John D Shaughnessy Jr

List of Publications by Year
in descending order

144 papers	17,783 citations	17405 63 h-index	14702 127 g-index
145 all docs	145 docs citations	145 times ranked	14818 citing authors

#	Article	IF	Citations
1	The Role of the Wnt-Signaling Antagonist DKK1 in the Development of Osteolytic Lesions in Multiple Myeloma. New England Journal of Medicine, 2003, 349, 2483-2494.	13.9	1,368
2	The molecular classification of multiple myeloma. Blood, 2006, 108, 2020-2028.	0.6	997
3	Frequent Engagement of the Classical and Alternative NF-ΐºB Pathways by Diverse Genetic Abnormalities in Multiple Myeloma. Cancer Cell, 2007, 12, 115-130.	7.7	899
4	A validated gene expression model of high-risk multiple myeloma is defined by deregulated expression of genes mapping to chromosome 1. Blood, 2007, 109, 2276-2284.	0.6	831
5	The MicroArray Quality Control (MAQC)-II study of common practices for the development and validation of microarray-based predictive models. Nature Biotechnology, 2010, 28, 827-838.	9.4	795
6	Genetics and Cytogenetics of Multiple Myeloma. Cancer Research, 2004, 64, 1546-1558.	0.4	642
7	CS1, a Potential New Therapeutic Antibody Target for the Treatment of Multiple Myeloma. Clinical Cancer Research, 2008, 14, 2775-2784.	3.2	491
8	F18-fluorodeoxyglucose positron emission tomography in the context of other imaging techniques and prognostic factors in multiple myeloma. Blood, 2009, 114, 2068-2076.	0.6	463
9	Fusion of the nucleoporin gene NUP98 to HOXA9 by the chromosome translocation t(7;11)(p15;p15) in human myeloid leukaemia. Nature Genetics, 1996, 12, 154-158.	9.4	459
10	Frequent gain of chromosome band 1q21 in plasma-cell dyscrasias detected by fluorescence in situ hybridization: incidence increases from MGUS to relapsed myeloma and is related to prognosis and disease progression following tandem stem-cell transplantation. Blood, 2006, 108, 1724-1732.	0.6	417
11	Antibody-based inhibition of DKK1 suppresses tumor-induced bone resorption and multiple myeloma growth in vivo. Blood, 2007, 109, 2106-2111.	0.6	414
12	High-resolution genomic profiles define distinct clinico-pathogenetic subgroups of multiple myeloma patients. Cancer Cell, 2006, 9, 313-325.	7.7	404
13	Gene expression profiling and correlation with outcome in clinical trials of the proteasome inhibitor bortezomib. Blood, 2007, 109, 3177-3188.	0.6	379
14	Magnetic Resonance Imaging in Multiple Myeloma: Diagnostic and Clinical Implications. Journal of Clinical Oncology, 2007, 25, 1121-1128.	0.8	369
15	The role of Dickkopf-1 in bone development, homeostasis, and disease. Blood, 2009, 113, 517-525.	0.6	350
16	Gene-expression signature of benign monoclonal gammopathy evident in multiple myeloma is linked to good prognosis. Blood, 2007, 109, 1692-1700.	0.6	328
17	Incorporating bortezomib into upfront treatment for multiple myeloma: early results of total therapy 3. British Journal of Haematology, 2007, 138, 176-185.	1.2	304
18	Cooperative activation of Hoxa and Pbx1-related genes in murine myeloid leukaemias. Nature Genetics, 1996, 12, 149-153.	9.4	287

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19	Heparanase Enhances Syndecan-1 Shedding. Journal of Biological Chemistry, 2007, 282, 13326-13333.	1.6	237
20	Inhibiting Dickkopf-1 (Dkk1) Removes Suppression of Bone Formation and Prevents the Development of Osteolytic Bone Disease in Multiple Myeloma. Journal of Bone and Mineral Research, 2009, 24, 425-436.	3.1	230
21	Myeloma-derived Dickkopf-1 disrupts Wnt-regulated osteoprotegerin and RANKL production by osteoblasts: a potential mechanism underlying osteolytic bone lesions in multiple myeloma. Blood, 2008, 112, 196-207.	0.6	223
22	Thalidomide arm of Total Therapy 2 improves complete remission duration and survival in myeloma patients with metaphase cytogenetic abnormalities. Blood, 2008, 112, 3115-3121.	0.6	223
23	Leukaemia disease genes: large-scale cloning and pathway predictions. Nature Genetics, 1999, 23, 348-353.	9.4	221
24	Superior results of Total Therapy 3 (2003-33) in gene expression profiling–defined low-risk multiple myeloma confirmed in subsequent trial 2006-66 with VRD maintenance. Blood, 2010, 115, 4168-4173.	0.6	196
25	Proliferation is a central independent prognostic factor and target for personalized and risk-adapted treatment in multiple myeloma. Haematologica, 2011, 96, 87-95.	1.7	188
26	High-risk myeloma is associated with global elevation of miRNAs and overexpression of <i>EIF2C2/AGO2</i>. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 7904-7909.	3.3	187
27	Frequent and specific immunity to the embryonal stem cell–associated antigen SOX2 in patients with monoclonal gammopathy. Journal of Experimental Medicine, 2007, 204, 831-840.	4.2	175
28	Infusion of haplo-identical killer immunoglobulin-like receptor ligand mismatched NK cells for relapsed myeloma in the setting of autologous stem cell transplantation. British Journal of Haematology, 2008, 143, 641-653.	1.2	175
29	Clinical, genomic, and imaging predictors of myeloma progression from asymptomatic monoclonal gammopathies (SWOG S0120). Blood, 2014, 123, 78-85.	0.6	173
30	Dickkopf Homolog 1 Mediates Endothelin-1-Stimulated New Bone Formation. Molecular Endocrinology, 2007, 21, 486-498.	3.7	169
31	High serum-free light chain levels and their rapid reduction in response to therapy define an aggressive multiple myeloma subtype with poor prognosis. Blood, 2007, 110, 827-832.	0.6	167
32	Combinatorial efficacy of anti-CS1 monoclonal antibody elotuzumab (HuLuc63) and bortezomib against multiple myeloma. Molecular Cancer Therapeutics, 2009, 8, 2616-2624.	1.9	161
33	Bortezomib down-regulates the cell-surface expression of HLA class I and enhances natural killer cell–mediated lysis of myeloma. Blood, 2008, 111, 1309-1317.	0.6	159
34	Sustained complete remissions in multiple myeloma linked to bortezomib in total therapy 3: comparison with total therapy 2. British Journal of Haematology, 2008, 140, 625-634.	1.2	156
35	Long-term outcome results of the first tandem autotransplant trial for multiple myeloma. British Journal of Haematology, 2006, 135, 158-164.	1.2	155
36	The role of IGF-1 as a major growth factor for myeloma cell lines and the prognostic relevance of the expression of its receptor. Blood, 2009, 113, 4614-4626.	0.6	150

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37	Pharmacogenomics of bortezomib test-dosing identifies hyperexpression of proteasome genes, especially PSMD4, as novel high-risk feature in myeloma treated with Total Therapy 3. Blood, 2011, 118, 3512-3524.	0.6	149
38	Dkk1-induced inhibition of Wnt signaling in osteoblast differentiation is an underlying mechanism of bone loss in multiple myeloma. Bone, 2008, 42, 669-680.	1.4	147
39	CKS1B, overexpressed in aggressive disease, regulates multiple myeloma growth and survival through SKP2- and p27Kip1-dependent and -independent mechanisms. Blood, 2007, 109, 4995-5001.	0.6	139
40	Bortezomib induces osteoblast differentiation via Wnt-independent activation of Î²-catenin/TCF signaling. Blood, 2009, 113, 4319-4330.	0.6	132
41	An analysis of the clinical and biologic significance of TP53 loss and the identification of potential novel transcriptional targets of TP53 in multiple myeloma. Blood, 2008, 112, 4235-4246.	0.6	124
42	The syndecan-1 heparan sulfate proteoglycan is a viable target for myeloma therapy. Blood, 2007, 110, 2041-2048.	0.6	122
43	Diagnostic Usefulness and Prognostic Impact of CD200 Expression in Lymphoid Malignancies and Plasma Cell Myeloma. American Journal of Clinical Pathology, 2012, 137, 93-100.	0.4	122
44	Thalidomide induces limb deformities by perturbing the Bmp/Dkkl/Wnt signaling pathway. FASEB Journal, 2007, 21, 1410-1421.	0.2	118
45	Dickkopf-1 (DKK) is a widely expressed and potent tumor-associated antigen in multiple myeloma. Blood, 2007, 110, 1587-1594.	0.6	115
46	Complete remission sustained 3 years from treatment initiation is a powerful surrogate for extended survival in multiple myeloma. Cancer, 2008, 113, 355-359.	2.0	115
47	The sumoylation pathway is dysregulated in multiple myeloma and is associated with adverse patient outcome. Blood, 2010, 115, 2827-2834.	0.6	106
48	Total Therapy 3 for multiple myeloma: prognostic implications of cumulative dosing and premature discontinuation of VTD maintenance components, bortezomib, thalidomide, and dexamethasone, relevant to all phases of therapy. Blood, 2010, 116, 1220-1227.	0.6	100
49	Benefit of Complete Response in Multiple Myeloma Limited to High-Risk Subgroup Identified by Gene Expression Profiling. Clinical Cancer Research, 2007, 13, 7073-7079.	3.2	99
50	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. Blood, 2009, 113, 4331-4340.	0.6	97
51	Highly activated and expanded natural killer cells for multiple myeloma immunotherapy. Haematologica, 2012, 97, 1348-1356.	1.7	97
52	The ephrinB2/EphB4 axis is dysregulated in osteoprogenitors from myeloma patients and its activation affects myeloma bone disease and tumor growth. Blood, 2009, 114, 1803-1812.	0.6	94
53	Complete remission in multiple myeloma examined as time-dependent variable in terms of both onset and duration in Total Therapy protocols. Blood, 2009, 114, 1299-1305.	0.6	92
54	Overexpression and involvement in migration by the metastasis-associated phosphatase PRL-3 in human myeloma cells. Blood, 2008, 111, 806-815.	0.6	90

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55	Seven-year median time to progression with thalidomide for smoldering myeloma: partial response identifies subset requiring earlier salvage therapy for symptomatic disease. Blood, 2008, 112, 3122-3125.	0.6	90
56	Wnt3a signaling within bone inhibits multiple myeloma bone disease and tumor growth. Blood, 2008, 112, 374-382.	0.6	87
57	The oxidative stress response regulates DKK1 expression through the JNK signaling cascade in multiple myeloma plasma cells. Blood, 2007, 109, 4470-4477.	0.6	80
58	Secondary genomic rearrangements involving immunoglobulin or MYC loci show similar prevalences in hyperdiploid and nonhyperdiploid myeloma tumors. Genes Chromosomes and Cancer, 2008, 47, 573-590.	1.5	79
59	Identification of early growth response protein 1 (EGR-1) as a novel target for JUN-induced apoptosis in multiple myeloma. Blood, 2010, 115, 61-70.	0.6	79
60	Multicolour spectral karyotyping identifies new translocations and a recurring pathway for chromosome loss in multiple myeloma. British Journal of Haematology, 2001, 112, 167-174.	1.2	74
61	Human Placenta-Derived Adherent Cells Prevent Bone loss, Stimulate Bone formation, and Suppress Growth of Multiple Myeloma in Bone. Stem Cells, 2011, 29, 263-273.	1.4	71
62	Gene Expression Profiles of Tumor Biology Provide a Novel Approach to Prognosis and May Guide the Selection of Therapeutic Targets in Multiple Myeloma. Journal of Clinical Oncology, 2009, 27, 4197-4203.	0.8	69
63	High-risk myeloma: a gene expression–based risk-stratification model for newly diagnosed multiple myeloma treated with high-dose therapy is predictive of outcome in relapsed disease treated with single-agent bortezomib or high-dose dexamethasone. Blood, 2008, 111, 968-969.	0.6	66
64	*TP53* deletion is not an adverse feature in multiple myeloma treated with total therapy 3. British Journal of Haematology, 2009, 147, 347-351.	1.2	65
65	Evi27 encodes a novel membrane protein with homology to the IL17 receptor. Oncogene, 2000, 19, 2098-2109.	2.6	64
66	Complete response in myeloma extends survival without, but not with history of prior monoclonal gammopathy of undetermined significance or smouldering disease. British Journal of Haematology, 2007, 136, 393-399.	1.2	63
67	An intermediate-risk multiple myeloma subgroup is defined by sIL-6r: levels synergistically increase with incidence of SNP rs2228145 and 1q21 amplification. Blood, 2012, 119, 503-512.	0.6	57
68	Characterization of Wnt/β–catenin signalling in osteoclasts in multiple myeloma. British Journal of Haematology, 2010, 148, 726-738.	1.2	55
69	Developing and Validating Continuous Genomic Signatures in Randomized Clinical Trials for Predictive Medicine. Clinical Cancer Research, 2012, 18, 6065-6073.	3.2	54
70	Interpreting the molecular biology and clinical behavior of multiple myeloma in the context of global gene expression profiling. Immunological Reviews, 2003, 194, 140-163.	2.8	47
71	First thalidomide clinical trial in multiple myeloma: a decade. Blood, 2008, 112, 1035-1038.	0.6	47
72	Testing standard and genetic parameters in 220 patients with multiple myeloma with complete data sets: superiority of molecular genetics. British Journal of Haematology, 2007, 137, 530-536.	1.2	44

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73	Tumor Cell Gene Expression Changes Following Short-term *In vivo* Exposure to Single Agent Chemotherapeutics are Related to Survival in Multiple Myeloma. Clinical Cancer Research, 2008, 14, 4821-4829.	3.2	44
74	Interleukin-6 Receptor Polymorphism Is Prevalent in HIV-negative Castleman Disease and Is Associated with Increased Soluble Interleukin-6 Receptor Levels. PLoS ONE, 2013, 8, e54610.	1.1	44
75	Expression of PAX5 in CD20-positive multiple myeloma assessed by immunohistochemistry and oligonucleotide microarray. Modern Pathology, 2004, 17, 1217-1222.	2.9	43
76	Clinical, Immunophenotypic, and Genetic Characterization of Small Lymphocyte–Like Plasma Cell Myeloma. American Journal of Clinical Pathology, 2010, 133, 265-270.	0.4	42
77	Reiterative Survival Analyses of Total Therapy 2 for Multiple Myeloma Elucidate Follow-Up Time Dependency of Prognostic Variables and Treatment Arms. Journal of Clinical Oncology, 2010, 28, 3023-3027.	0.8	39
78	Consequences of Daily Administered Parathyroid Hormone on Myeloma Growth, Bone Disease, and Molecular Profiling of Whole Myelomatous Bone. PLoS ONE, 2010, 5, e15233.	1.1	38
79	Prediction of cytogenetic abnormalities with gene expression profiles. Blood, 2012, 119, e148-e150.	0.6	36
80	High expression of *BCL3* in human myeloma cells is associated with increased proliferation and inferior prognosis. European Journal of Haematology, 2009, 82, 354-363.	1.1	32
81	International staging system and metaphase cytogenetic abnormalities in the era of gene expression profiling data in multiple myeloma treated with total therapy 2 and 3 protocols. Cancer, 2011, 117, 1001-1009.	2.0	30
82	Immunoglobulin isotypes in multiple myeloma: laboratory correlates and prognostic implications in total therapy protocols. British Journal of Haematology, 2009, 145, 134-137.	1.2	29
83	Translating a gene expression signature for multiple myeloma prognosis into a robust high-throughput assay for clinical use. BMC Medical Genomics, 2014, 7, 25.	0.7	29
84	Role of osteoblast suppression in multiple myeloma. Journal of Cellular Biochemistry, 2006, 98, 1-13.	1.2	28
85	Establishment and exploitation of hyperdiploid and non–hyperdiploid human myeloma cell lines. British Journal of Haematology, 2007, 138, 802-811.	1.2	27
86	Prospective Evaluation of Operating Characteristics of Prostate Cancer Detection Biomarkers. Journal of Urology, 2011, 185, 104-110.	0.2	27
87	The use of molecular-based risk stratification and pharmacogenomics for outcome prediction and personalized therapeutic management of multiple myeloma. International Journal of Hematology, 2011, 94, 321-333.	0.7	27
88	Proteasome Inhibitors and Bone Disease. Seminars in Hematology, 2012, 49, 243-248.	1.8	26
89	CYR61/CCN1 overexpression in the myeloma microenvironment is associated with superior survival and reduced bone disease. Blood, 2014, 124, 2051-2060.	0.6	26
90	The distinct gene expression profiles of chronic lymphocytic leukemia and multiple myeloma suggest different anti-apoptotic mechanisms but predict only some differences in phenotype. Leukemia Research, 2003, 27, 765-774.	0.4	25

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91	Inhibitor of DASH proteases affects expression of adhesion molecules in osteoclasts and reduces myeloma growth and bone disease. British Journal of Haematology, 2009, 145, 775-787.	1.2	25
92	<scp>TRIM</scp>13 (<scp>RFP</scp>2) downregulation decreases tumour cell growth in multiple myeloma through inhibition of <scp>NF K</scp>appa <scp>B</scp> pathway and proteasome activity. British Journal of Haematology, 2013, 162, 210-220.	1.2	22
93	Using Genomics to Identify High-Risk Myeloma after Autologous Stem Cell Transplantation. Biology of Blood and Marrow Transplantation, 2006, 12, 77-80.	2.0	20
94	RARÎ±2 expression is associated with disease progression and plays a crucial role in efficacy of ATRA treatment in myeloma. Blood, 2009, 114, 600-607.	0.6	20
95	Gene expression profiling of plasma cells at myeloma relapse from tandem transplantation trial Total Therapy 2 predicts subsequent survival. Blood, 2009, 113, 6572-6575.	0.6	20
96	Identification of Novel Transcriptional Consequences of Activation and Inactivation of TP53 in Multiple Myeloma.. Blood, 2007, 110, 393-393.	0.6	20
97	Thalidomide in Total Therapy 2 Overcomes Inferior Prognosis of Myeloma with Low Expression of the Glucocorticoid Receptor Gene <i>NR3C1</i>. Clinical Cancer Research, 2012, 18, 5499-5506.	3.2	19
98	Global Gene Expression Profiling in the Study of Multiple Myeloma. International Journal of Hematology, 2003, 77, 213-225.	0.7	15
99	Ellipticine derivative NSC 338258 represents a potential new antineoplastic agent for the treatment of multiple myeloma. Molecular Cancer Therapeutics, 2008, 7, 500-509.	1.9	15
100	Duration of Survival in Patients with Myeloma Treated with Thalidomide. New England Journal of Medicine, 2008, 359, 210-212.	13.9	12
101	Genetic Analysis of Multiple Myeloma Identifies Cytogenetic Alterations Implicated in Disease Complexity and Progression. Cancers, 2021, 13, 517.	1.7	12
102	Integration of DNA Copy Number and Gene Expression Alterations Reveal Novel Insights into the Molecular Pathogenesis and Prognosis of Multiple Myeloma. Blood, 2008, 112, 250-250.	0.6	12
103	Clustering of significant genes in prognostic studies with microarrays: Application to a clinical study for multiple myeloma. Statistics in Medicine, 2008, 27, 1106-1120.	0.8	11
104	CGO: utilizing and integrating gene expression microarray data in clinical research and data management. Bioinformatics, 2002, 18, 327-328.	1.8	10
105	TRIP13 modulates protein deubiquitination and accelerates tumor development and progression of B cell malignancies. Journal of Clinical Investigation, 2021, 131, .	3.9	10
106	Changes in the Expression of Proteasome Genes in Tumor Cells Following Short-Term Proteasome Inhibitor Therapy Predicts Survival in Multiple Myeloma Treated with Bortezomib-Containing Multi-Agent Chemotherapy. Blood, 2008, 112, 733-733.	0.6	10
107	Jumping Translocations 1q12 Contribute to Copy Number (CN) Alterations in Multiple Myeloma (MM): Unexpected Focal Amplifications of Receptor Chromosomes (RC). Blood, 2011, 118, 298-298.	0.6	10
108	Gene Expression Profiling Reveals Aberrant T-cell Marker Expression on Tumor Cells of Waldenström's Macroglobulinemia. Clinical Cancer Research, 2019, 25, 201-209.	3.2	9

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109	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.	0.6	9
110	Integrating cytogenetics and gene expression profiling in the molecular analysis of Multiple Myeloma. International Journal of Hematology, 2002, 76, 59-64.	0.7	7
111	An unexpected addiction. Nature, 2008, 454, 172-173.	13.7	7
112	Cytogenetic abnormalities in multiple myeloma: poor prognosis linked to concomitant detection in random and focal lesion bone marrow samples and associated with high€risk gene expression profile. British Journal of Haematology, 2009, 145, 637-641.	1.2	7
113	Modeling for Cure with Total Therapy (TT) Trials for Newly Diagnosed Multiple Myeloma (MM): Let the Math Speak.. Blood, 2009, 114, 744-744.	0.6	7
114	Maximum predictive power of the microarray-based models for clinical outcomes is limited by correlation between endpoint and gene expression profile. BMC Genomics, 2011, 12, S3.	1.2	6
115	Cell Surface CXCR4 and BTK Expression Are Associated in Myeloma Cells and Osteoclast Precursors and Mediate Myeloma Cell Homing and Clonogenicity, and Osteoclastogenesis. Blood, 2011, 118, 884-884.	0.6	6
116	Allelic mutations in noncoding genomic sequences construct novel transcription factor binding sites that promote gene overexpression. Genes Chromosomes and Cancer, 2015, 54, 692-701.	1.5	5
117	A Validated Gene Expression Signature of High Risk Multiple Myeloma Is Defined by Deregulated Expression of Genes Mapping to Chromosome 1.. Blood, 2006, 108, 111-111.	0.6	5
118	Gene Expression Profiling (GEP) Analysis of Plasma Cells (PC) Obtained From MRI-Defined Focal Lesions (FL) Under CT-Guided Fine-Needle Aspiration Provides Better Risk Stratification in Patients with Multiple Myeloma. Blood, 2011, 118, 2896-2896.	0.6	5
119	Bispecific CAR-T Cells Targeting Both BCMA and CD24: A Potentially Treatment Approach for Multiple Myeloma. Blood, 2021, 138, 2802-2802.	0.6	4
120	Inducible Heme Oxygenase 1 (HMOX1) Promotes Osteoblastogenesis, and Inhibits Osteoclastogenesis and Myeloma-Induced Bone Disease. Blood, 2011, 118, 627-627.	0.6	3
121	Going with the flow, and beyond, in myeloma. Blood, 2008, 112, 3917-3918.	0.6	2
122	NEK2 Inhibition Enhances the Efficacy of PD-1/PD-L1 Blockade in Multiple Myeloma. Blood, 2021, 138, 2671-2671.	0.6	2
123	Interphase FISH of Chromosome 1 and 13 in Newly Diagnosed Myeloma and the Disease Prognosis. , 2009, , .		1
124	A Gene Expression Signature of Benign Monoclonal Gammopathy Evident in Multiple Myeloma Is Linked to Good Prognosis.. Blood, 2006, 108, 3393-3393.	0.6	1
125	A Gene Expression-Based Risk Stratification Model Developed in Newly Diagnosed Multiple Myeloma Treated with High Dose Therapy Is Predictive of Outcome in Relapsed Disease Treated with Single Agent Bortezomib.. Blood, 2007, 110, 656-656.	0.6	1
126	Secreted Frizzled-Related Protein-3 (sFRP3) Is Produced by Myeloma Cells and Augments Wnt3a-Induced Differentiation of Mesenchymal Stem Cells and OPG Production in Osteoblasts. Blood, 2011, 118, 808-808.	0.6	1

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127	Proteasome Inhibitor, Bortezomib Induces Mesenchymal Stem Cells toward Osteoblast Differentiation through Wnt-Independent Activation of Beta-catenin/TCF Signaling. Blood, 2008, 112, 644-644.	0.6	1
128	Clinical use of genomics in multiple myeloma. Clinical Advances in Hematology and Oncology, 2006, 4, 419-21.	0.3	1
129	New Insights into the Molecular Basis of Multiple Myeloma Pathogenesis and Prognosis. Clinical Lymphoma and Myeloma, 2009, 9, S10-S11.	1.4	0
130	Reply to J. Mehta. Journal of Clinical Oncology, 2011, 29, e125-e126.	0.8	0
131	Proteasome Inhibitors: Introduction. Seminars in Hematology, 2012, 49, 193-195.	1.8	0
132	Dkk1 Transgenic Mice for the Study of Bone Lesions in Human Multiple Myeloma.. Blood, 2005, 106, 2505-2505.	0.6	0
133	DKK-1 Is a Widely Expressed, Potent Tumor-Associated Antigen in Multiple Myeloma Recognized by Cytotoxic T Lymphocytes.. Blood, 2005, 106, 3467-3467.	0.6	0
134	JNK Regulates DKK1 Expression in Multiple Myeloma Cells.. Blood, 2006, 108, 3411-3411.	0.6	0
135	Bone Morphogenic Protein 6: A Prognostic Factor Expressed by Normal Plasma Cells and Multiple Myeloma Cells Inhibiting Their Proliferation and Angiogenesis Induction. Blood, 2008, 112, 2701-2701.	0.6	0
136	Proteomic Profiling of Multiple Myeloma: Correlation of Protein and Gene Expression Data.. Blood, 2008, 112, 1705-1705.	0.6	0
137	Molecular Indicators of High-Risk Disease.. Blood, 2008, 112, sci-6-sci-6.	0.6	0
138	Bortezomib Induces Osteoblast Differentiation Via Wnt-Independent Activation of Beta-catenin/TCF Signaling. Blood, 2008, 112, 846-846.	0.6	0
139	High-Risk Multiple Myeloma Is Characterized by Uniform Over-Expression of Mirnas and Increased Copy Number and Expression of Argonaute 2, A Master Regulator of Mirna Maturation and B-Cell Development.. Blood, 2009, 114, 1804-1804.	0.6	0
140	Deregulated Cellular Iron Metabolism Factors Mediate Iron Overload in Myeloma Cells and Osteoclasts, and Promote Myeloma Growth and Bone Disease,. Blood, 2011, 118, 3941-3941.	0.6	0
141	Gene Expression Profiling (GEP) in MGUS and AMM: Predictors of Progression.. Blood, 2012, 120, 2933-2933.	0.6	0
142	Gene Expression Signature in MGUS and Multiple Myeloma. , 2013, , 17-41.		0
143	Mutation Burden in Multiple Myeloma Is Captured By Gene Expression Profiles. Blood, 2016, 128, 4450-4450.	0.6	0
144	N-Cadherin Stabilizes Î²-Catenin and Promotes Î²-Catenin/TCF Transcriptional Activation and Cell Adhesion-Mediated Drug Resistance in Multiple Myeloma. Blood, 2021, 138, 1572-1572.	0.6	0