⁺ CD16 ⁺ monocytes expand in multiple myeloma patients leading to increased osteoclasts. Haematologica, 2017, 102, 773-784.	1.7	36
34	Targeting COPZ1 non-oncogene addiction counteracts the viability of thyroid tumor cells. Cancer Letters, 2017, 410, 201-211.	3.2	15
35	EphA3 targeting reduces in vitro adhesion and invasion and in vivo growth and angiogenesis of multiple myeloma cells. Cellular Oncology (Dordrecht), 2017, 40, 483-496.	2.1	15
36	Cutaneous localization in multiple myeloma in the context of bortezomib-based treatment: how do myeloma cells escape from the bone marrow to the skin?. International Journal of Hematology, 2017, 105, 104-108.	0.7	14

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37	Disentangling the microRNA regulatory <i>milieu</i> 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
38	In Silico Characterization of miRNA and Long Non-Coding RNA Interplay in Multiple Myeloma. Genes, 2016, 7, 107.	1.0	17
39	Distinct lncRNA transcriptional fingerprints characterize progressive stages of multiple myeloma. Oncotarget, 2016, 7, 14814-14830.	0.8	79
40	Gene expression profiling reveals novel protective effects of Aminaphtone on ECV304 endothelial cells. European Journal of Pharmacology, 2016, 782, 59-69.	1.7	7
41	Primary Plasma Cell Leukemia: Identity Card 2016. Current Treatment Options in Oncology, 2016, 17, 19.	1.3	17
42	Dependence on glutamine uptake and glutamine addiction characterize myeloma cells: a new attractive target. Blood, 2016, 128, 667-679.	0.6	128
43	Compendium of <i><scp>FAM</scp>46C</i> gene mutations in plasma cell dyscrasias. British Journal of Haematology, 2016, 174, 642-645.	1.2	34
44	Prospective validation of predictive value of abdominal computed tomography scan on time to first treatment in Rai O chronic lymphocytic leukemia patients: results of the multicenter Oâ€ <scp>CLL</scp> 1â€ <scp>GISL</scp> study. European Journal of Haematology, 2016, 96, 36-45.	1.1	7
45	Identification of a new subclass of ALK-negative ALCL expressing aberrant levels of ERBB4 transcripts. Blood, 2016, 127, 221-232.	0.6	97
46	Time-course gene expression data on the transcriptional effects of Aminaphtone on ECV304 endothelial cells. Data in Brief, 2016, 8, 836-850.	0.5	3
47	Primary plasma cell leukemia 2.0: advances in biology and clinical management. Expert Review of Hematology, 2016, 9, 1063-1073.	1.0	15
48	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
49	Multiple myeloma-derived Jagged ligands increases autocrine and paracrine interleukin-6 expression in bone marrow niche. Oncotarget, 2016, 7, 56013-56029.	0.8	34
50	Molecular spectrum of <i>TP53</i> mutations in plasma cell dyscrasias by next generation sequencing: an Italian cohort study and overview of the literature. Oncotarget, 2016, 7, 21353-21361.	0.8	40
51	miR-451a is underexpressed and targets AKT/mTOR pathway in papillary thyroid carcinoma. Oncotarget, 2016, 7, 12731-12747.	0.8	77
52	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
53	Whole-exome sequencing of primary plasma cell leukemia discloses heterogeneous mutational patterns. Oncotarget, 2015, 6, 17543-17558.	0.8	55
54	The ribonuclease DIS3 promotes let-7 miRNA maturation by degrading the pluripotency factor LIN28B mRNA. Nucleic Acids Research, 2015, 43, 5182-5193.	6.5	31

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55	ls ZAP70 still a key prognostic factor in early stage chronic lymphocytic leukaemia? Results of the analysis from a prospective multicentre observational study. British Journal of Haematology, 2015, 168, 455-459.	1.2	9
56	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
57	A compendium of <i>DIS3</i> mutations and associated transcriptional signatures in plasma cell dyscrasias. Oncotarget, 2015, 6, 26129-26141.	0.8	40
58	ldentification of thyroid tumor cell vulnerabilities through a siRNA-based functional screening. Oncotarget, 2015, 6, 34629-34648.	0.8	26
59	Molecular events underlying interleukinâ€6 independence in a subclone of the CMAâ€03 multiple myeloma cell line. Genes Chromosomes and Cancer, 2014, 53, 154-167.	1.5	6
60	Lenalidomide and low-dose dexamethasone for newly diagnosed primary plasma cell leukemia. Leukemia, 2014, 28, 222-225.	3.3	77
61	Notch signaling drives multiple myeloma induced osteoclastogenesis. Oncotarget, 2014, 5, 10393-10406.	0.8	45
62	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
63	Genomeâ€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
64	Single-agent Smac-mimetic compounds induce apoptosis in B chronic lymphocytic leukaemia (B-CLL). Leukemia Research, 2013, 37, 809-815.	0.4	11
65	Improved risk stratification in myeloma using a micro <scp>RNA</scp> â€based classifier. British Journal of Haematology, 2013, 162, 348-359.	1.2	53
66	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
67	Biological and Clinical Relevance of miRNA Expression Signatures in Primary Plasma Cell Leukemia. Clinical Cancer Research, 2013, 19, 3130-3142.	3.2	86
68	The HDAC inhibitor Givinostat modulates the hematopoietic transcription factors NFE2 and C-MYB in JAK2V617F myeloproliferative neoplasm cells. Experimental Hematology, 2012, 40, 634-645.e10.	0.2	36
69	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
70	Canonical and noncanonical Hedgehog pathway in the pathogenesis of multiple myeloma. Blood, 2012, 120, 5002-5013.	0.6	121
71	HOXB7 expression by myeloma cells regulates their pro-angiogenic properties in multiple myeloma patients. Leukemia, 2011, 25, 527-537.	3.3	39
72	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

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73	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
74	Dioxin exposure of human CD34+ hemopoietic cells induces gene expression modulation that recapitulates its in vivo clinical and biological effects. Toxicology, 2011, 283, 18-23.	2.0	12
75	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
76	Impact of Host Genes and Strand Selection on miRNA and miRNA* Expression. PLoS ONE, 2011, 6, e23854.	1.1	37
77	Pleiotropic anti-myeloma activity of ITF2357: inhibition of interleukin-6 receptor signaling and repression of miR-19a and miR-19b. Haematologica, 2010, 95, 260-269.	1.7	36
78	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
79	The clinical and biological features of a series of immunophenotypic variant of Bâ€CLL. European Journal of Haematology, 2010, 85, 120-129.	1.1	13
80	Bone osteoblastic and mesenchymal stromal cells lack primarily tumoral features in multiple myeloma patients. Leukemia, 2010, 24, 1368-1370.	3.3	8
81	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
82	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
83	Effects of enzastaurin, alone or in combination, on signaling pathway controlling growth and survival of B-cell lymphoma cell lines. Leukemia and Lymphoma, 2010, 51, 671-679.	0.6	14
84	Does Adiponectin Act as an Antiangiogenic Factor in B-Cell Chronic Lymphocytic Leukemia?. Advances in Hematology, 2009, 2009, 1-6.	0.6	3
85	Gene Expression Profiling of Bone Marrow Endothelial Cells in Patients with Multiple Myeloma. Clinical Cancer Research, 2009, 15, 5369-5378.	3.2	91
86	Molecular targeting of the PKCâ€ <i>β</i> inhibitor enzastaurin (LY317615) in multiple myeloma involves a coordinated downregulation of MYC and IRF4 expression. Hematological Oncology, 2009, 27, 23-30.	0.8	20
87	Gene array profile identifies collagen type XV as a novel human osteoblastâ€secreted matrix protein. Journal of Cellular Physiology, 2009, 220, 401-409.	2.0	30
88	Integrative highâ€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
89	A SNP microarray and FISHâ€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
90	<i>In vitro</i> antiâ€leukaemia activity of sphingosine kinase inhibitor. British Journal of Haematology, 2009, 144, 350-357.	1.2	25

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91	Definition of progression risk based on combinations of cellular and molecular markers in patients with Binet stage A chronic lymphocytic leukaemia. British Journal of Haematology, 2009, 146, 44-53.	1.2	50
92	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
93	CRITICAL ANALYSIS OF TRANSCRIPTIONAL AND POST-TRANSCRIPTIONAL REGULATORY NETWORKS IN MULTIPLE MYELOMA. , 2009, , 397-408.		5
94	Prognostic relevance of serum levels and cellular expression of adiponectin in B-cell chronic lymphocytic leukemia. International Journal of Hematology, 2008, 88, 374-380.	0.7	12
95	Molecular and transcriptional characterization of 17p loss in Bâ€ɛell chronic lymphocytic leukemia. Genes Chromosomes and Cancer, 2008, 47, 781-793.	1.5	59
96	Serum thrombopoietin compared with ZAP-70 and immunoglobulin heavy-chain gene mutation status as a predictor of time to first treatment in early chronic lymphocytic leukemia. Leukemia and Lymphoma, 2008, 49, 62-67.	0.6	4
97	Biological and Clinical Relevance of Surrogate Markers of IgVH Mutational Status in B-Cell Chronic Lymphocytic Leukemia Blood, 2008, 112, 1062-1062.	0.6	0
98	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
99	Molecular and transcriptional characterization of the novel 17p11.2â€p12 amplicon in multiple myeloma. Genes Chromosomes and Cancer, 2007, 46, 1109-1118.	1.5	20
100	Transcriptional features of multiple myeloma patients with chromosome 1q gain. Leukemia, 2007, 21, 1113-1116.	3.3	45
101	Upregulation of translational machinery and distinct genetic subgroups characterise hyperdiploidy in multiple myeloma. British Journal of Haematology, 2007, 136, 565-573.	1.2	66
102	Molecular and Transcriptional Characterization of the Novel 17p11.2-p12 Chromosome Amplification in Multiple Myeloma Blood, 2007, 110, 2486-2486.	0.6	0
103	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
104	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
105	Molecular and biological characterization of three novel interleukin-6-dependent human myeloma cell lines. Haematologica, 2005, 90, 1541-8.	1.7	11