Jerome Moreaux

List of Publications by Year
in descending order

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145 papers	5,194 citations	81839 39 h-index	98753 67 g-index
153 all docs	153 docs citations	153 times ranked	6579 citing authors

#	Article	IF	Citations
1	BAFF and APRIL protect myeloma cells from apoptosis induced by interleukin 6 deprivation and dexamethasone. Blood, 2004, 103, 3148-3157.	0.6	488
2	The level of TACI gene expression in myeloma cells is associated with a signature of microenvironment dependence versus a plasmablastic signature. Blood, 2005, 106, 1021-1030.	0.6	245
3	Embryonic stem cell markers expression in cancers. Biochemical and Biophysical Research Communications, 2009, 383, 157-162.	1.0	219
4	CD200 is a new prognostic factor in multiple myeloma. Blood, 2006, 108, 4194-4197.	0.6	205
5	Survival and Proliferation Factors of Normal and Malignant Plasma Cells. International Journal of Hematology, 2003, 78, 106-113.	0.7	195
6	Proliferation is a central independent prognostic factor and target for personalized and risk-adapted treatment in multiple myeloma. Haematologica, 2011, 96, 87-95.	1.7	188
7	The role of IGF-1 as a major growth factor for myeloma cell lines and the prognostic relevance of the expression of its receptor. Blood, 2009, 113, 4614-4626.	0.6	150
8	A high-risk signature for patients with multiple myeloma established from the molecular classification of human myeloma cell lines. Haematologica, 2011, 96, 574-582.	1.7	141
9	Induction of angiogenesis by normal and malignant plasma cells. Blood, 2009, 114, 128-143.	0.6	127
10	Overexpression of Claspin and Timeless protects cancer cells from replication stress in a checkpoint-independent manner. Nature Communications, 2019, 10, 910.	5.8	105
11	APRIL and TACI interact with syndecanâ€1 on the surface of multiple myeloma cells to form an essential survival loop. European Journal of Haematology, 2009, 83, 119-129.	1.1	98
12	Expression of EGF-family receptors and amphiregulin in multiple myeloma. Amphiregulin is a growth factor for myeloma cells. Oncogene, 2005, 24, 3512-3524.	2.6	97
13	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. Blood, 2009, 113, 4331-4340.	0.6	97
14	CD200: A putative therapeutic target in cancer. Biochemical and Biophysical Research Communications, 2008, 366, 117-122.	1.0	96
15	Heparan sulphate proteoglycans are essential for the myeloma cell growth activity of EGF-family ligands in multiple myeloma. Oncogene, 2006, 25, 7180-7191.	2.6	86
16	Clinical and prognostic role of annexin A2 in multiple myeloma. Blood, 2012, 120, 1087-1094.	0.6	81
17	EZH2 in normal hematopoiesis and hematological malignancies. Oncotarget, 2016, 7, 2284-2296.	0.8	77
18	Bone morphogenic protein 6: a member of a novel class of prognostic factors expressed by normal and malignant plasma cells inhibiting proliferation and angiogenesis. Oncogene, 2009, 28, 3866-3879.	2.6	71

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19	Atacicept in relapsed/refractory multiple myeloma or active WaldenstrÃ¶m's macroglobulinemia: a phase I study. British Journal of Cancer, 2009, 101, 1051-1058.	2.9	71
20	MMSET is overexpressed in cancers: Link with tumor aggressiveness. Biochemical and Biophysical Research Communications, 2009, 379, 840-845.	1.0	69
21	SULFs in human neoplasia: implication as progression and prognosis factors. Journal of Translational Medicine, 2011, 9, 72.	1.8	68
22	RECQ1 helicase is involved in replication stress survival and drug resistance in multiple myeloma. Leukemia, 2017, 31, 2104-2113.	3.3	68
23	STEAP1 is overexpressed in cancers: A promising therapeutic target. Biochemical and Biophysical Research Communications, 2012, 429, 148-155.	1.0	67
24	Chetomin, targeting HIF-1Î±/p300 complex, exhibits antitumour activity in multiple myeloma. British Journal of Cancer, 2016, 114, 519-523.	2.9	64
25	APRIL is overexpressed in cancer: link with tumor progression. BMC Cancer, 2009, 9, 83.	1.1	63
26	Growth factors in multiple myeloma: a comprehensive analysis of their expression in tumor cells and bone marrow environment using Affymetrix microarrays. BMC Cancer, 2010, 10, 198.	1.1	60
27	Osteoclast-gene expression profiling reveals osteoclast-derived CCR2 chemokines promoting myeloma cell migration. Blood, 2011, 117, 1280-1290.	0.6	60
28	Microarray-based understanding of normal and malignant plasma cells. Immunological Reviews, 2006, 210, 86-104.	2.8	56
29	Lymphocytes of dogs immunised with purified excreted-secreted antigens of Leishmania infantum co-incubated with Leishmania infected macrophages produce IFN gamma resulting in nitric oxide-mediated amastigote apoptosis. Veterinary Immunology and Immunopathology, 2005, 106, 247-257.	0.5	55
30	Targeting NF-ÎºB pathway with an IKK2 inhibitor induces inhibition of multiple myeloma cell growth. British Journal of Haematology, 2007, 138, 160-168.	1.2	55
31	DNA repair pathways in human multiple myeloma. Cell Cycle, 2013, 12, 2760-2773.	1.3	52
32	Gene expression-based prediction of myeloma cell sensitivity to histone deacetylase inhibitors. British Journal of Cancer, 2013, 109, 676-685.	2.9	50
33	Comprehensive characterization of the mutational landscape in multiple myeloma cell lines reveals potential drivers and pathways associated with tumor progression and drug resistance. Theranostics, 2019, 9, 540-553.	4.6	49
34	Myeloid-derived suppressor cells induce multiple myeloma cell survival by activating the AMPK pathway. Cancer Letters, 2019, 442, 233-241.	3.2	49
35	Development of Gene Expressionâ€"Based Score to Predict Sensitivity of Multiple Myeloma Cells to DNA Methylation Inhibitors. Molecular Cancer Therapeutics, 2012, 11, 2685-2692.	1.9	47
36	Inhibition of Ataxia-Telangiectasia Mutated and RAD3-Related (<i>ATR</i>) Overcomes Oxaliplatin Resistance and Promotes Antitumor Immunity in Colorectal Cancer. Cancer Research, 2019, 79, 2933-2946.	0.4	46

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37	TACI expression is associated with a mature bone marrow plasma cell signature and C-MAF overexpression in human myeloma cell lines. Haematologica, 2007, 92, 803-811.	1.7	45
38	Genes with a spike expression are clustered in chromosome (sub)bands and spike (sub)bands have a powerful prognostic value in patients with multiple myeloma. Haematologica, 2012, 97, 622-630.	1.7	44
39	Discovery of Candidate DNA Methylation Cancer Driver Genes. Cancer Discovery, 2021, 11, 2266-2281.	7.7	42
40	A DNA repair pathway score predicts survival in human multiple myeloma: the potential for therapeutic strategy. Oncotarget, 2014, 5, 2487-2498.	0.8	42
41	Extracellular S100A9 Protein in Bone Marrow Supports Multiple Myeloma Survival by Stimulating Angiogenesis and Cytokine Secretion. Cancer Immunology Research, 2017, 5, 839-846.	1.6	41
42	miRNAs in multiple myeloma - a survival relevant complex regulator of gene expression. Oncotarget, 2015, 6, 39165-39183.	0.8	40
43	Global miRNA expression analysis identifies novel key regulators of plasma cell differentiation and malignant plasma cell. Nucleic Acids Research, 2017, 45, 5639-5652.	6.5	33
44	EZH2 is overexpressed in transitional preplasmablasts and is involved in human plasma cell differentiation. Leukemia, 2019, 33, 2047-2060.	3.3	33
45	Kinome expression profiling to target new therapeutic avenues in multiple myeloma. Haematologica, 2020, 105, 784-795.	1.7	33
46	Inhibiting the anaphase promoting complex/cyclosome induces a metaphase arrest and cell death in multiple myeloma cells. Oncotarget, 2016, 7, 4062-4076.	0.8	33
47	PRC2 targeting is a therapeutic strategy for EZ score defined high-risk multiple myeloma patients and overcome resistance to IMiDs. Clinical Epigenetics, 2018, 10, 121.	1.8	32
48	DNMTi/HDACi combined epigenetic targeted treatment induces reprogramming of myeloma cells in the direction of normal plasma cells. British Journal of Cancer, 2018, 118, 1062-1073.	2.9	30
49	RNA-sequencing data-driven dissection of human plasma cell differentiation reveals new potential transcription regulators. Leukemia, 2021, 35, 1451-1462.	3.3	30
50	<i>CD24</i>, <i>CD27</i>, <i>CD36</i> and <i>CD302</i> gene expression for outcome prediction in patients with multiple myeloma. Oncotarget, 2017, 8, 98931-98944.	0.8	29
51	The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. Haematologica, 2015, 100, e110-e113.	1.7	27
52	Loss of RASSF4 Expression in Multiple Myeloma Promotes RAS-Driven Malignant Progression. Cancer Research, 2018, 78, 1155-1168.	0.4	27
53	Kruppel-like factor 4 blocks tumor cell proliferation and promotes drug resistance in multiple myeloma. Haematologica, 2013, 98, 1442-1449.	1.7	25
54	Antioxidant Defenses Confer Resistance to High Dose Melphalan in Multiple Myeloma Cells. Cancers, 2019, 11, 439.	1.7	25

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55	<i>In vivo</i>treatment with epigenetic modulating agents induces transcriptional alterations associated with prognosis and immunomodulation in multiple myeloma. Oncotarget, 2015, 6, 3319-3334.	0.8	25
56	Critical role of the NOTCH ligand JAG2 in self-renewal of myeloma cells. Blood Cells, Molecules, and Diseases, 2012, 48, 247-253.	0.6	24
57	Inhibition of DEPDC1A, a Bad Prognostic Marker in Multiple Myeloma, Delays Growth and Induces Mature Plasma Cell Markers in Malignant Plasma Cells. PLoS ONE, 2013, 8, e62752.	1.1	24
58	Tumor-associated neutrophils correlate with poor prognosis in diffuse large B-cell lymphoma patients. Blood Cancer Journal, 2018, 8, 66.	2.8	24
59	Input of DNA Microarrays to Identify Novel Mechanisms in Multiple Myeloma Biology and Therapeutic Applications. Clinical Cancer Research, 2007, 13, 7289-7295.	3.2	23
60	The hydroxymethylome of multiple myeloma identifies FAM72D as a 1q21 marker linked to proliferation. Haematologica, 2020, 105, 774-783.	1.7	23
61	Drug metabolism and clearance system in tumor cells of patients with multiple myeloma. Oncotarget, 2015, 6, 6431-6447.	0.8	23
62	Development of gene expression-based risk score in cytogenetically normal acute myeloid leukemia patients. Oncotarget, 2012, 3, 824-832.	0.8	22
63	Characterization of human FCRL4-positive B cells. PLoS ONE, 2017, 12, e0179793.	1.1	21
64	MYEOV is a prognostic factor in multiple myeloma. Experimental Hematology, 2010, 38, 1189-1198.e3.	0.2	20
65	Gene expression-based risk score in diffuse large B-cell lymphoma. Oncotarget, 2012, 3, 1700-1710.	0.8	20
66	Identification of a 20-Gene Expression-Based Risk Score as a Predictor of Clinical Outcome in Chronic Lymphocytic Leukemia Patients. BioMed Research International, 2014, 2014, 1-10.	0.9	19
67	G9a/GLP targeting in MM promotes autophagy-associated apoptosis and boosts proteasome inhibitorâ€“mediated cell death. Blood Advances, 2021, 5, 2325-2338.	2.5	19
68	Differential effects of lenalidomide during plasma cell differentiation. Oncotarget, 2016, 7, 28096-28111.	0.8	19
69	Identification of Pluripotent and Adult Stem Cell Genes Unrelated to Cell Cycle and Associated with Poor Prognosis in Multiple Myeloma. PLoS ONE, 2012, 7, e42161.	1.1	18
70	Expression and role of RIP140/NRIP1 in chronic lymphocytic leukemia. Journal of Hematology and Oncology, 2015, 8, 20.	6.9	17
71	RECQ helicases are deregulated in hematological malignancies in association with a prognostic value. Biomarker Research, 2016, 4, 3.	2.8	16
72	Dihydropyrimidinase protects from DNA replication stress caused by cytotoxic metabolites. Nucleic Acids Research, 2020, 48, 1886-1904.	6.5	16

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73	Nucleotide excision DNA repair pathway as a therapeutic target in patients with high-risk diffuse large B cell lymphoma. Cell Cycle, 2013, 12, 1811-1812.	1.3	15
74	Identifying high-risk adult AML patients: epigenetic and genetic risk factors and their implications for therapy. Expert Review of Hematology, 2016, 9, 351-360.	1.0	15
75	Treatment May Be Harmful: Mechanisms/Prediction/Prevention of Drug-Induced DNA Damage and Repair in Multiple Myeloma. Frontiers in Genetics, 2019, 10, 861.	1.1	15
76	<scp>DNA</scp> methylation score is predictive of myeloma cell sensitivity to 5â€azacitidine. British Journal of Haematology, 2014, 164, 613-616.	1.2	14
77	Clinical Correlations of Polycomb Repressive Complex 2 in Different Tumor Types. Cancers, 2021, 13, 3155.	1.7	14
78	Targeting Cellular Iron Homeostasis with Ironomycin in Diffuse Large B-cell Lymphoma. Cancer Research, 2022, 82, 998-1012.	0.4	14
79	Residual malignant and normal plasma cells shortly after high dose melphalan and stem cell transplantation. Highlight of a putative therapeutic window in Multiple Myeloma?. Oncotarget, 2012, 3, 1335-1347.	0.8	13
80	Identification and characterization of new Leishmania promastigote surface antigens, LaPSA-38S and LiPSA-50S, as major immunodominant excreted/secreted components of L. amazonensis and L. infantum. Infection, Genetics and Evolution, 2014, 24, 1-14.	1.0	12
81	Factors influencing extramedullary relapse after allogeneic transplantation for multiple myeloma. Blood Cancer Journal, 2015, 5, e341-e341.	2.8	12
82	<scp>DNA</scp> repair in diffuse large Bâ€cell lymphoma: a molecular portrait. British Journal of Haematology, 2015, 169, 296-299.	1.2	12
83	The anaphase-promoting complex/cyclosome: a new promising target in diffuse large B-cell lymphoma and mantle cell lymphoma. British Journal of Cancer, 2019, 120, 1137-1146.	2.9	12
84	A Phase I/II Study of Atacicept (TACI-Ig) To Neutralize APRIL and BLyS in Patients with Refractory or Relapsed Multiple Myeloma (MM) or Active Previously Treated Waldenstromâ€™s Macroglobulinemia (WM).. Blood, 2006, 108, 3578-3578.	0.6	12
85	The Glycome of Normal and Malignant Plasma Cells. PLoS ONE, 2013, 8, e83719.	1.1	12
86	Forced KLF4 expression increases the generation of mature plasma cells and uncovers a network linked with plasma cell stage. Cell Cycle, 2016, 15, 1919-1928.	1.3	11
87	An epigenetic regulator-related score (EpiScore) predicts survival in patients with diffuse large B cell lymphoma and identifies patients who may benefit from epigenetic therapy. Oncotarget, 2018, 9, 19079-19099.	0.8	11
88	Physiological and druggable skipping of immunoglobulin variable exons in plasma cells. Cellular and Molecular Immunology, 2019, 16, 810-819.	4.8	11
89	Targeting the methyltransferase SETD8 impairs tumor cell survival and overcomes drug resistance independently of p53 status in multiple myeloma. Clinical Epigenetics, 2021, 13, 174.	1.8	11
90	Hypoxia favors the generation of human plasma cells. Cell Cycle, 2017, 16, 1104-1117.	1.3	10

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91	Comprehensive characterization of the epigenetic landscape in Multiple Myeloma. Theranostics, 2022, 12, 1715-1729.	4.6	10
92	Efficient transduction of healthy and malignant plasma cells by lentiviral vectors pseudotyped with measles virus glycoproteins. Leukemia, 2012, 26, 1663-1670.	3.3	9
93	Automated and simplified identification of normal and abnormal plasma cells in Multiple Myeloma by flow cytometry. Cytometry Part B - Clinical Cytometry, 2018, 94, 484-492.	0.7	9
94	Role of Polycomb Complexes in Normal and Malignant Plasma Cells. International Journal of Molecular Sciences, 2020, 21, 8047.	1.8	9
95	The microenvironment of DLBCL is characterized by noncanonical macrophages recruited by tumor-derived CCL5. Blood Advances, 2021, 5, 4338-4351.	2.5	9
96	New prognostic markers, determined using gene expression analyses, reveal two distinct subtypes of chronic myelomonocytic leukaemia patients. British Journal of Haematology, 2012, 157, 347-356.	1.2	8
97	BrdU incorporation in multiparameter flow cytometry: A new cell cycle assessment approach in multiple myeloma. Cytometry Part B - Clinical Cytometry, 2019, 96, 209-214.	0.7	8
98	Targeting EZH2 in Multiple Myeloma Could be Promising for a Subgroup of MM Patients in Combination with IMiDs. Blood, 2016, 128, 311-311.	0.6	8
99	Prospective target assessment and multimodal prediction of survival for personalized and risk-adapted treatment strategies in multiple myeloma in the GMMG-MM5 multicenter trial. Journal of Hematology and Oncology, 2019, 12, 65.	6.9	7
100	Maternal embryonic leucine zipper kinase is a novel target for diffuse large B cell lymphoma and mantle cell lymphoma. Blood Cancer Journal, 2019, 9, 87.	2.8	7
101	A Retrospective Comparison of DLI and gDLI for Post-Transplant Treatment. Journal of Clinical Medicine, 2020, 9, 2204.	1.0	7
102	Characterization of immortalized human islet stromal cells reveals a MSC-like profile with pancreatic features. Stem Cell Research and Therapy, 2020, 11, 158.	2.4	7
103	Transcription/Replication Conflicts in Tumorigenesis and Their Potential Role as Novel Therapeutic Targets in Multiple Myeloma. Cancers, 2021, 13, 3755.	1.7	7
104	NPM1 is overexpressed in hyperdiploid multiple myeloma due to a gain of chromosome 5 but is not delocalized to the cytoplasm. Genes Chromosomes and Cancer, 2010, 49, 333-341.	1.5	6
105	Phenotypic Characterization of Diffuse Large B-Cell Lymphoma Cells and Prognostic Impact. Journal of Clinical Medicine, 2019, 8, 1074.	1.0	6
106	Immunotherapy perspectives in the new era of B-cell editing. Blood Advances, 2021, 5, 1770-1779.	2.5	6
107	RNA-Sequencing-Based Transcriptomic Score with Prognostic and Theranostic Values in Multiple Myeloma. Journal of Personalized Medicine, 2021, 11, 988.	1.1	6
108	Analysis of Global Gene Expression Profiles. Methods in Molecular Biology, 2018, 1792, 157-166.	0.4	5

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109	PIM2 kinase has a pivotal role in plasmablast generation and plasma cell survival, opening up novel treatment options in myeloma. Blood, 2022, 139, 2316-2337.	0.6	5
110	In Vitro Differentiation Model of Human Normal Memory B Cells to Long-lived Plasma Cells. Journal of Visualized Experiments, 2019, , .	0.2	3
111	DNA Repair Expression Profiling to Identify High-Risk Cytogenetically Normal Acute Myeloid Leukemia and Define New Therapeutic Targets. Cancers, 2020, 12, 2874.	1.7	3
112	Inhibition of SUV39H Methyltransferase As a Potent Therapeutic Target in Multiple Myeloma. Blood, 2015, 126, 1771-1771.	0.6	3
113	The role of fluorescence in situ hybridization and gene expression profiling in myeloma risk stratification. Srpski Arhiv Za Celokupno Lekarstvo, 2011, 139, 84-89.	0.1	3
114	Inhibition of the Protein Arginine Methyltransferase PRMT5 in High-Risk Multiple Myeloma as a Novel Treatment Approach. Frontiers in Cell and Developmental Biology, 0, 10, .	1.8	3
115	RASSF4 functions as a tumor suppressor in Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e227.	0.2	1
116	PO-481 Alteration in epigenetic-related genes and histones modifications levels revealed as a potential resistance factor to oxaliplatin in colorectal cancer cells. ESMO Open, 2018, 3, A210-A211.	2.0	1
117	The origin of preplasmablastic cells. Blood, 2021, 137, 1134-1135.	0.6	1
118	RAS Association Domain Family Member 4 (RASSF4): A New Potent Tumor Suppressor in Multiple Myeloma. Blood, 2016, 128, 2057-2057.	0.6	1
119	A Small Molecule That Selectively Targets BLM Helicase Has a Therapeutic Interest in Multiple Myeloma. Blood, 2016, 128, 4433-4433.	0.6	1
120	Genomic Characterization of in Vitro Acquired-Resistance to Proteasome Inhibitors. Blood, 2021, 138, 2651-2651.	0.6	1
121	Targeting DNA Repair to Overcome Drug Resistance in Hodgkin Lymphoma. Blood, 2020, 136, 26-26.	0.6	1
122	Cytokine Pathways in Myeloma Growth and Survival. Clinical Lymphoma and Myeloma, 2009, 9, S16-S17.	1.4	0
123	CCR2 (chemokine (C-C motif) receptor 2). Atlas of Genetics and Cytogenetics in Oncology and Haematology, 2012, , .	0.1	0
124	Inhibition of H3K9 methyltransferase as a potent therapeutic target in multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e214-e215.	0.2	0
125	Role of RECQ1 helicase in multiple myeloma drug resistance. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e67.	0.2	0
126	SNaPshot as a Valuable Option for the Identification of Mutations in Myeloma. EBioMedicine, 2015, 2, 13-14.	2.7	0

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127	Vaccine based immunotherapy as a strategy to bypass drug resistance in multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2015, 15, e285-e286.	0.2	0
128	CeVi: A UNIQUE CRYOPRESERVED HUMAN VIABLE CELL COLLECTION FROM LYMPHOMA PATIENTS, A CALYM INITIATIVE TO ACCELERATE INNOVATION AND ITS TRANSFER TO LYMPHOMA FIELD. Hematological Oncology, 2019, 37, 370-372.	0.8	0
129	Multi-omics tumor profiling technologies to develop precision medicine in multiple myeloma. Exploration of Targeted Anti-tumor Therapy, 0, , .	0.5	0
130	Multi-omics tumor profiling technologies to develop precision medicine in multiple myeloma. Exploration of Targeted Anti-tumor Therapy, 0, , .	0.5	0
131	Growth Factors in Multiple Myeloma. , 2013, , 65-84.		0
132	The in vivo Transcriptional Response Towards Epigenetic Modulating Agents in Multiple Myeloma. Blood, 2014, 124, 3375-3375.	0.6	0
133	Identification of a Gene Signature Associated to Treatment Response to Palbociclib in Multiple Myeloma. Blood, 2016, 128, 5666-5666.	0.6	0
134	Patterns of Microrna in Plasma Cells: From Normal Differentiation to Multiple Myeloma. Blood, 2016, 128, 2069-2069.	0.6	0
135	SET8 Is a Potential Therapeutic Target in MM. Blood, 2016, 128, 4435-4435.	0.6	0
136	On the Redox Profile of B- Cell Terminal Differentiation and Multiple Myeloma: New Insights and Therapeutic Opportunities. Blood, 2016, 128, 5644-5644.	0.6	0
137	Abstract A147: Synthetic lethality screening reveals ATR as responsible for oxaliplatin resistance in colorectal cancer cells. , 2018, , .		0
138	PF577 TARGETING PROTEIN ARGININE METHYLTRANFERASE PRMT5 IN HIGHâ€RISK MULTIPLE MYELOMA: A NEW TREATMENT STRATEGY?. HemaSphere, 2019, 3, 240-241.	1.2	0
139	Ironomycin Induces Diffuse Large B-Cell Lymphoma Cell Death By Targeting Iron Metabolism Addiction. Blood, 2019, 134, 3960-3960.	0.6	0
140	Prediction of Malingant Plasma Cell Biology Related Survival in AL-Amyloidosis. Blood, 2019, 134, 3078-3078.	0.6	0
141	RNA-Sequencing Based Assessment of Targets, Risk and Long Term Survival for Personalized Treatment of Multiple Myeloma. Blood, 2019, 134, 1801-1801.	0.6	0
142	Angiogenic factors could help us to define patients obtaining complete response with undetectable minimal residual disease in untreated CLL patients treated by FCR: results from the CLL2010FMP, a FILO study. Leukemia and Lymphoma, 2021, 62, 3160-3169.	0.6	0
143	Comprehensive Characterization of the Epigenetic Landscape in Multiple Myeloma. Blood, 2020, 136, 2-3.	0.6	0
144	Robust Discovery of Candidate DNA Methylation Cancer Drivers. Blood, 2020, 136, 33-34.	0.6	0

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145	DNA Repair Expression Profiling to Identify High-Risk Cytogenetically Normal Acute Myeloid Leukemia and Define New Therapeutic Targets. Blood, 2020, 136, 35-35.	0.6	0