Gareth J Morgan

List of Publications by Year
in descending order

595 papers	36,252 citations	3933 88 h-index	4015 176 g-index
607 all docs	607 docs citations	607 times ranked	25833 citing authors

#	Article	IF	Citations
1	Design and standardization of PCR primers and protocols for detection of clonal immunoglobulin and T-cell receptor gene recombinations in suspect lymphoproliferations: Report of the BIOMED-2 Concerted Action BMH4-CT98-3936. Leukemia, 2003, 17, 2257-2317.	7.2	2,788
2	International Staging System for Multiple Myeloma. Journal of Clinical Oncology, 2005, 23, 3412-3420.	1.6	2,404
3	High-Dose Chemotherapy with Hematopoietic Stem-Cell Rescue for Multiple Myeloma. New England Journal of Medicine, 2003, 348, 1875-1883.	27.0	1,648
4	Revised International Staging System for Multiple Myeloma: A Report From International Myeloma Working Group. Journal of Clinical Oncology, 2015, 33, 2863-2869.	1.6	1,525
5	Thalidomide and immunomodulatory derivatives augment natural killer cell cytotoxicity in multiple myeloma. Blood, 2001, 98, 210-216.	1.4	869
6	Prevention of thalidomide- and lenalidomide-associated thrombosis in myeloma. Leukemia, 2008, 22, 414-423.	7.2	787
7	The genetic architecture of multiple myeloma. Nature Reviews Cancer, 2012, 12, 335-348.	28.4	741
8	Risk of progression and survival in multiple myeloma relapsing after therapy with IMiDs and bortezomib: A multicenter international myeloma working group study. Leukemia, 2012, 26, 149-157.	7.2	664
9	First-line treatment with zoledronic acid as compared with clodronic acid in multiple myeloma (MRC) Tj ETQq1 1 0.784314 rgBT /Over	13.7	505
10	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. Journal of Clinical Oncology, 2015, 33, 3911-3920.	1.6	463
11	Early Mortality After Diagnosis of Multiple Myeloma: Analysis of Patients Entered Onto the United Kingdom Medical Research Council Trials Between 1980 and 2002â€"Medical Research Council Adult Leukaemia Working Party. Journal of Clinical Oncology, 2005, 23, 9219-9226.	1.6	402
12	Myeloma management guidelines: a consensus report from the Scientific Advisors of the International Myeloma Foundation. The Hematology Journal, 2003, 4, 379-398.	1.4	374
13	Minimal Residual Disease Assessed by Multiparameter Flow Cytometry in Multiple Myeloma: Impact on Outcome in the Medical Research Council Myeloma IX Study. Journal of Clinical Oncology, 2013, 31, 2540-2547.	1.6	372
14	Genetic variation in TNF and IL10 and risk of non-Hodgkin lymphoma: a report from the InterLymph Consortium. Lancet Oncology, The, 2006, 7, 27-38.	10.7	345
15	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. Blood, 2018, 132, 587-597.	1.4	335
16	International Myeloma Working Group Consensus Statement for the Management, Treatment, and Supportive Care of Patients With Myeloma Not Eligible for Standard Autologous Stem-Cell Transplantation. Journal of Clinical Oncology, 2014, 32, 587-600.	1.6	330
17	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. Blood, 2010, 116, e56-e65.	1.4	315
18	The role of maintenance thalidomide therapy in multiple myeloma: MRC Myeloma IX results and meta-analysis. Blood, 2012, 119, 7-15.	1.4	315

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19	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. Leukemia, 2019, 33, 159-170.	7.2	313
20	Personalized therapy in multiple myeloma according to patient age and vulnerability: a report of the European Myeloma Network (EMN). Blood, 2011, 118, 4519-4529.	1.4	309
21	Monoclonal B lymphocytes with the characteristics of â€œindolentâ€•chronic lymphocytic leukemia are present in 3.5% of adults with normal blood counts. Blood, 2002, 100, 635-639.	1.4	305
22	A novel prognostic model in myeloma based on co-segregating adverse FISH lesions and the ISS: analysis of patients treated in the MRC Myeloma IX trial. Leukemia, 2012, 26, 349-355.	7.2	298
23	The Requirement for DNAM-1, NKG2D, and NKp46 in the Natural Killer Cell-Mediated Killing of Myeloma Cells. Cancer Research, 2007, 67, 8444-8449.	0.9	284
24	Antimyeloma activity of heat shock protein-90 inhibition. Blood, 2005, 107, 1092-1100.	1.4	278
25	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. Nature Communications, 2017, 8, 268.	12.8	277
26	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Nature Communications, 2015, 6, 6997.	12.8	261
27	Germinal center phenotype and bcl-2 expression combined with the International Prognostic Index improves patient risk stratification in diffuse large B-cell lymphoma. Blood, 2002, 99, 1136-1143.	1.4	252
28	Guidelines for the diagnosis and management of multiple myeloma 2011. British Journal of Haematology, 2011, 154, 32-75.	2.5	252
29	Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. Leukemia, 2014, 28, 384-390.	7.2	252
30	Quantitation of minimal disease levels in chronic lymphocytic leukemia using a sensitive flow cytometric assay improves the prediction of outcome and can be used to optimize therapy. Blood, 2001, 98, 29-35.	1.4	249
31	Lenalidomide maintenance versus observation for patients with newly diagnosed multiple myeloma (Myeloma XI): a multicentre, open-label, randomised, phase 3 trial. Lancet Oncology, The, 2019, 20, 57-73.	10.7	245
32	Polymorphism in glutathione S -transferase P1 is associated with susceptibility to chemotherapy-induced leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 11592-11597.	7.1	233
33	Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. Blood, 2012, 120, 1077-1086.	1.4	231
34	Heat shock protein inhibition is associated with activation of the unfolded protein response pathway in myeloma plasma cells. Blood, 2007, 110, 2641-2649.	1.4	219
35	Aberrant global methylation patterns affect the molecular pathogenesis and prognosis of multiple myeloma. Blood, 2011, 117, 553-562.	1.4	217
36	Insights into the multistep transformation of MGUS to myeloma using microarray expression analysis. Blood, 2003, 102, 4504-4511.	1.4	212

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37	Polymorphisms in the thymidylate synthase and serine hydroxymethyltransferase genes and risk of adult acute lymphocytic leukemia. Blood, 2002, 99, 3786-3791.	1.4	210
38	Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. Leukemia, 2014, 28, 1705-1715.	7.2	207
39	Structure of the Ire1 autophosphorylation complex and implications for the unfolded protein response. EMBO Journal, 2011, 30, 894-905.	7.8	201
40	Bortezomib (Velcade?) in the treatment of multiple myeloma. Therapeutics and Clinical Risk Management, 2006, 2, 271-279.	2.0	197
41	Preclinical evaluation of the proteasome inhibitor bortezomib in cancer therapy. Cancer Cell International, 2005, 5, 18.	4.1	196
42	Flow cytometric disease monitoring in multiple myeloma: the relationship between normal and neoplastic plasma cells predicts outcome after transplantation. Blood, 2002, 100, 3095-3100.	1.4	194
43	Curing myeloma at last: defining criteria and providing the evidence. Blood, 2014, 124, 3043-3051.	1.4	194
44	Oral ixazomib maintenance following autologous stem cell transplantation (TOURMALINE-MM3): a double-blind, randomised, placebo-controlled phase 3 trial. Lancet, The, 2019, 393, 253-264.	13.7	187
45	Cyclophosphamide, thalidomide, and dexamethasone (CTD) as initial therapy for patients with multiple myeloma unsuitable for autologous transplantation. Blood, 2011, 118, 1231-1238.	1.4	179
46	Evolutionary biology of high-risk multiple myeloma. Nature Reviews Cancer, 2017, 17, 543-556.	28.4	178
47	Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. Leukemia, 2018, 32, 102-110.	7.2	177
48	Integration of global SNP-based mapping and expression arrays reveals key regions, mechanisms, and genes important in the pathogenesis of multiple myeloma. Blood, 2006, 108, 1733-1743.	1.4	176
49	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. Blood, 2016, 128, 1735-1744.	1.4	170
50	Circulating plasma cells in multiple myeloma: characterization and correlation with disease stage. British Journal of Haematology, 1997, 97, 46-55.	2.5	165
51	Immunoglobulin gene rearrangements and the pathogenesis of multiple myeloma. Blood, 2007, 110, 3112-3121.	1.4	157
52	Effects of zoledronic acid versus clodronic acid on skeletal morbidity in patients with newly diagnosed multiple myeloma (MRC Myeloma IX): secondary outcomes from a randomised controlled trial. Lancet Oncology, The, 2011, 12, 743-752.	10.7	151
53	Mapping of Chromosome 1p Deletions in Myeloma Identifies FAM46C at 1p12 and CDKN2C at 1p32.3 as Being Genes in Regions Associated with Adverse Survival. Clinical Cancer Research, 2011, 17, 7776-7784.	7.0	147
54	Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. Blood, 2013, 122, 219-226.	1.4	147

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55	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	12.8	146
56	Cyclophosphamide, thalidomide, and dexamethasone as induction therapy for newly diagnosed multiple myeloma patients destined for autologous stem-cell transplantation: MRC Myeloma IX randomized trial results. Haematologica, 2012, 97, 442-450.	3.5	144
57	Safety and efficacy of pomalidomide plus low-dose dexamethasone in STRATUS (MM-010): a phase 3b study in refractory multiple myeloma. Blood, 2016, 128, 497-503.	1.4	144
58	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	21.4	143
59	Long-term Follow-up of MRC Myeloma IX Trial: Survival Outcomes with Bisphosphonate and Thalidomide Treatment. Clinical Cancer Research, 2013, 19, 6030-6038.	7.0	143
60	Translocations at 8q24 juxtapose MYC with genes that harbor superenhancers resulting in overexpression and poor prognosis in myeloma patients. Blood Cancer Journal, 2014, 4, e191-e191.	6.2	142
61	Deletion of chromosome 13 detected by conventional cytogenetics is a critical prognostic factor in myeloma. Leukemia, 2006, 20, 1610-1617.	7.2	141
62	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	21.4	137
63	Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. Blood, 2007, 110, 3291-3300.	1.4	133
64	Essential Role of Caveolae in Interleukin-6- and Insulin-like Growth Factor I-triggered Akt-1-mediated Survival of Multiple Myeloma Cells. Journal of Biological Chemistry, 2003, 278, 5794-5801.	3.4	128
65	Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. Blood, 2013, 121, 3413-3419.	1.4	128
66	Low NAD(P)H:quinone oxidoreductase 1 activity is associated with increased risk of acute leukemia in adults. Blood, 2001, 97, 1422-1426.	1.4	125
67	Homozygous Deletion Mapping in Myeloma Samples Identifies Genes and an Expression Signature Relevant to Pathogenesis and Outcome. Clinical Cancer Research, 2010, 16, 1856-1864.	7.0	124
68	The clinical relevance and management of monoclonal gammopathy of undetermined significance and related disorders: recommendations from the European Myeloma Network. Haematologica, 2014, 99, 984-996.	3.5	124
69	Rearrangement of the BCL6 locus at 3q27 is an independent poor prognostic factor in nodal diffuse large B-cell lymphoma. British Journal of Haematology, 2002, 117, 322-332.	2.5	113
70	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. Leukemia, 2019, 33, 1713-1722.	7.2	112
71	Potent and Selective KDM5 Inhibitor Stops Cellular Demethylation of H3K4me3 at Transcription Start Sites and Proliferation of MM1S Myeloma Cells. Cell Chemical Biology, 2017, 24, 371-380.	5.2	111
72	Percutaneous Device Closure of Paravalvular Leak. Circulation, 2016, 134, 934-944.	1.6	109

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73	Genetic variation in XPD predicts treatment outcome and risk of acute myeloid leukemia following chemotherapy. Blood, 2004, 104, 3872-3877.	1.4	108
74	Expert panel consensus statement on the optimal use of pomalidomide in relapsed and refractory multiple myeloma. Leukemia, 2014, 28, 1573-1585.	7.2	108
75	Trends in autologous hematopoietic cell transplantation for multiple myeloma in Europe: increased use and improved outcomes in elderly patients in recent years. Bone Marrow Transplantation, 2015, 50, 209-215.	2.4	108
76	Results of the MRC pilot study show autografting for younger patients with chronic lymphocytic leukemia is safe and achieves a high percentage of molecular responses. Blood, 2005, 105, 397-404.	1.4	107
77	XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. Blood, 2010, 116, 250-253.	1.4	107
78	MMSET deregulation affects cell cycle progression and adhesion regulons in t(4;14) myeloma plasma cells. Haematologica, 2009, 94, 78-86.	3.5	106
79	Prediction of high- and low-risk multiple myeloma based on gene expression and the International Staging System. Blood, 2015, 126, 1996-2004.	1.4	106
80	The impact of attaining a minimal disease state after highâ€dose melphalan and autologous transplantation for multiple myeloma. British Journal of Haematology, 2001, 112, 814-819.	2.5	103
81	Cancer-Selective Targeting of the NF-Î²B Survival Pathway with GADD45Î²/MKK7 Inhibitors. Cancer Cell, 2014, 26, 495-508.	16.8	99
82	The impact of extramedullary disease at presentation on the outcome of myeloma. Leukemia and Lymphoma, 2009, 50, 230-235.	1.3	97
83	The sialyltransferase ST3GAL6 influences homing and survival in multiple myeloma. Blood, 2014, 124, 1765-1776.	1.4	97
84	Assessment of Total Lesion Glycolysis by 18F FDG PET/CT Significantly Improves Prognostic Value of GEP and ISS in Myeloma. Clinical Cancer Research, 2017, 23, 1981-1987.	7.0	97
85	Lenalidomide (Revlimid), in combination with cyclophosphamide and dexamethasone (RCD), is an effective and tolerated regimen for myeloma patients. British Journal of Haematology, 2007, 137, 268-269.	2.5	96
86	Subclonal evolution in disease progression from MGUS/SMM to multiple myeloma is characterised by clonal stability. Leukemia, 2019, 33, 457-468.	7.2	96
87	Genetic Factors Underlying the Risk of Thalidomide-Related Neuropathy in Patients With Multiple Myeloma. Journal of Clinical Oncology, 2011, 29, 797-804.	1.6	95
88	High-Producer Haplotypes of Tumor Necrosis Factor Alpha and Lymphotoxin Alpha Are Associated With an Increased Risk of Myeloma and Have an Improved Progression-Free Survival After Treatment. Journal of Clinical Oncology, 2000, 18, 2843-2851.	1.6	91
89	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	21.4	91
90	The impact of intra-clonal heterogeneity on the treatment of multiple myeloma. British Journal of Haematology, 2014, 165, 441-454.	2.5	91

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91	Polymorphic variation in GSTP1 modulates outcome following therapy for multiple myeloma. Blood, 2003, 102, 2345-2350.	1.4	90
92	European Perspective on Multiple Myeloma Treatment Strategies in 2014. Oncologist, 2014, 19, 829-844.	3.7	90
93	Carfilzomib resistance due to ABCB1/MDR1 overexpression is overcome by nelfinavir and lopinavir in multiple myeloma. Leukemia, 2018, 32, 391-401.	7.2	89
94	Deletions of CDKN2C in Multiple Myeloma: Biological and Clinical Implications. Clinical Cancer Research, 2008, 14, 6033-6041.	7.0	88
95	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	12.8	86
96	Myeloma management guidelines: a consensus report from the Scientific Advisors of the International Myeloma Foundation. The Hematology Journal, 2003, 4, 379-98.	1.4	86
97	Current Multiple Myeloma Treatment Strategies with Novel Agents: A European Perspective. Oncologist, 2010, 15, 6-25.	3.7	85
98	Polymorphic variation within the glutathione S-transferase genes and risk of adult acute leukaemia. Carcinogenesis, 2000, 21, 43-47.	2.8	84
99	Differentiation stage of myeloma plasma cells: biological and clinical significance. Leukemia, 2017, 31, 382-392.	7.2	83
100	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794.	7.0	81
101	Overexpression of EZH2 in multiple myeloma is associated with poor prognosis and dysregulation of cell cycle control. Blood Cancer Journal, 2017, 7, e549-e549.	6.2	81
102	Revealing the Impact of Structural Variants in Multiple Myeloma. Blood Cancer Discovery, 2020, 1, 258-273.	5.0	81
103	Gastric marginal zone lymphoma is associated with polymorphisms in genes involved in inflammatory response and antioxidative capacity. Blood, 2003, 102, 1007-1011.	1.4	79
104	Non-Hodgkin's lymphoma, obesity and energy homeostasis polymorphisms. British Journal of Cancer, 2005, 93, 811-816.	6.4	79
105	The interleukin-6 receptor alpha-chain (CD126) is expressed by neoplastic but not normal plasma cells. Blood, 2000, 96, 3880-3886.	1.4	78
106	Genetic variants of NHEJ DNA ligase IV can affect the risk of developing multiple myeloma, a tumour characterised by aberrant class switch recombination. Journal of Medical Genetics, 2002, 39, 900-905.	3.2	77
107	Untangling the unfolded protein response. Cell Cycle, 2008, 7, 865-869.	2.6	76
108	Genetic abnormalities during transition from Helicobacter-pylori-associated gastritis to low-grade MALToma. Lancet, The, 1995, 345, 26-27.	13.7	75

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109	Bâ€lymphocyte suppression in multiple myeloma is a reversible phenomenon specific to normal Bâ€cell progenitors and plasma cell precursors. British Journal of Haematology, 1998, 100, 176-183.	2.5	74
110	Age has a profound effect on the incidence and significance of chromosome abnormalities in myeloma. Leukemia, 2005, 19, 1634-1642.	7.2	73
111	Removing batch effects from purified plasma cell gene expression microarrays with modified ComBat. BMC Bioinformatics, 2015, 16, 63.	2.6	73
112	Myeloma aetiology and epidemiology. Biomedicine and Pharmacotherapy, 2002, 56, 223-234.	5.6	72
113	Risk of Non-Hodgkin Lymphoma Associated with Polymorphisms in Folate-Metabolizing Genes. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 2999-3003.	2.5	72
114	The combination of cyclophosphamide, velcade and dexamethasone (CVD) induces high response rates with comparable toxicity to velcade alone (V) and velcade plus dexamethasone (VD). Haematologica, 2007, 92, 1149-1150.	3.5	71
115	Targeting heat shock protein 72 enhances Hsp90 inhibitor-induced apoptosis in myeloma. Leukemia, 2010, 24, 1804-1807.	7.2	71
116	The spectrum of somatic mutations in monoclonal gammopathy of undetermined significance indicates a less complex genomic landscape than that in multiple myeloma. Haematologica, 2017, 102, 1617-1625.	3.5	71
117	A clinical prediction model for outcome and therapy delivery in transplant-ineligible patients with myeloma (UK Myeloma Research Alliance Risk Profile): a development and validation study. Lancet Haematology,the, 2019, 6, e154-e166.	4.6	71
118	Serum free immunoglobulin light chain evaluation as a marker of impact from intraclonal heterogeneity on myeloma outcome. Blood, 2014, 123, 3414-3419.	1.4	68
119	Second malignancies in the context of lenalidomide treatment: an analysis of 2732 myeloma patients enrolled to the Myeloma XI trial. Blood Cancer Journal, 2016, 6, e506-e506.	6.2	68
120	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. Nature Communications, 2021, 12, 1861.	12.8	68
121	Poor metabolizers at the cytochrome P450 2D6 and 2C19 loci are at increased risk of developing adult acute leukaemia. Pharmacogenetics and Genomics, 2000, 10, 605-615.	5.7	67
122	Maintenance Treatment and Survival in Patients With Myeloma. JAMA Oncology, 2018, 4, 1389.	7.1	67
123	Clonal evolution in myeloma: the impact of maintenance lenalidomide and depth of response on the genetics and sub-clonal structure of relapsed disease in uniformly treated newly diagnosed patients. Haematologica, 2019, 104, 1440-1450.	3.5	67
124	Aetiology of bone disease and the role of bisphosphonates in multiple myeloma. Lancet Oncology, The, 2003, 4, 284-292.	10.7	66
125	Treatment of relapsed and refractory multiple myeloma in the era of novel agents. Cancer Treatment Reviews, 2011, 37, 266-283.	7.7	66
126	Long-term outcomes after autologous stem cell transplantation for multiple myeloma. Blood Advances, 2020, 4, 422-431.	5.2	66

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127	Non-Hodgkin Lymphoma Secondary to Cancer Chemotherapy. Cancer Epidemiology Biomarkers and Prevention, 2007, 16, 377-380.	2.5	65
128	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. Blood, 2008, 112, 4924-4934.	1.4	65
129	The role of second autografts in the management of myeloma at first relapse. Haematologica, 2006, 91, 141-2.	3.5	62
130	Inherited genetic susceptibility to multiple myeloma. Leukemia, 2014, 28, 518-524.	7.2	60
131	Karyotype and age in acute myeloid leukemia.. Cancer Genetics and Cytogenetics, 2001, 126, 155-161.	1.0	59
132	Factors Influencing the Outcome of a Second Autologous Stem Cell Transplant (ASCT) in Relapsed Multiple Myeloma: A Study from the British Society ofÂBlood and Marrow Transplantation Registry. Biology of Blood and Marrow Transplantation, 2011, 17, 1638-1645.	2.0	59
133	The clinical impact and molecular biology of del(17p) in multiple myeloma treated with conventional or thalidomideâ€based therapy. Genes Chromosomes and Cancer, 2011, 50, 765-774.	2.8	59
134	Epigenetic consequences of AML1-ETO action at the human c-FMS locus. EMBO Journal, 2003, 22, 2798-2809.	7.8	58
135	Clinical value of molecular subtyping multiple myeloma using gene expression profiling. Leukemia, 2016, 30, 423-430.	7.2	58
136	Thrombosis in patients with myeloma treated in the Myeloma IX and Myeloma XI phase 3 randomized controlled trials. Blood, 2020, 136, 1091-1104.	1.4	58
137	Antitumor Effects and Anticancer Applications of Bisphosphonates. Seminars in Oncology, 2010, 37, S30-S40.	2.2	57
138	The addition of cyclophosphamide to lenalidomide and dexamethasone in multiply relapsed/refractory myeloma patients; a phase I/II study. British Journal of Haematology, 2010, 150, 326-333.	2.5	57
139	Lenalidomide-induced diarrhea in patients with myeloma is caused by bile acid malabsorption that responds to treatment. Blood, 2014, 124, 2467-2468.	1.4	57
140	MAF protein mediates innate resistance to proteasome inhibition therapy in multiple myeloma. Blood, 2016, 128, 2919-2930.	1.4	57
141	The level of deletion 17p and bi-allelic inactivation of TP53 has a significant impact on clinical outcome in multiple myeloma. Haematologica, 2017, 102, e364-e367.	3.5	57
142	Tobacco and Alcohol Consumption and the Risk of Non-Hodgkin Lymphoma. Cancer Causes and Control, 2004, 15, 771-780.	1.8	55
143	Assessing myeloma bone disease with whole-body diffusion-weighted imaging: comparison with x-ray skeletal survey by regionÂand relationship with laboratory estimatesÂof disease burden. Clinical Radiology, 2015, 70, 614-621.	1.1	54
144	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. Nature Communications, 2021, 12, 293.	12.8	54

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145	Mutations of theAML1 gene in acute myeloid leukemia of FAB types M0 and M7. Genes Chromosomes and Cancer, 2002, 34, 24-32.	2.8	53
146	Cleavage of BLOC1S1 mRNA by IRE1 Is Sequence Specific, Temporally Separate from XBP1 Splicing, and Dispensable for Cell Viability under Acute Endoplasmic Reticulum Stress. Molecular and Cellular Biology, 2015, 35, 2186-2202.	2.3	53
147	A Global Expression-based Analysis of the Consequences of the t(4;14) Translocation in Myeloma. Clinical Cancer Research, 2004, 10, 5692-5701.	7.0	51
148	t(3;14)(p14;q32) Results in aberrant expression of FOXP1 in a case of diffuse large Bâ€cell lymphoma. Genes Chromosomes and Cancer, 2006, 45, 164-168.	2.8	51
149	Efficacy and outcome of autologous transplantation in rare myelomas. Haematologica, 2010, 95, 2126-2133.	3.5	51
150	Characterisation of immunoparesis in newly diagnosed myeloma and its impact on progression-free and overall survival in both old and recent myeloma trials. Leukemia, 2018, 32, 1727-1738.	7.2	50
151	Combinations of ZAP-70, CD38 and IGHV mutational status as predictors of time to first treatment in CLL. Leukemia and Lymphoma, 2008, 49, 2108-2115.	1.3	48
152	Genetic factors underlying the risk of bortezomib induced peripheral neuropathy in multiple myeloma patients. Haematologica, 2011, 96, 1728-1732.	3.5	48
153	Bi-allelic inactivation is more prevalent at relapse in multiple myeloma, identifying RB1 as an independent prognostic marker. Blood Cancer Journal, 2017, 7, e535-e535.	6.2	48
154	Treatment to suppression of focal lesions on positron emission tomography-computed tomography is a therapeutic goal in newly diagnosed multiple myeloma. Haematologica, 2018, 103, 1047-1053.	3.5	47
155	Immunologic approaches for the treatment of multiple myeloma. Cancer Treatment Reviews, 2017, 55, 190-199.	7.7	46
156	HSF1 Is Essential for Myeloma Cell Survival and A Promising Therapeutic Target. Clinical Cancer Research, 2018, 24, 2395-2407.	7.0	46
157	COVID-19 Infections and Clinical Outcomes in Patients with Multiple Myeloma in New York City: A Cohort Study from Five Academic Centers. Blood Cancer Discovery, 2020, 1, 234-243.	5.0	46
158	Residual disease detection using fluorescent polymerase chain reaction at 20 weeks of therapy predicts clinical outcome in childhood acute lymphoblastic leukemia.. Journal of Clinical Oncology, 1998, 16, 3616-3627.	1.6	45
159	Long-term outcomes of previously untreated myeloma patients: responses to induction chemotherapy and high-dose melphalan incorporated within a risk stratification model can help to direct the use of novel treatments. British Journal of Haematology, 2005, 129, 607-614.	2.5	45
160	Genomic variation in myeloma: design, content, and initial application of the Bank On A Cure SNP Panel to detect associations with progression-free survival. BMC Medicine, 2008, 6, 26.	5.5	45
161	Assessment of IgH PCR strategies in multiple myeloma.. Journal of Clinical Pathology, 1996, 49, 672-675.	2.0	44
162	Minimal residual disease monitoring in multiple myeloma. Best Practice and Research in Clinical Haematology, 2002, 15, 197-222.	1.7	44

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163	High-dose cyclophosphamide with stem cell rescue for severe rheumatoid arthritis: Short-term efficacy correlates with reduction of macroscopic and histologic synovitis. Arthritis and Rheumatism, 2002, 46, 837-839.	6.7	44
164	Aminopeptidase inhibition as a targeted treatment strategy in myeloma. Molecular Cancer Therapeutics, 2009, 8, 762-770.	4.1	44
165	Four genes predict high risk of progression from smoldering to symptomatic multiple myeloma (SWOG S0120). Haematologica, 2015, 100, 1214-1221.	3.5	44
166	The combination of cyclophosphomide, thalidomide and dexamethasone is an effective alternative to cyclophosphamide â€“ vincristine â€“ doxorubicin â€“ methylprednisolone as induction chemotherapy prior to autologous transplantation for multiple myeloma: a case-matched analysis. Leukemia and Lymphoma, 2006, 47, 2335-2338.	1.3	43
167	Haplotypes in the tumour necrosis factor region and myeloma. British Journal of Haematology, 2005, 129, 358-365.	2.5	42
168	Advances in oral therapy for multiple myeloma. Lancet Oncology, The, 2006, 7, 316-325.	10.7	42
169	Response-adapted intensification with cyclophosphamide, bortezomib, and dexamethasone versus no intensification in patients with newly diagnosed multiple myeloma (Myeloma XI): a multicentre, open-label, randomised, phase 3 trial. Lancet Haematology,the, 2019, 6, e616-e629.	4.6	42
170	Microhomology-mediated end joining drives complex rearrangements and overexpression of MYC and PVT1 in multiple myeloma. Haematologica, 2020, 105, 1055-1066.	3.5	42
171	CYP1A1*2B (Val) allele is overrepresented in a subgroup of acute myeloid leukemia patients with poor-risk karyotype associated with NRAS mutation, but not associated withFLT3 internal tandem duplication. Blood, 2003, 101, 2770-2774.	1.4	41
172	Evidence of an epigenetic origin for high-risk 1q21 copy number aberrations in multiple myeloma. Blood, 2015, 125, 3756-3759.	1.4	41
173	Disentangling the microRNA regulatorymilieuin 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.	1.8	41
174	Minimal residual disease following autologous stem cell transplant in myeloma: impact on outcome is independent of induction regimen. Haematologica, 2016, 101, e69-e71.	3.5	41
175	Accelerated single cell seeding in relapsed multiple myeloma. Nature Communications, 2020, 11, 3617.	12.8	41
176	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. Oncotarget, 2015, 6, 19132-19147.	1.8	41
177	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	6.2	40
178	The Detection of t(14;18) in Archival Lymph Nodes. Journal of Molecular Diagnostics, 2003, 5, 168-175.	2.8	39
179	A single-tube six-colour flow cytometry screening assay for the detection of minimal residual disease in myeloma. Leukemia, 2007, 21, 2046-2049.	7.2	39
180	Lenalidomide: A new therapy for multiple myeloma. Cancer Treatment Reviews, 2008, 34, 283-291.	7.7	39

#	Article	IF	Citations
181	Gender Disparities in the Tumor Genetics and Clinical Outcome of Multiple Myeloma. Cancer Epidemiology Biomarkers and Prevention, 2011, 20, 1703-1707.	2.5	39
182	Loss of heterozygosity as a marker of homologous repair deficiency in multiple myeloma: a role for PARP inhibition?. Leukemia, 2018, 32, 1561-1566.	7.2	39
183	Role of AID in the temporal pattern of acquisition of driver mutations in multiple myeloma. Leukemia, 2020, 34, 1476-1480.	7.2	39
184	Variability of polymerase chain reaction detection of the bcl-2-IgH translocation in an international multicentre study. Annals of Oncology, 1999, 10, 1349-1354.	1.2	38
185	BRAF and DIS3 Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. Clinical Cancer Research, 2020, 26, 2422-2432.	7.0	37
186	A TC classification-based predictor for multiple myeloma using multiplexed real-time quantitative PCR. Leukemia, 2013, 27, 1754-1757.	7.2	36
187	Clinical characteristics and prognostic factors in multiple myeloma patients with light chain deposition disease. American Journal of Hematology, 2017, 92, 739-745.	4.1	36
188	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. Leukemia, 2020, 34, 1866-1874.	7.2	36
189	Maintenance Thalidomide May Improve Progression Free but Not Overall Survival; Results from the Myeloma IX Maintenance Randomisation. Blood, 2008, 112, 656-656.	1.4	35
190	Peripheral blood or bone marrow cells in reduced-intensity or myeloablative conditioning allogeneic HLA identical sibling donor transplantation for multiple myeloma. Haematologica, 2007, 92, 1513-1518.	3.5	34
191	Proteomic evaluation of pathways associated with dexamethasone-mediated apoptosis and resistance in multiple myeloma. British Journal of Haematology, 2007, 139, 559-567.	2.5	34
192	Diagnosis and monitoring for light chain only and oligosecretory myeloma using serum free light chain tests. British Journal of Haematology, 2017, 178, 220-230.	2.5	34
193	RAD51 homologous recombination repair gene haplotypes and risk of acute myeloid leukaemia. Leukemia Research, 2007, 31, 169-174.	0.8	33
194	Thalidomide Combinations Improve Response Rates; Results from the MRC IX Study.. Blood, 2007, 110, 3593-3593.	1.4	33
195	Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. PLoS Medicine, 2020, 17, e1003323.	8.4	33
196	Haplotypic structure across the IÎºBÎ± gene (NFKBIA) and association with multiple myeloma. Cancer Letters, 2007, 246, 92-99.	7.2	32
197	Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. Nature Communications, 2016, 7, 13656.	12.8	32
198	Genome-wide association study of immunoglobulin light chain amyloidosis in three patient cohorts: comparison with myeloma. Leukemia, 2017, 31, 1735-1742.	7.2	32

#	Article	IF	Citations
199	The mutagenic impact of melphalan in multiple myeloma. Leukemia, 2021, 35, 2145-2150.	7.2	32
200	Demonstration of changes in plasma cell subsets in multiple myeloma. Haematologica, 2007, 92, 1135-1138.	3.5	31
201	Hsp70 inhibition induces myeloma cell death via the intracellular accumulation of immunoglobulin and the generation of proteotoxic stress. Cancer Letters, 2013, 339, 49-59.	7.2	31
202	Phase II Study of Vincristine Sulfate Liposome Injection (Marqibo) and Rituximab for Patients With Relapsed and Refractory Diffuse Large B-Cell Lymphoma or Mantle Cell Lymphoma in Need of Palliative Therapy. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, 37-42.	0.4	31
203	A molecular diagnostic approach able to detect the recurrent genetic prognostic factors typical of presenting myeloma. Genes Chromosomes and Cancer, 2015, 54, 91-98.	2.8	31
204	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290.	12.8	31
205	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	3.3	31
206	The Pattern of Mesenchymal Stem Cell Expression Is an Independent Marker of Outcome in Multiple Myeloma. Clinical Cancer Research, 2018, 24, 2913-2919.	7.0	30
207	A molecular study of the t(4;14) in multiple myeloma. British Journal of Haematology, 2002, 118, 514-520.	2.5	29
208	DNA mismatch repair pathway defects in the pathogenesis and evolution of myeloma. Carcinogenesis, 2004, 25, 1795-1803.	2.8	29
209	Biologic Frontiers in Multiple Myeloma: From Biomarker Identification to Clinical Practice. Clinical Cancer Research, 2014, 20, 804-813.	7.0	29
210	Subclonal TP53 copy number is associated with prognosis in multiple myeloma. Blood, 2018, 132, 2465-2469.	1.4	29
211	Minimal Residual Disease After Autologous Stem-Cell Transplant for Patients With Myeloma: Prognostic Significance and the Impact of Lenalidomide Maintenance and Molecular Risk. Journal of Clinical Oncology, 2022, 40, 2889-2900.	1.6	29
212	Association between non-Hodgkin lymphoma and haplotypes in the TNF region. British Journal of Haematology, 2006, 133, 293-300.	2.5	28
213	A Gene Expressionâ€“Based Predictor for Myeloma Patients at High Risk of Developing Bone Disease on Bisphosphonate Treatment. Clinical Cancer Research, 2011, 17, 6347-6355.	7.0	27
214	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.	3.5	27
215	Hyperhaploidy is a novel high-risk cytogenetic subgroup in multiple myeloma. Leukemia, 2017, 31, 637-644.	7.2	27
216	Search for multiple myeloma risk factors using Mendelian randomization. Blood Advances, 2020, 4, 2172-2179.	5.2	27

#	Article	IF	Citations
217	Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. Blood Cancer Journal, 2020, 10, 70.	6.2	27
218	Copy number signatures predict chromothripsis and clinical outcomes in newly diagnosed multiple myeloma. Nature Communications, 2021, 12, 5172.	12.8	27
219	Metabolic Enzyme Polymorphisms and Susceptibility to Acute Leukemia in Adults. Molecular Diagnosis and Therapy, 2002, 2, 79-92.	3.3	26
220	Benzene and the hemopoietic stem cell. Chemico-Biological Interactions, 2005, 153-154, 217-222.	4.0	26
221	High expression levels of the mammalian target of rapamycin inhibitorDEPTORare predictive of response to thalidomide in myeloma. Leukemia and Lymphoma, 2010, 51, 2126-2129.	1.3	26
222	The prognostic value of the depth of response in multiple myeloma depends on the time of assessment, risk status and molecular subtype. Haematologica, 2017, 102, e313-e316.	3.5	26
223	Kinase domain activation through gene rearrangement in multiple myeloma. Leukemia, 2018, 32, 2435-2444.	7.2	26
224	MAFb protein confers intrinsic resistance to proteasome inhibitors in multiple myeloma. BMC Cancer, 2018, 18, 724.	2.6	26
225	Lenalidomide Is a Highly Effective Maintenance Therapy in Myeloma Patients of All Ages; Results of the Phase III Myeloma XI Study. Blood, 2016, 128, 1143-1143.	1.4	26
226	Results of a Prospective Clinical Trial of Pre-DLI Lymphoreduction Using Oral Fludarabine In Patients with Mixed Chimerism Post Allogeneic Transplant.. Blood, 2010, 116, 1299-1299.	1.4	26
227	A phase 1 study to address the safety and efficacy of granulocyte colony-stimulating factor for the mobilization of hematopoietic progenitor cells in active rheumatoid arthritis. Arthritis and Rheumatism, 1997, 40, 1838-1842.	6.7	25
228	Autologous stem cell transplantation for rapidly progressive joâ€1â€positive polymyositis with longâ€term followâ€up. British Journal of Haematology, 2001, 113, 840-841.	2.5	25
229	Isotype class switching and the pathogenenesis of multiple myeloma. Hematological Oncology, 2002, 20, 75-85.	1.7	25
230	How to use new biology to guide therapy in multiple myeloma. Hematology American Society of Hematology Education Program, 2012, 2012, 342-349.	2.5	25
231	Understanding the multiple biological aspects leading to myeloma. Haematologica, 2014, 99, 605-612.	3.5	25
232	The varied distribution and impact of RAS codon and other key DNA alterations across the translocation cyclin D subgroups in multiple myeloma. Oncotarget, 2017, 8, 27854-27867.	1.8	25
233	Follicular lymphoma with a novel t(14;18) breakpoint involving the immunoglobulin heavy chain switch mu region indicates an origin from germinal center B cells. Blood, 2002, 99, 716-718.	1.4	24
234	Genomewide profiling of copyâ€number alteration in monoclonal gammopathy of undetermined significance. European Journal of Haematology, 2016, 97, 568-575.	2.2	24

#	Article	IF	Citations
235	Serum free light chain levels and renal function at diagnosis in patients with multiple myeloma. BMC Nephrology, 2018, 19, 178.	1.8	24
236	A Modified Method for Whole Exome Resequencing from Minimal Amounts of Starting DNA. PLoS ONE, 2012, 7, e32617.	2.5	24
237	Perspectives on the Risk-Stratified Treatment of Multiple Myeloma. Blood Cancer Discovery, 2022, 3, 273-284.	5.0	24
238	Comparison of fluorescent consensus IgH PCR and alleleâ€specific oligonucleotide probing in the detection of minimal residual disease in childhood ALL. British Journal of Haematology, 1997, 97, 457-459.	2.5	23
239	An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. Blood Cancer Journal, 2019, 9, 62.	6.2	23
240	Gene Expression Profiling of Extramedullary Disease-Related Toward Identification of a Terminal Disease Pathway in Multiple Myeloma. Blood, 2015, 126, 1777-1777.	1.4	23
241	Role of thalidomide in the treatment of patients with multiple myeloma. Critical Reviews in Oncology/Hematology, 2013, 88, S14-S22.	4.4	22
242	Understanding the interplay between the proteasome pathway and autophagy in response to dual PI3K/mTOR inhibition in myeloma cells is essential for their effective clinical application. Leukemia, 2013, 27, 2397-2403.	7.2	22
243	The multiple myeloma risk allele at 5q15 lowers ELL2 expression and increases ribosomal gene expression. Nature Communications, 2018, 9, 1649.	12.8	22
244	Phenome-wide association analysis of LDL-cholesterol lowering genetic variants in PCSK9. BMC Cardiovascular Disorders, 2019, 19, 240.	1.7	22
245	Chromothripsis as a pathogenic driver of multiple myeloma. Seminars in Cell and Developmental Biology, 2022, 123, 115-123.	5.0	22
246	Genetic polymorphisms in microsomal epoxide hydrolase â€and susceptibility to adult acute myeloid leukaemia â€with defined cytogenetic abnormalities. British Journal of Haematology, 2002, 116, 587-594.	2.5	21
247	Genomic characterization of the chromosomal breakpoints of t(4;14) of multiple myeloma suggests more than one possible aetiological mechanism. Oncogene, 2003, 22, 1103-1113.	5.9	21
248	Association of metabolic gene polymorphisms with tobacco consumption in healthy controls. International Journal of Cancer, 2004, 110, 266-270.	5.1	21
249	Successful mobilization of PBSCs predicts favorable outcomes in multiple myeloma patients treated with novel agents and autologous transplantation. Bone Marrow Transplantation, 2015, 50, 673-678.	2.4	21
250	Overall survival of relapsed and refractory multiple myeloma patients after adjusting for crossover in the <scp>MM</scp>â€003 trial for pomalidomide plus lowâ€dose dexamethasone. British Journal of Haematology, 2015, 168, 820-823.	2.5	21
251	Reconstructing the evolutionary history of multiple myeloma. Best Practice and Research in Clinical Haematology, 2020, 33, 101145.	1.7	21
252	Polymorphisms in cytochrome P450 17A1 and risk of non-Hodgkin lymphoma. British Journal of Haematology, 2005, 129, 618-621.	2.5	20

#	Article	IF	Citations
253	Neutral tumor evolution in myeloma is associated with poor prognosis. Blood, 2017, 130, 1639-1643.	1.4	20
254	Investigation of a gene signature to predict response to immunomodulatory derivatives for patients with multiple myeloma: an exploratory, retrospective study using microarray datasets from prospective clinical trials. Lancet Haematology,the, 2017, 4, e443-e451.	4.6	20
255	The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. Journal of Hematology and Oncology, 2020, 13, 108.	17.0	20
256	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. Haematologica, 2021, 106, 736-745.	3.5	20
257	Designing Evolutionary-based Interception Strategies to Block the Transition from Precursor Phases to Multiple Myeloma. Clinical Cancer Research, 2021, 27, 15-23.	7.0	20
258	Peripheral blood stem cell transplantation in myeloma using CD34 selected cells. Bone Marrow Transplantation, 1996, 17, 723-7.	2.4	20
259	Streptolysin-O reversible permeabilisation is an effective method to transfect siRNAs into myeloma cells. Journal of Immunological Methods, 2008, 333, 147-155.	1.4	19
260	Bendamustine, thalidomide and dexamethasone combination therapy for relapsed/refractory myeloma patients: results of the MUKone randomized dose selection trial. British Journal of Haematology, 2015, 170, 336-348.	2.5	19
261	Evolving treatment strategies for myeloma. British Journal of Cancer, 2005, 92, 217-221.	6.4	18
262	Mesenchymal stem cells gene signature in highâ€risk myeloma bone marrow linked to suppression of distinct IGFBP2â€expressing small adipocytes. British Journal of Haematology, 2019, 184, 578-593.	2.5	18
263	Carfilzomib, lenalidomide, dexamethasone, and cyclophosphamide (KRdc) as induction therapy for transplant-eligible, newly diagnosed multiple myeloma patients (Myeloma XI+): Interim analysis of an open-label randomised controlled trial. PLoS Medicine, 2021, 18, e1003454.	8.4	18
264	Genetic Associations with Bortezomib Mediated Neuropathy in Multiple Myeloma.. Blood, 2009, 114, 1794-1794.	1.4	18
265	Natural History of Multiple Myeloma Relapsing After Therapy with IMiDs and Bortezomib: A Multicenter International Myeloma Working Group Study.. Blood, 2009, 114, 2878-2878.	1.4	18
266	Differential transcription factor occupancy but evolutionarily conserved chromatin features at the human and mouse M-CSF (CSF-1) receptor loci. Nucleic Acids Research, 2003, 31, 5805-5816.	14.5	17
267	Use of Single Nucleotide Polymorphismâ€"Based Mapping Arrays to Detect Copy Number Changes and Loss of Heterozygosity in Multiple Myeloma. Clinical Lymphoma and Myeloma, 2006, 7, 186-192.	1.4	17
268	Genetic polymorphisms of EPHX1, Gsk3Î², TNFSF8 and myeloma cell DKK-1 expression linked to bone disease in myeloma. Leukemia, 2009, 23, 1913-1919.	7.2	17
269	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	6.4	17
270	p53 gene mutations in multiple myeloma.. Journal of Clinical Pathology, 1997, 50, 18-20.	1.9	16

#	Article	IF	Citations
271	Survival and outcome of blastoid variant myeloma following treatment with the novel thalidomide containing regime DTâ€PACE. European Journal of Haematology, 2008, 81, 432-436.	2.2	16
272	Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. Scientific Reports, 2015, 5, 12473.	3.3	16
273	Immunotherapy in Multiple Myeloma: Accelerating on the Path to the Patient. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, 332-344.	0.4	16
274	Lenalidomide before and after ASCT for transplant-eligible patients of all ages in the randomized, phase III, Myeloma XI trial. Haematologica, 2020, 106, haematol.2020.247130.	3.5	16
275	High Absolute T Regulatory Cell Counts and Resistance of CD8 Central Memory Cells to Killing by Fludarabine Predicts for Poor Responses to DLI in the Context of a Pre-DLI Lymphoreduction Strategy. Blood, 2011, 118, 1912-1912.	1.4	16
276	Autologous stem cell transplantation is safe and effective for fit older myeloma patients: exploratory results from the Myeloma XI trial. Haematologica, 2020, Online ahead of print, 0-0.	3.5	16
277	New Developments in the Epidemiology of Cancer Prognosis: Traditional and Molecular Predictors of Treatment Response and Survival. Cancer Epidemiology Biomarkers and Prevention, 2006, 15, 2042-2046.	2.5	15
278	Position statement on the use of bortezomib in multiple myeloma. International Journal of Laboratory Hematology, 2008, 30, 1-10.	1.3	15
279	Nonâ€Homologous Endâ€Joining Gene Profiling Reveals Distinct Expression Patterns Associated with Lymphoma and Multiple Myeloma. British Journal of Haematology, 2010, 149, 258-262.	2.5	15
280	Biology and Treatment of Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2014, 14, S65-S70.	0.4	15
281	Phase 2 Study of Venetoclax Plus Carfilzomib and Dexamethasone in Patients with Relapsed/Refractory Multiple Myeloma. Blood, 2018, 132, 303-303.	1.4	15
282	The use of genetic microarray analysis to classify and predict prognosis in haematological malignancies. International Journal of Laboratory Hematology, 2003, 25, 209-220.	0.2	14
283	Understanding the molecular biology of myeloma and its therapeutic implications. Expert Review of Hematology, 2012, 5, 603-617.	2.2	14
284	Impact of Genes Highly Correlated with MMSET Myeloma on the Survival of Non-MMSET Myeloma Patients. Clinical Cancer Research, 2016, 22, 4039-4044.	7.0	14
285	The efficacy and tolerability of pomalidomide in relapsed/refractory myeloma patients in a â€œreal-worldâ€•study: the Royal Marsden Hospital experience. Leukemia and Lymphoma, 2017, 58, 494-497.	1.3	14
286	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	2.9	14
287	Genome-wide interaction and pathway-based identification of key regulators in multiple myeloma. Communications Biology, 2019, 2, 89.	4.4	14
288	Optimising the value of immunomodulatory drugs during induction and maintenance in transplant ineligible patients with newly diagnosed multiple myeloma: results from Myeloma XI, a multicentre, openâ€label, randomised, Phase III trial. British Journal of Haematology, 2021, 192, 853-868.	2.5	14

#	Article	IF	Citations
289	The Addition of Thalidomide to the Induction Treatment of Newly Presenting Myeloma Patients Increases the CR Rate Which Is Likely to Translate Into Improved PFS and OS.. Blood, 2009, 114, 352-352.	1.4	14
290	Interleukin 6, tumour necrosis factor Î± and lymphotoxin Î± polymorphisms in monoclonal gammopathy of uncertain significance and multiple myeloma. British Journal of Haematology, 2001, 112, 249-250.	2.5	13
291	Allele and haplotype frequency at human leucocyte antigen class I/II and immunomodulatory cytokine loci in patients with myelodysplasia and acute myeloid leukaemia: in search of an autoimmune aetiology. British Journal of Haematology, 2002, 117, 541-545.	2.5	13
292	Translocation t(11;14) in multiple myeloma: Analysis of translocation breakpoints on der(11) and der(14) chromosomes suggests complex molecular mechanisms of recombination. Genes Chromosomes and Cancer, 2004, 39, 151-155.	2.8	13
293	Haplotypic variation in MRE11, RAD50 and NBS1 and risk of non-Hodgkin's lymphoma. Leukemia and Lymphoma, 2006, 47, 2567-2583.	1.3	13
294	Haplotype uncertainty in association studies. Genetic Epidemiology, 2007, 31, 348-357.	1.3	13
295	Identification of Autophosphorylation Inhibitors of the Inositol-Requiring Enzyme 1 Alpha (IRE1Î±) by High-Throughput Screening Using a DELFIA Assay. Journal of Biomolecular Screening, 2013, 18, 298-308.	2.6	13
296	Proof of the Concept to Use a Malignant B Cell Line Drug Screen Strategy for Identification and Weight of Melphalan Resistance Genes in Multiple Myeloma. PLoS ONE, 2013, 8, e83252.	2.5	13
297	Adverse Metaphase Cytogenetics Can Be Overcome by Adding Bortezomib and Thalidomide to Fractionated Melphalan Transplants. Clinical Cancer Research, 2017, 23, 2665-2672.	7.0	13
298	Thalidomide Maintenance Significantly Improves Progression-Free Survival (PFS) and Overall Survival (OS) of Myeloma Patients When Effective Relapse Treatments Are Used: MRC Myeloma IX Results. Blood, 2010, 116, 623-623.	1.4	13
299	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of TP53. Oncotarget, 2019, 10, 732-737.	1.8	13
300	Characterising the TP53-deleted subgroup of chronic lymphocytic leukemia: an analysis of additional cytogenetic abnormalities detected by interphase fluorescencein situhybridisation and array-based comparative genomic hybridisation. Leukemia and Lymphoma, 2008, 49, 1879-1886.	1.3	12
301	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. Blood Cancer Journal, 2017, 7, e573-e573.	6.2	12
302	The genomic landscape of plasma cells in systemic light chain amyloidosis. Blood, 2018, 132, 2775-2777.	1.4	12
303	Lack of Spleen Signal on Diffusion Weighted MRI is associated with High Tumor Burden and Poor Prognosis in Multiple Myeloma: A Link to Extramedullary Hematopoiesis?. Theranostics, 2019, 9, 4756-4763.	10.0	12
304	Stem cell mutations can be detected in myeloma patients years before onset of secondary leukemias. Blood Advances, 2019, 3, 3962-3967.	5.2	12
305	Sex Differences in Multiple Myeloma Biology but not Clinical Outcomes: Results from 3894 Patients in the Myeloma XI Trial. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, 667-675.	0.4	12
306	Minimal Residual Disease in the Maintenance Setting in Myeloma: Prognostic Significance and Impact of Lenalidomide. Blood, 2017, 130, 904-904.	1.4	12

#	Article	IF	Citations
307	The Bone Marrow Microenvironment Influences the Differential Chemokine Receptor Expression of Normal and Neoplastic Plasma Cells.. Blood, 2004, 104, 2353-2353.	1.4	12
308	Current and potential epigenetic targets in multiple myeloma. Epigenomics, 2014, 6, 215-228.	2.1	11
309	Genetic factors influencing the risk of multiple myeloma bone disease. Leukemia, 2016, 30, 883-888.	7.2	11
310	Where are we now with the treatment of multiple myeloma?. Nature Reviews Clinical Oncology, 2017, 14, 461-462.	27.6	11
311	Bortezomib, Vorinostat, and Dexamethasone Combination Therapy in Relapsed Myeloma: Results of the Phase 2 MUK four Trial. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, 154-161.e3.	0.4	11
312	Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. Leukemia, 2021, 35, 3017-3020.	7.2	11
313	Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget, 2017, 8, 36203-36210.	1.8	11
314	Inflammation and infection in plasma cell disorders: how pathogens shape the fate of patients. Leukemia, 2022, 36, 613-624.	7.2	11
315	Genetic subtypes of smoldering multiple myeloma are associated with distinct pathogenic phenotypes and clinical outcomes. Nature Communications, 2022, 13, .	12.8	11
316	An update on drug combinations for treatment of myeloma. Expert Opinion on Investigational Drugs, 2008, 17, 1-12.	4.1	10
317	Positive selection as the unifying force for clonal evolution in multiple myeloma. Leukemia, 2021, 35, 1511-1515.	7.2	10
318	Analysis of Intestinal Microbiome in Multiple Myeloma Reveals Progressive Dysbiosis Compared to MGUS and Healthy Individuals. Blood, 2019, 134, 3076-3076.	1.4	10
319	Adjusting for Patient Crossover in Clinical Trials Using External Data: A Case Study of Lenalidomide for Advanced Multiple Myeloma. Value in Health, 2011, 14, 672-678.	0.3	9
320	Extensive Remineralization of Large Pelvic Lytic Lesions Following Total Therapy Treatment in Patients With Multiple Myeloma. Journal of Bone and Mineral Research, 2017, 32, 1261-1266.	2.8	9
321	Maintenance Therapy with the Oral Proteasome Inhibitor (PI) Ixazomib Significantly Prolongs Progression-Free Survival (PFS) Following Autologous Stem Cell Transplantation (ASCT) in Patients with Newly Diagnosed Multiple Myeloma (NDMM): Phase 3 Tourmaline-MM3 Trial. Blood, 2018, 132, 301-301.	1.4	9
322	Response Adapted Induction Treatment Improves Outcomes for Myeloma Patients; Results of the Phase III Myeloma XI Study. Blood, 2016, 128, 244-244.	1.4	9
323	A Favorable BCL-2 Family Expression Profile May Explain the Increased Susceptibility of the t(11;14) Multiple Myeloma Subgroup to Single Agent Venetoclax. Blood, 2016, 128, 5613-5613.	1.4	9
324	Regional differences in the treatment approaches for relapsed multiple myeloma: An IMF study.. Journal of Clinical Oncology, 2012, 30, 8095-8095.	1.6	9

#	Article	IF	Citations
325	The combination of HDAC and aminopeptidase inhibitors is highly synergistic in myeloma and leads to disruption of the NFÎºB signalling pathway. Oncotarget, 2015, 6, 17314-17327.	1.8	9
326	The Genetic Contribution to the Aetiology of Thalidomide Associated VTE.. Blood, 2006, 108, 246-246.	1.4	9
327	Poor metabolizer status at the cytochrome p450 2c19 and 2d6 loci does not modulate susceptibility to therapy-related acute myeloid leukaemia. British Journal of Haematology, 2003, 121, 192-194.	2.5	8
328	Risk of multiple myeloma in a caseâ€“spouse study. Leukemia and Lymphoma, 2016, 57, 1450-1459.	1.3	8
329	Maintaining therapeutic progress in multiple myeloma by integrating genetic and biological advances into the clinic. Expert Review of Hematology, 2018, 11, 513-523.	2.2	8
330	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. Leukemia, 2021, , .	7.2	8
331	The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. Blood, 2016, 128, 4431-4431.	1.4	8
332	Daratumumab Single Agent and Daratumumab Plus Pomalidomide and Dexametasone in Relapsed/Refractory Multiple Myeloma: A Real Life Retrospective Evaluation. Blood, 2016, 128, 4516-4516.	1.4	8
333	The Combination of Velcade, Idarubicin and Melphalan (VIM) Demonstrates Significant Clinical Activity in Relapsed/Refractory Myeloma Patients.. Blood, 2007, 110, 2727-2727.	1.4	8
334	Ixazomib with cyclophosphamide and dexamethasone in relapsed or refractory myeloma: MUKeight phase II randomised controlled trial results. Blood Cancer Journal, 2022, 12, 52.	6.2	8
335	Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers. Genome Research, 2022, 32, 1343-1354.	5.5	8
336	High dose immunosuppressive therapy and stem cell transplantation in autoimmune and inflammatory diseases. International Immunopharmacology, 2002, 2, 399-414.	3.8	7
337	The outcome of high-dose chemotherapy and auto-SCT in patients with multiple myeloma: a UK/Ireland and European benchmarking comparative analysis. Bone Marrow Transplantation, 2011, 46, 1210-1218.	2.4	7
338	Identification of a novel t(7;14) translocation in multiple myeloma resulting in overexpression of EGFR. Genes Chromosomes and Cancer, 2013, 52, 817-822.	2.8	7
339	Transplants for the elderly in myeloma. Blood, 2013, 122, 1332-1334.	1.4	7
340	A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. Leukemia and Lymphoma, 2015, 56, 594-601.	1.3	7
341	Genome-wide association study of clinical parameters in immunoglobulin light chain amyloidosis in three patient cohorts. Haematologica, 2017, 102, e411-e414.	3.5	7
342	Renal outcome in patients with newly diagnosed multiple myeloma: results from the UK NCRI Myeloma XI trial. Blood Advances, 2020, 4, 5836-5845.	5.2	7

#	Article	IF	Citations
343	Novel Drugs in Myeloma: Harnessing Tumour Biology to Treat Myeloma. Recent Results in Cancer Research, 2011, 183, 151-187.	1.8	7
344	TRUE SPECTRUM OF 14q32 TRANSLOCATIONS IN MULTIPLE MYELOMA. British Journal of Haematology, 1998, 103, 1209-1210.	2.5	7
345	Economic Evaluation of Lenalidomide Combined with Dexamethasone for the Treatment of Multiple Myeloma in the UK. Blood, 2008, 112, 2400-2400.	1.4	7
346	High Risk Multiple Myeloma Demonstrates Marked Spatial Genomic Heterogeneity Between Focal Lesions and Random Bone Marrow; Implications for Targeted Therapy and Treatment Resistance. Blood, 2015, 126, 20-20.	1.4	7
347	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. Blood Cancer Journal, 2022, 12, .	6.2	7
348	Transfection of siRNAs in Multiple Myeloma Cell Lines. Methods in Molecular Biology, 2010, 623, 299-309.	0.9	6
349	Monoclonal antibody therapy in multiple myeloma: where do we stand and where are we going?. Immunotherapy, 2016, 8, 367-384.	2.0	6
350	The safety of pomalidomide for the treatment of multiple myeloma. Expert Opinion on Drug Safety, 2016, 15, 535-547.	2.4	6
351	Response comparison of multiple myeloma and monoclonal gammopathy of undetermined significance to the same anti-myeloma therapy: a retrospective cohort study. Lancet Haematology,the, 2017, 4, e584-e594.	4.6	6
352	Sequential minimal residual disease (MRD) monitoring: Results from the UK Myeloma XI trial. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e45-e46.	0.4	6
353	Plasma cells expression from smouldering myeloma to myeloma reveals the importance of the PRC2 complex, cell cycle progression, and the divergent evolutionary pathways within the different molecular subgroups. Leukemia, 2022, 36, 591-595.	7.2	6
354	A Quadruplet Regimen Comprising Carfilzomib, Cyclophosphamide, Lenalidomide, Dexamethasone (KCRD) Vs an Immunomodulatory Agent Containing Triplet (CTD/CRD) Induction Therapy Prior to Autologous Stem Cell Transplant: Results of the Myeloma XI Study. Blood, 2018, 132, 302-302.	1.4	6
355	Clinical Development of a Non-Gene-Edited Allogeneic Bcma-Targeting CAR T-Cell Product in Relapsed or Refractory Multiple Myeloma. Blood, 2020, 136, 27-28.	1.4	6
356	The Combination of Cyclophosphamide, Velcade and Dexamethasone (CVD) Induces High Response Rates with Minimal Toxicity Compared to Velcade Alone (V) and Velcade Plus Dexamethasone (VD).. Blood, 2006, 108, 3537-3537.	1.4	6
357	Carfilzomib, Cyclophosphamide and Dexamethasone (KCD) Versus Bortezomib, Cyclophosphamide and Dexamethasone (VCD) for Treatment of First Relapse or Primary Refractory Multiple Myeloma (MM): First Final Analysis of the Phase 2 Muk Five Study. Blood, 2017, 130, 835-835.	1.4	6
358	The genomic features associated with high-risk multiple myeloma. Oncotarget, 2018, 9, 35478-35479.	1.8	6
359	Proteasome inhibition and multiple myeloma. Current Opinion in Investigational Drugs, 2007, 8, 447-51.	2.3	6
360	Myeloma Genome Project Panel is a Comprehensive Targeted Genomics Panel for Molecular Profiling of Patients with Multiple Myeloma. Clinical Cancer Research, 2022, 28, 2854-2864.	7.0	6

#	Article	IF	Citations
361	Patients entered into MRC AML trials are biologically representative of the totality of the disease in the UK. International Journal of Laboratory Hematology, 2002, 24, 263-265.	0.2	5
362	The bone marrow microenvironment influences the differential chemokine receptor expression of normal and neoplastic plasma cells. Blood, 2005, 105, 4895-4896.	1.4	5
363	A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. Blood Advances, 2018, 2, 2400-2411.	5.2	5
364	Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregulate Gene Function By a Range of Mechanisms. Blood, 2019, 134, 3767-3767.	1.4	5
365	Economic Evaluation of Bortezomib (VELCADE) for Relapsed and Refractory Multiple Myeloma.. Blood, 2004, 104, 268-268.	1.4	5
366	Sequential Immunomodulatory Drug (IMiD) and Proteosome Inhibitor Therapy Improves Response Rates in Newly Diagnosed Multiple Myeloma: Preliminary Results From the Myeloma XI Trial. Blood, 2012, 120, 335-335.	1.4	5
367	Higher Expressions of PTH Receptor Type 1 and/or 2 in Bone Marrow Is Associated to Longer Survival in Newly Diagnosed Myeloma Patients Enrolled in Total Therapy 3. Blood, 2014, 124, 3409-3409.	1.4	5
368	Primary IMiD Refractory Myeloma; Results from 3894 Patients Treated in the Phase III Myeloma XI Study. Blood, 2016, 128, 1144-1144.	1.4	5
369	A Phase I Dose-Escalation Study of the Class 1 Selective Histone Deacetylase Inhibitor CHR-3996 in Combination with Tosedostat for Patients with Relapsed, Refractory Multiple Myeloma: Results of the Muk Three Trial. Blood, 2016, 128, 3321-3321.	1.4	5
370	A Novel Functional Role for MMSET in RNA Processing Based on the Link Between the REIIBP Isoform and Its Interaction with the SMN Complex. PLoS ONE, 2014, 9, e99493.	2.5	5
371	Proteomic Evaluation of Pathways Associated with Dexamethasone-Induced Apoptosis and Resistance in Multiple Myeloma.. Blood, 2004, 104, 642-642.	1.4	5
372	What is the evidence for the use of bisphosphonate therapy in newly diagnosed multiple myeloma patients lacking bone disease?. Hematology American Society of Hematology Education Program, 2012, 2012, 350-353.	2.5	4
373	Response and biological subtype of myeloma are independent prognostic factors and combine to define outcome after highâ€dose therapy. British Journal of Haematology, 2013, 161, 291-294.	2.5	4
374	Thymic PTH Increases After Thyroparathyroidectomy in C57BL/KaLwRij Mice. Endocrinology, 2018, 159, 1561-1569.	2.8	4
375	Highâ€risk transcriptional profiles in multiple myeloma are an acquired feature that can occur in any subtype and more frequently with each subsequent relapse. British Journal of Haematology, 2021, 195, 283-286.	2.5	4
376	Targeting Bone in Myeloma. Recent Results in Cancer Research, 2012, 192, 127-143.	1.8	4
377	CRD: A Phase 1 Dose Escalation Study to Determine the Maximum Tolerated Dose of Cyclophosphamide in Combination with Lenalidomide and Dexamethasone in Relapsed/Refractory Myeloma. Blood, 2008, 112, 3707-3707.	1.4	4
378	Low Expression Of The FUCA1 Gene Is An Adverse Prognostic Factor In Myeloma and Combined With High Sialyltransferase Gene Expression Identifies Patients At Increased Risk Of Early Disease Progression and Death. Blood, 2013, 122, 1864-1864.	1.4	4

#	Article	IF	Citations
379	Multiple Myeloma Cells Express Functional E-Selectin Ligands Which Can be Inhibited Both in-Vitro and in-Vivo Leading to Prolongation of Survival in a Murine Transplant Model. Blood, 2014, 124, 4718-4718.	1.4	4
380	Targeted MEK Inhibition in Patients with Previously Treated Multiple Myeloma. Blood, 2014, 124, 4775-4775.	1.4	4
381	Hyperhaploid karyotypes in multiple myeloma. Oncotarget, 2017, 8, 78259-78260.	1.8	4
382	Genome-Wide Identification of Gene Expression Networks Affected by Genomic Changes in Multiple Myeloma.. Blood, 2007, 110, 2494-2494.	1.4	4
383	Residual Monoclonal Free Light Chain Positivity By Mass Spectrometry Identifies Patients at Increased Risk of Early Relapse Following First-Line Anti-Myeloma Treatment. Blood, 2021, 138, 820-820.	1.4	4
384	Insights into high-risk multiple myeloma from an analysis of the role of PHF19 in cancer. Journal of Experimental and Clinical Cancer Research, 2021, 40, 380.	8.6	4
385	Neuron-specific enolase expression in multiple myeloma. Lancet Oncology, The, 2006, 7, 960.	10.7	3
386	Collection of peripheral blood stem cells in new patients with myeloma receiving minimal or no prior cytoreductive therapy. Hematology, 2007, 12, 113-115.	1.5	3
387	p53 protein overexpression in bone marrow biopsies from chronic lymphocytic leukaemia is associated with TP53 deletion and resistance to fludarabine. Journal of Hematopathology, 2010, 3, 61-68.	0.4	3
388	Targeting Bone as a Therapy for Myeloma. Cancer Microenvironment, 2011, 4, 299-311.	3.1	3
389	Could DNA methylation become a useful measure for multiple myeloma prognoses?. Expert Review of Hematology, 2011, 4, 125-127.	2.2	3
390	Preclinical evaluation of the new GPRC5DxCD3 (JNJ-7564) bispecific antibody for the treatment of multiple myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e122-e123.	0.4	3
391	FRAX is a robust predictor of baseline vertebral fractures in multiple myeloma patients. Bone, 2019, 121, 134-138.	2.9	3
392	Case Report: Two Cases of Cryptosporidiosis in Heavily Pretreated Patients With Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, 21, e545-e547.	0.4	3
393	Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. Blood, 2018, 132, 1882-1882.	1.4	3
394	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. Blood, 2018, 132, 408-408.	1.4	3
395	Genetic Variation in ADME Genes Is Associated with Thalidomide Related Peripheral Neuropathy in Multiple Myeloma Patients.. Blood, 2008, 112, 1675-1675.	1.4	3
396	Optimising Bone Disease In Myeloma; Zoledronic Acid Plus Thalidomide Combinations Improves Survival and Bone Endpoints: Results of the MRC Myeloma IX Trial. Blood, 2010, 116, 311-311.	1.4	3

#	Article	IF	Citations
397	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. Blood, 2010, 116, 782-782.	1.4	3
398	The Value Of Serum Free Light Chain Monitoring Compared To Urinary Bence-Jones Measurement In Light Chain Only Myeloma. Blood, 2013, 122, 1895-1895.	1.4	3
399	Curing Multiple Myeloma (MM) with Total Therapy (TT). Blood, 2014, 124, 195-195.	1.4	3
400	Characterization of the Mutational Landscape of Multiple Myeloma Using Comprehensive Genomic Profiling. Blood, 2014, 124, 3418-3418.	1.4	3
401	Mesenchymal Stem Cells Preconditioned with Myeloma Cells from High-Risk Patients Support the Growth of Myeloma Cells from Low-Risk Patients. Blood, 2016, 128, 3304-3304.	1.4	3
402	Incidence of Second Malignant Neoplasms (SMN) after Haematopoetic Stem Cell Transplant.. Blood, 2006, 108, 551-551.	1.4	3
403	Spatial-Temporal Genomic Analyses Reveal a Component of "Big Bang" Kinetics in Multiple Myeloma Evolution. Blood, 2016, 128, 239-239.	1.4	3
404	MYC Rearrangements in Multiple Myeloma Are Complex, Can Involve More Than Five Different Chromosomes, and Correlate with Increased Expression of MYC and a Distinct Downstream Gene Expression Pattern. Blood, 2017, 130, 65-65.	1.4	3
405	Outcome of high-dose cytarabine-based induction therapy followed by hematopoietic stem cell transplantation in acute myeloid leukemia: influence of karyotype. Leukemia and Lymphoma, 2008, 49, 2284-2290.	1.3	2
406	Myeloma:diagnosis complications and supportive care. Hematology, 2012, 17, s109-s111.	1.5	2
407	Active multiple myeloma suppresses and typically eliminates coexisting MGUS. British Journal of Cancer, 2017, 117, 835-839.	6.4	2
408	Integration of Genomics Into Treatment: Are We There Yet?. American Society of Clinical Oncology Educational Book / ASCO American Society of Clinical Oncology Meeting, 2017, 37, 569-574.	3.8	2
409	Distinct promoter methylation profile reveals spatial epigenetic heterogeneity in 2 myeloma patients with multifocal extramedullary relapses. Clinical Epigenetics, 2018, 10, 158.	4.1	2
410	Antibody-based targeting of BCMA in multiple myeloma. Lancet Oncology, The, 2020, 21, 186-187.	10.7	2
411	Heterogenous mutation spectrum and deregulated cellular pathways in aberrant plasma cells underline molecular pathology of light-chain amyloidosis. Haematologica, 2021, 106, 601-604.	3.5	2
412	The Mutational Landscape of Primary Plasma Cell Leukemia. Blood, 2018, 132, 114-114.	1.4	2
413	A High-Risk Multiple Myeloma Group Identified By Integrative Multi-Omics Segmentation of Newly Diagnosed Patients. Blood, 2018, 132, 3165-3165.	1.4	2
414	The Spectrum of Exomic Mutation in Elderly Myeloma Differs Substantially from Patients at Younger Ages Consistent with a Different Evolutionary Trajectory to Full Blown Disease Based on Age of Onset. Blood, 2019, 134, 4346-4346.	1.4	2

#	Article	IF	Citations
415	Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive Versus Stable Myeloma Precursor Disease. Blood, 2020, 136, 47-48.	1.4	2
416	Fine Mapping and Expression Analysis of Chromosome 1 with the Aim of Defining Critically Deregulated Genes Important in the Pathogenesis of Myeloma.. Blood, 2006, 108, 112-112.	1.4	2
417	Lenolidamide (Revlimid), in Combination with Cyclophosphamide and Dexamethasone (CRD) Is an Effective Regimen for Heavily Pre-Treated Myeloma Patients.. Blood, 2006, 108, 3555-3555.	1.4	2
418	Different IGH Rearrangement and Somatic Hypermutation Patterns in Hairy-Cell Leukemia, Hairy-Cell Leukemia Variant and Splenic Marginal Zone Lymphoma.. Blood, 2007, 110, 2082-2082.	1.4	2
419	Aminopeptidase Inhibition as a Targeted Treatment Strategy in Myeloma.. Blood, 2007, 110, 2505-2505.	1.4	2
420	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. Blood, 2009, 114, 426-426.	1.4	2
421	MRC Myeloma IX, 6 Year Median Follow-up (FU) Highlights the Importance of Long-Term FU in Myeloma Clinical Trials and Differential Effects of Thalidomide in High- and Low-Risk Disease. Blood, 2011, 118, 993-993.	1.4	2
422	The Spectrum of Epigenetic Mutations in Myeloma and Their Clinical Impact. Blood, 2014, 124, 2194-2194.	1.4	2
423	Safety and Efficacy in the Stratus (MM-010) Trial, a Single-Arm Phase 3b Study Evaluating Pomalidomide + Low-Dose Dexamethasone in Patients with Refractory or Relapsed and Refractory Multiple Myeloma. Blood, 2014, 124, 80-80.	1.4	2
424	The Composition and Clinical Impact of Focal Lesions and Their Impact on the Microenvironment in Myeloma. Blood, 2015, 126, 1806-1806.	1.4	2
425	Melphalan Affects Genes Critical for Myeloma Survival, Homing, and Response to Cytokines and Chemokines. Blood, 2015, 126, 1808-1808.	1.4	2
426	Impact of Minimal Residual Disease in High and Standard Risk Multiple Myeloma. Blood, 2015, 126, 2979-2979.	1.4	2
427	Specific Exosomal microRNA Are Differentially Expressed Between High and Low-Risk Myeloma Suggesting They Are Pathogenically Important. Blood, 2015, 126, 4189-4189.	1.4	2
428	The Co-Occurrence of MAF Translocations in RAS Mutated Multiple Myeloma Confers Resistance to MEK Inhibition. Blood, 2016, 128, 1138-1138.	1.4	2
429	Myeloma-Derived Exosomes and Soluble Factors Suppress Natural Killer Cell Function. Blood, 2016, 128, 2066-2066.	1.4	2
430	Myeloma Exosomes Prime the Microenvironment to Support Survival and Growth of Myeloma Cells. Blood, 2016, 128, 2067-2067.	1.4	2
431	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278.	1.4	2
432	Identifying Ultra-High Risk Myeloma By Integrated Molecular Genetic and Gene Expression Profiling. Blood, 2016, 128, 4407-4407.	1.4	2

#	Article	IF	Citations
433	The Impact of Maintenance Lenalidomide on the Mutational Status of the Myeloma Clone at Relapse in the NCRI Myeloma XI Trial for Newly Diagnosed Multiple Myeloma Patients (NDMM). Blood, 2016, 128, 4412-4412.	1.4	2
434	A Phase I Study of CHR-2797, an Orally Active Aminopeptidase Inhibitor in Elderly and/or Treatment Refractory Patients with Acute Myeloid Leukemia or Multiple Myeloma.. Blood, 2007, 110, 443-443.	1.4	2
435	MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. Blood, 2013, 122, 274-274.	1.4	2
436	A Prognostic 51-Gene Signature Linked to Abnormal Metaphase Cytogenetics Identifies Myeloma Patients Who Benefit from Fractionated Melphalan Dosing and Added Bortezomib, Thalidomide and Dexamethasone As Conditioning for Autologous Stem Cell Transplant. Blood, 2015, 126, 3181-3181.	1.4	2
437	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. Blood, 2016, 128, 196-196.	1.4	2
438	Translocations and Jumping Rearrangements at 8q24 Result in over-Expression of MYC and are Key Drivers of Disease Progression. Blood, 2016, 128, 115-115.	1.4	2
439	Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. Blood, 2016, 128, 3271-3271.	1.4	2
440	Maximizing Pre-Transplant Response Is Associated with Improved Outcome for Myeloma Patients: Exploratory Analysis of the Myeloma XI Trial. Blood, 2018, 132, 3280-3280.	1.4	2
441	Genetic Segmentation and Targeted Therapeutics for Multiple Myeloma. Oncology & Hematology Review, 2019, 15, 87.	0.2	2
442	Allele Imbalance at Tumour Suppressor Loci During the Indolent Phase of Follicle Centre Cell Lymphoma. Leukemia and Lymphoma, 1996, 22, 113-117.	1.3	1
443	Long Distance Vectorette PCR (LDV PCR). , 2002, 192, 275-284.		1
444	Targeting both BET and CBP/EP300 proteins with the novel dual inhibitors NEO2734 and NEO1132 leads to anti-tumor activity in Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e120-e121.	0.4	1
445	Quadruplet KCRD (Carfilzomib, Cyclophosphamide, Lenalidomide and Dexamethasone) Induction for Newly Diagnosed Myeloma Patients. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e2.	0.4	1
446	A detailed exploration of using RNA-Seq data in established multiple myeloma gene expression profile microarray based risk scores. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e57-e58.	0.4	1
447	From Bench to Bedside. Cancer Journal (Sudbury, Mass), 2021, 27, 213-221.	2.0	1
448	Deep Immunoprofiling of the Bone Marrow Microenvironmental Changes Underlying the Multistep Progression of Multiple Myeloma. Blood, 2018, 132, 243-243.	1.4	1
449	Long-Term Follow-up Identifies Double Hit and Key Mutations As Impacting Progression Free and Overall Survival in Multiple Myeloma. Blood, 2018, 132, 110-110.	1.4	1
450	A Phase I Trial of CHIR-258, a Multitargeted RTK Inhibitor, in Acute Myeloid Leukemia (AML).. Blood, 2005, 106, 2794-2794.	1.4	1

#	Article	IF	Citations
451	Integration of Gene Mapping and Expression Arrays Identifies Mechanisms by Which Genes Are Dysregulated as a Result of Copy Number Loss and Gain Associated with IgH Translocations in Multiple Myeloma.. Blood, 2007, 110, 395-395.	1.4	1
452	Developing a SNP Classifier for Predicting Peripheral Neuropathy by Bortezomib in Multiple Myeloma Patients.. Blood, 2009, 114, 1800-1800.	1.4	1
453	Abnormal Serum IgA Kappa / IgA Lambda Ratios at Maximum Response Predict Poor Progression Free Survival in Myeloma Patients.. Blood, 2009, 114, 4879-4879.	1.4	1
454	Hypermethylation Is A Key Feature of the Transition of Multiple Myeloma to Plasma Cell Leukemia. Blood, 2010, 116, 535-535.	1.4	1
455	Further Evolution of Metronomic Therapy Extended to 28 Days (Metro28) for Relapsed Refractory Multiple Myeloma (RRMM). Blood, 2014, 124, 2128-2128.	1.4	1
456	Somatic Mutation Spectrum in Monoclonal Gammopathy of Undetermined Significance Compared to Multiple Myeloma. Blood, 2014, 124, 3346-3346.	1.4	1
457	Minimal Residual Disease (MRD) in Myeloma: Independent Outcome Prediction and Sequential Survival Benefits per Log Tumour Reduction. Blood, 2014, 124, 3416-3416.	1.4	1
458	Upfront 28-Day Metronomic Therapy for High-Risk Multiple Myeloma (HRMM). Blood, 2015, 126, 1843-1843.	1.4	1
459	Myeloma XI Trial for Newly Diagnosed Multiple Myeloma (NDMM); A Report of Second Primary Malignancy (SPM) Rates and the Importance of Review of Reported Cases. Blood, 2015, 126, 1847-1847.	1.4	1
460	Comprehensive Genomic Profiling of Multiple Myeloma in the Course of Clinical Care Identifies Targetable and Prognostically Significant Genomic Alterations. Blood, 2015, 126, 369-369.	1.4	1
461	The Impact of Combination Chemotherapy and Tandem Stem Cell Transplant on Clonal Substructure and Mutational Pattern at Relapse of MM. Blood, 2015, 126, 372-372.	1.4	1
462	Signatures of Mesenchymal Cell Lineages and Microenvironment Factors Are Dysregulated in High Risk Myeloma. Blood, 2016, 128, 2065-2065.	1.4	1
463	Concurrent Amplification of MYC and 1q21 in Multiple Myeloma: Focal and Segmental Jumping Translocations of MYC. Blood, 2016, 128, 3266-3266.	1.4	1
464	The 70-Gene MyPRSR prognostic Risk Score Signature Predicts Increased Risk of Progression from MGUS to Multiple Myeloma Requring Treatment. Blood, 2016, 128, 3275-3275.	1.4	1
465	Automated Multiparameter Flow Cytometry (MFC) Immunophenotyping for Reproducible Identification of High Risk Smoldering Multiple Myeloma (SMM). Blood, 2016, 128, 373-373.	1.4	1
466	Comparison of MRD Detection By MFC, NGS and PET-CT in Patients at Different Treatment Stages for Multiple Myeloma. Blood, 2016, 128, 377-377.	1.4	1
467	Use of Multiple Myeloma 70-Gene Prognostic Risk Score As a Continuous Predicitor of Patient Outcome. Blood, 2016, 128, 5614-5614.	1.4	1
468	DNA Methylation Profiling of Myeloma Trial Patients Reveals Specific Epigenetic Changes Associated with Outcome. Blood, 2016, 128, 804-804.	1.4	1

#	Article	IF	Citations
469	Efficacy and side-effect profile of long-term bisphosphonate therapy in patients (pts) with multiple myeloma (MM): MRC myeloma IX study results.. Journal of Clinical Oncology, 2012, 30, 8015-8015.	1.6	1
470	Newly Diagnosed Myeloma Pateints Are at Risk of Venous Thrombotic Events - High Risk Patients Need To Be Identified and Recieve Thromboprophylaxis: The MRC Experience.. Blood, 2004, 104, 2395-2395.	1.4	1
471	IgH Rearrangements and Mutational Status in Class-Switched IgG B-CLL.. Blood, 2004, 104, 2793-2793.	1.4	1
472	Follow up Analysis for MRC Myeloma VII Trial.. Blood, 2004, 104, 927-927.	1.4	1
473	A Comparative Analysis of Outcomes in Primary Myelodysplastic Syndrome (MDS) and Therapy-Related MDS Reveals Two Subgroups with Differing Risk Profiles: Implications for the Application of a Prognostic Classification.. Blood, 2005, 106, 2532-2532.	1.4	1
474	Abnormalities of 16q in Multiple Myeloma Are Associated with Poor Prognosis: 500K Gene Mapping and Expression Correlations Identify Two Potential Tumor Suppressor Genes, WWOX and CYLD.. Blood, 2006, 108, 110-110.	1.4	1
475	Defining Complete Response in Multiple Myeloma: Role of the Serum Free Light Chain Assay and Multiparameter Flow Cytometry.. Blood, 2007, 110, 1479-1479.	1.4	1
476	The Impact of Constitutional Copy Number Variants in Myeloma. Blood, 2008, 112, 496-496.	1.4	1
477	Inhibitors of Heat Shock Protein 72 Induction Enhance Apoptosis Induced by Hsp90 Inhibitors. Blood, 2008, 112, 2625-2625.	1.4	1
478	Inhibition of HDACs and Aminopeptidases Is Highly Synergistic in Myeloma Cells Resulting in Cell Death Via the Upregulation of BIRC3, a Key Mediator of NF-KappaB Signalling.. Blood, 2009, 114, 607-607.	1.4	1
479	Non-Cycling Cells From Acute Myeloid Leukemia Patients Harbor the FLT3-ITD Mutation and Are Insensitive to TKI258, a Potent FLT3-Directed Inhibitor, in Vitro.. Blood, 2009, 114, 479-479.	1.4	1
480	Defining High Risk Myeloma Using Co-Segregating FISH Variables; Results of MRC Myeloma IX. Blood, 2010, 116, 1907-1907.	1.4	1
481	Autophagy Is a Key Myeloma Survival Pathway That Can Be Manipulated Therapeutically to Enhance Apoptosis. Blood, 2010, 116, 4083-4083.	1.4	1
482	Whole Genome Sequencing Illuminates the Genetic and Biological Features Underlying the Transition of SMM to MM. Blood, 2011, 118, 296-296.	1.4	1
483	Mafb Protein Confers Primary Resistance of Myeloma to Proteasome Inhibitors. Blood, 2014, 124, 2091-2091.	1.4	1
484	Stem Cell-like Characteristics of MM Plasma Cells Vary By ROS Levels: Implications for Targeted Therapy. Blood, 2015, 126, 1820-1820.	1.4	1
485	Defining the Impact of Tandem Autologous Stem Cell Transplantation in Multiple Myeloma: A Case-Match Analysis in the Total Therapy Trials. Blood, 2015, 126, 3182-3182.	1.4	1
486	Identification of Biomarkers Associated with MAF-Mediated Resistance to Proteasome Inhibitors in t(14;16) Multiple Myeloma. Blood, 2015, 126, 3020-3020.	1.4	1

#	Article	IF	Citations
487	A Survey of Fusion Genes in Myeloma Identifies Kinase Domain Activation Which Could be Targeted with Available Treatments. Blood, 2016, 128, 117-117.	1.4	1
488	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. Blood, 2016, 128, 4416-4416.	1.4	1
489	Expression Signature of Myeloma Residual Cells Is Characterized By Genes Associated with Proliferation, Epigenetic Modification, and Stem Cell Maintenance. Blood, 2018, 132, 4465-4465.	1.4	1
490	Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. Blood, 2018, 132, 1906-1906.	1.4	1
491	An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. Blood, 2018, 132, 4489-4489.	1.4	1
492	The Leukaemia-Associated AML1-ETO Fusion Protein Acts as a Sequence Specific Transcriptional Repressor in vivo by Altering the Chromatin Structure of Target Genes. Clinical Science, 2003, 104, 30P-30P.	0.0	0
493	Response to Goodman et al.: Amyloidosis, not myeloma. British Journal of Haematology, 2005, 129, 159-160.	2.5	0
494	The genetic and epigenetic mechanisms underlying the behavior of myeloma. , 0, , 48-63.		0
495	B-cell malignancies: capture-sequencing strategies for identification of gene rearrangements and translocations into immunoglobulin gene loci. Blood and Lymphatic Cancer: Targets and Therapy, 2014, , 107.	2.7	0
496	Optimizing the treatment of multiple myeloma. Nature Reviews Clinical Oncology, 2014, 11, 686-688.	27.6	0
497	Reply to M. Roschewski et al. Journal of Clinical Oncology, 2014, 32, 476-477.	1.6	0
498	An Outbreak of Respiratory Syncytial Virus Infections in an Outpatient Cancer Unit: Clinical Characteristics and Molecular Investigations. Open Forum Infectious Diseases, 2016, 3, .	0.9	0
499	Long-term Analysis Of Multiple Sequential Samples Reveals Patterns Of Progression In Smoldering Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e59-e60.	0.4	0
500	Enrichment for copy number alterations and a unique pattern of gene mutations characterize multiple myeloma in elderly patients. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e81-e82.	0.4	0
501	Large deletions (>10.9 MB) in 17p and bi-allelic TP53 inactivation events in newly-diagnosed multiple myeloma are associated with higher clonal cell fraction and poor prognosis. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e81.	0.4	0
502	Circulating cell free DNA is a biomarker for GEP70 risk score and tumor burden in myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e62.	0.4	0
503	Deep sequencing as an approach to understanding the complexity and improving the treatment of multiple myeloma. Expert Review of Precision Medicine and Drug Development, 2020, 5, 363-370.	0.7	0
504	The evolving role and utility of off-label drug use in multiple myeloma. Exploration of Targeted Anti-tumor Therapy, 0, , .	0.8	0

#	Article	IF	Citations
505	Impact of Etiological Cytogenetic Abnormalities on the Depth of Immunoparesis and Survival in Newly Diagnosed Multiple Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2021, , .	0.4	0
506	Innovative approaches for diagnosis and monitoring. , 2004, , 164-178.		0
507	Responses to Induction Chemotherapy and High Dose Melphalan Can Be Incorporated within a Risk Stratification Model and Help to Identify Myeloma Patients Who May Benefit from Novel Therapies.. Blood, 2004, 104, 2394-2394.	1.4	0
508	Comparison of IgH Gene Rearrangement Configuration between Hairy Cell Leukemia (HCL) and Hairy Cell Leukemia Variant (HCL-v).. Blood, 2005, 106, 4997-4997.	1.4	0
509	Insights into the Basis of Chromosomal Imbalances during the Clonal Evolution of Multiple Myeloma Using SNP Array Analysis.. Blood, 2005, 106, 621-621.	1.4	0
510	SNP Genotypes as Prognostic Factors Associated with Staging in Myeloma: The First Combined SNP Association Analysis of SWOG, ECOG, and MRC Clinical Trials from the Bank on a Cure.. Blood, 2005, 106, 3489-3489.	1.4	0
511	Development of a Panel of 3,500 SNP Based Functional Genetic Variants Relevant to the Etiology and Outcome in Multiple Myeloma.. Blood, 2005, 106, 620-620.	1.4	0
512	Ultra-Rapid, High-Throughput Molecular Diagnostics in Hemato-Oncology.. Blood, 2005, 106, 3270-3270.	1.4	0
513	Combinations of ZAP-70, CD38 and IgVH Mutational Status as Predictors of Time to First Treatment in CLL.. Blood, 2005, 106, 711-711.	1.4	0
514	B- Cell Chronic Lymphocytic Leukaemia Complicated by Aggressive T-Cell Lymphoma: Clinical and Molecular Analysis of a Rare Variant of Richterâ€™s Syndrome.. Blood, 2005, 106, 4999-4999.	1.4	0
515	Identification of Collaborating Oncogeneic Events Leading to Disease Progression in Myeloma Cases with a t(4;14) and t(11;14) Using SNP and Gene Expression Arrays.. Blood, 2005, 106, 1542-1542.	1.4	0
516	Status of Chromosome 13 in Multiple Myeloma: Integrated Approach Using SNP Mapping Array and Gene Expression Array.. Blood, 2005, 106, 1563-1563.	1.4	0
517	Genetic variation in Th1/Th2 cytokines and the risk of developing childhood leukaemia. FASEB Journal, 2006, 20, LB123.	0.5	0
518	Lymphocyte Count on Day 56 Predicts for Reduced Risk of Infection Related Mortality Following Non-Myeloablative Allogeneic Haematopoietic Stem Cell Transplantation.. Blood, 2006, 108, 5324-5324.	1.4	0
519	Prophylactic Defibrotide in Allogeneic Stem Cell Transplantation: Low Morbidity and Zero Mortality from Veno-Occlusive Disease.. Blood, 2006, 108, 2968-2968.	1.4	0
520	Sub-Classification of Hyperdiploid Myeloma Using Global Gene Expression Profiling and SNP-Based Mapping Arrays.. Blood, 2006, 108, 3390-3390.	1.4	0
521	Pregnancy Outcome Following Haematopoietic Stem Cell Transplantation.. Blood, 2006, 108, 3367-3367.	1.4	0
522	High Dose Methylprednisolone and Rituximab Is an Effective Therapy in Advanced Refractory Chronic Lymphocytic Leukaemia Resistant to Fludarabine Therapy.. Blood, 2007, 110, 3125-3125.	1.4	0

#	Article	IF	Citations
523	The Tyrosine Kinase Inhibitor TK258 Differentially Targets Proliferating Human Hematopoietic Progenitor Cells but Does Not Eliminate the Quiescent Fraction.. Blood, 2007, 110, 3356-3356.	1.4	0
524	Immunoglobulin Gene Translocations Are Frequent in Unclassifiable CD5+ Small B-Cell Leukemias and in Particular, a Novel Subtype Characterised by t(14;19)(q32;q13) and Deregulation of BCL3 Is Described.. Blood, 2007, 110, 4230-4230.	1.4	0
525	Thalidomide in Combination with Idarubicin, Dexamethasone and Etoposide (TIDE) Is an Effective Oral Combination in Heavily Pre-Treated Myeloma Patients.. Blood, 2007, 110, 4841-4841.	1.4	0
526	Correlation between TP53 Deletion and Protein Overexpression in Chronic Lymphocytic Leukaemia and Its Impact on Prognostic.. Blood, 2007, 110, 2076-2076.	1.4	0
527	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. Blood, 2007, 110, 2473-2473.	1.4	0
528	Maintenance Chemotherapy (MC) after Autotransplantation in First-Remission Acute Lymphoblastic Leukemia (ALL): Single-Center Experience of 100 Patients.. Blood, 2007, 110, 2874-2874.	1.4	0
529	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. Blood, 2007, 110, 2474-2474.	1.4	0
530	An Integrated Pharmacogenomic Strategy for the Definition of Thalidomide Response Signatures in Presenting Cases of Multiple Myeloma.. Blood, 2007, 110, 2493-2493.	1.4	0
531	An Early CT-Diagnosis Based Treatment Strategy for Invasive Fungal Infection in Allogeneic Transplant Recipients Using Caspofungin First Line: An Effective Strategy with Low Mortality.. Blood, 2008, 112, 1149-1149.	1.4	0
532	Autologous Transplantation Is the Optimum Approach to the Management of Myeloma Patients with Extramedullary Disease at Presentation. Blood, 2008, 112, 3313-3313.	1.4	0
533	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling Identifies Kinase Pathway Alterations.. Blood, 2008, 112, 1694-1694.	1.4	0
534	Analytical Approaches for the BOAC SNP Panel Association with Progression Free Survival in Myeloma. Blood, 2008, 112, 2715-2715.	1.4	0
535	High Resolution Genomic Profiling Using Single Nucleotide Polymorphism Microarrays Identifies Multiple Novel Genomic Minimally Deleted Regions in Multiple Myeloma. Blood, 2008, 112, 625-625.	1.4	0
536	High Resolution Genomic Profiling Using Single Nucleotide Polymorphism Microarrays Reveals Novel Genomic Lesions in Hairy Cell Leukaemia and Hairy-Cell Leukaemia Variant. Blood, 2008, 112, 3136-3136.	1.4	0
537	A Single Institutionâ€™s Experience with Allogeneic Haematopoietic Stem Cell Transplantation for Acute Lymphoblastic Leukaemia: Analysis of Factors Leading to Improved Outcome. Blood, 2008, 112, 4322-4322.	1.4	0
538	XBP1 Expression Is An Important Prognostic Factor for Newly Diagnosed Myeloma Patients.. Blood, 2008, 112, 1686-1686.	1.4	0
539	Large Scale Evaluation of Genetic Variation and the Risk of Multiple Myeloma.. Blood, 2008, 112, 1679-1679.	1.4	0
540	Homozygous Deletions Can Be Used to Define a Cell Death Specific Gene Expression Signature Able to Predict Outcome in Myeloma. Blood, 2008, 112, 2725-2725.	1.4	0

#	Article	IF	Citations
541	Genome-Wide Profiling of DNA Copy Number Variation in CLL Cases Lacking 17p- (TP53) or 11q- (ATM) Abnormalities Selected from the CLL4 Study. Blood, 2008, 112, 3140-3140.	1.4	0
542	Gene Expression Profiling Classifies Splenic Marginal Zone Lymphoma and Hairy Cell Leukemia-Variant as Related Diseases That Are Distinct From Typical Hairy Cell Leukemia.. Blood, 2009, 114, 3467-3467.	1.4	0
543	Global Methylation Array Analysis of Multiple Myeloma Samples Indicate An Alteration of Epigenetics During the Transition From MGUS to Myeloma and An Increased Frequency of Gene Methylation in t(4;14) Myeloma.. Blood, 2009, 114, 121-121.	1.4	0
544	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling.. Blood, 2009, 114, 1793-1793.	1.4	0
545	UTX, a Histone Demethylase, Is Inactivated through Homozygous Deletion, Mutation, and DNA Methylation in Multiple Myeloma.. Blood, 2009, 114, 1798-1798.	1.4	0
546	Serum Free Light Chain and Serum Heavy / Light Chain Ratios Are Independently Prognostic in Multiple Myeloma Patients.. Blood, 2009, 114, 4880-4880.	1.4	0
547	Identification of Single Nucleotide Polymorphism Interactions Associated with Survival and Risk In Multiple Myeloma Using Novel Data Mining Methods. Blood, 2010, 116, 2973-2973.	1.4	0
548	Expression Profile and up-Regulation of Telomere-Associated Proteins In Multiple Myeloma. Blood, 2010, 116, 4050-4050.	1.4	0
549	Deletion 13, Detected by Metaphase Analysis, Is Not a Significant Prognostic Indicator In Myeloma. Blood, 2010, 116, 2980-2980.	1.4	0
550	The Introduction of Novel Agents Improves Outcomes of Young Patients with Myeloma (MM) Treated with Autologous Stem Cell Transplant (ASCT). Blood, 2010, 116, 1348-1348.	1.4	0
551	Cost-Effectiveness of Zoledronic Acid Versus Clodronate In Patients with Multiple Myeloma From a Canadian Healthcare System Perspective.. Blood, 2010, 116, 3812-3812.	1.4	0
552	The Interaction of Response and FISH-Based Risk Stratification to Better Define Clinical Outcome in Myeloma. Blood, 2011, 118, 1823-1823.	1.4	0
553	A Novel Mouse Model of Multiple Myeloma Representative of Human Disease and Its Use in Preclinical Therapeutic Assessment. Blood, 2011, 118, 2907-2907.	1.4	0
554	High Readmission Rates Are Associated with a Significant Economic Burden and Poor Outcome in Patients with Grade 3/4 Acute GvHD. Blood, 2011, 118, 2061-2061.	1.4	0
555	Differences in Patterns of Treatment and Outcome Among Patients with Relapsed Refractory Myeloma From United States, Europe and Asia,. Blood, 2011, 118, 3989-3989.	1.4	0
556	Exome Sequencing of the t(4;14) and t(11;14) Translocation Specific Subgroups of MM. Blood, 2011, 118, 1817-1817.	1.4	0
557	The Natural History of Myeloma Patients Who Relapse Early After High Dose Therapy.. Blood, 2012, 120, 3125-3125.	1.4	0
558	Base-Pair Resolution Mapping of IGH Translocations in Multiple Myeloma Using Targeted Capture and Massively Parallel Sequencing. Blood, 2012, 120, 3490-3490.	1.4	0

#	Article	IF	Citations
559	Single-Cell Genetic Analysis Reveals The Genetic Composition Of Founder Clones, Phylogenetic Patterns Of Branching and Parallel Evolution, and Clonal Fluctuations Following Patient Treatment In Multiple Myeloma. Blood, 2013, 122, 398-398.	1.4	0
560	Flow Cytometry Defined Cytoplasmic Immunoglobulin Index Is a Major Prognostic Factor for Progression of Asymptomatic Monoclonal Gammopathies to Clinical Multiple Myeloma. Blood, 2014, 124, 2079-2079.	1.4	0
561	Identifying a Gene Expression (GEP)-Based Model Predicting for Progression from AMM to Cmm Requiring Therapy in S0120 Patients Treated at Mirt. Blood, 2014, 124, 2078-2078.	1.4	0
562	PET-CT Defined Focal Lesions at Baseline and Day 7 Predict Outcome in GEP 70 Defined High Risk Multiple Myeloma Patients. Blood, 2014, 124, 3407-3407.	1.4	0
563	High Resolution Genome Wide DNA Methylation Analysis in a Large Trial Group Reveals a Novel Epigenetically Defined Subgroup of Myeloma Patients Characterized By Developmental Gene Hypermethylation. Blood, 2014, 124, 2189-2189.	1.4	0
564	Prediction of High and Low-Risk Multiple Myeloma Based on the EMC92 Gene Expression Signature and the International Staging System. Blood, 2014, 124, 3358-3358.	1.4	0
565	Apobec Family Mutational Signatures Are Associated with Poor Prognosis Translocations in Multiple Myeloma. Blood, 2014, 124, 723-723.	1.4	0
566	Defining Risk of MGUS and AMM Progression to Myeloma By Ig Heavy-Chain FISH. Blood, 2014, 124, 3408-3408.	1.4	0
567	Outcomes of Autologous Transplantation for Treatment-Related AML and MDS in Previously Treated Multiple Myeloma Patients (pts). Blood, 2015, 126, 1997-1997.	1.4	0
568	Assessment of Total Lesion Glycolysis and Metabolic Tumor Volume Improve the Clinical Value of Focal Lesion Assessment By FDG PET/CT in Myeloma. Blood, 2015, 126, 724-724.	1.4	0
569	Deletion of TP53 (17p13) Is Associated with Poor Outcome for Newly Diagnosed High-Risk Multiple Myeloma. Blood, 2015, 126, 2982-2982.	1.4	0
570	Molecular Subtyping and Risk Stratification for the Classification of Myeloma. Blood, 2015, 126, 4173-4173.	1.4	0
571	Identifying Targets for Therapy in High Risk t(4;14) Myeloma Using Multi-Level Molecular and Phenotypic Analysis of Isogenic MMSET and MMSET Knock out Cell Lines. Blood, 2015, 126, 1792-1792.	1.4	0
572	Differential ICAM3 Gene Expression Correlates with Susceptibility to Natural Killer Cell-Mediated Lysis in Multiple Myeloma. Blood, 2015, 126, 2990-2990.	1.4	0
573	Profound Impact of Sample Processing Delay on Gene Expression of Multiple Myeloma Plasma Cells. Blood, 2015, 126, 2996-2996.	1.4	0
574	Extending Metronomic Therapy to 28 Days (metro28) for Relapsed Refractory Multiple Myeloma (RRMM). Blood, 2015, 126, 5395-5395.	1.4	0
575	Re-Mineralization of Large Pelvic Lytic Lesions By CT Imaging in Patients with Multiple Myeloma: The Arkansas Experience. Blood, 2015, 126, 4193-4193.	1.4	0
576	Next Generation Sequencing (NGS) Based Minimal Residual Disease (MRD) Testing Is Highly Predictive of Overall and Progression Free Survival in the Total Therapy Trials and Shows Different Prognostic Implications in High Vs Standard Risk Multiple Myeloma. Blood, 2016, 128, 2064-2064.	1.4	0

#	Article	IF	Citations
577	The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. Blood, 2016, 128, 4441-4441.	1.4	0
578	The Metabolic Phenotype of Myeloma Plasma Cells Differs Between Active and Residual Disease States. Blood, 2016, 128, 4438-4438.	1.4	0
579	Clinical Application of Epigenetic Modifier Mutations in Myeloma. Blood, 2018, 132, SCI-39-SCI-39.	1.4	0
580	Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. Blood, 2018, 132, 4457-4457.	1.4	0
581	Poor Overall Survival in Hyperhaploid Multiple Myeloma Is Defined By Double-Hit Bi-Allelic Inactivation of TP53. Blood, 2018, 132, 4441-4441.	1.4	0
582	Sequential Improvements in the Outcome of Autologous Stem Cell Transplantation for Multiple Myeloma over Time. Blood, 2018, 132, 3168-3168.	1.4	0
583	Myeloma Patient-Derived Bone Marrow Serum Negatively Regulates Natural Killer Cell Activity. Blood, 2018, 132, 4468-4468.	1.4	0
584	Mutations and Copy Number Changes Predict Progression from Smoldering Myeloma to Symptomatic Myeloma in the Era of Novel IMWG Criteria. Blood, 2018, 132, 4456-4456.	1.4	0
585	Global 3D-Epigenetic Dysregulation of Cyclin D1 and D2 Actively Controls Their Expression Pattern in Multiple Myeloma. Blood, 2018, 132, 3904-3904.	1.4	0
586	Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. Blood, 2018, 132, 3185-3185.	1.4	0
587	Lack of a Spleen Signal on Diffusion Weighted MRI Is Associated with High Tumor Burden and Poor Prognosis in Multiple Myeloma. Blood, 2018, 132, 4471-4471.	1.4	0
588	Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. Blood, 2018, 132, 4454-4454.	1.4	0
589	Mesenchymal Stem Cells Gene Signature in High-Risk Myeloma Bone Marrow Linked to Suppression of Distinct IGFBP2-Expressing Small Adipocytes. Blood, 2018, 132, 4448-4448.	1.4	0
590	Characterisation of Long-Term Responders to First-Line Myeloma Therapy - Results from the UK Myeloma IX and XI Trials. Blood, 2018, 132, 2000-2000.	1.4	0
591	High Levels of APOBEC3B Gene Expression Contribute to Poor Prognosis in Multiple Myeloma Patients. Blood, 2018, 132, 3897-3897.	1.4	0
592	Mutant KRAS and Brafs Upregulate Stress Granules and Mediate Drug Resistance, Which Can be Modulated By Cox2 Inhibition in Multiple Myeloma. Blood, 2018, 132, 3166-3166.	1.4	0
593	Characterization of the Immune Impact of Daratumumab By Mass Cytometry in Multiple Myeloma. Blood, 2018, 132, 4466-4466.	1.4	0
594	Proliferation and Molecular Risk Score of Low Risk Myeloma Cells Are Increased in High Risk Microenvironment Via Augmented Bioavailability of Growth Factors. Blood, 2018, 132, 1929-1929.	1.4	0

#	Article	IF	Citations
595	Multiomic Mapping of Copy Number and Structural Variation on Chromosome 1 (Chr1) Highlights Multiple Recurrent Disease Drivers. Blood, 2021, 138, 721-721.	1.4	0