John D Shaughnessy Jr

List of Publications by Year
in descending order

144 papers	17,783 citations	20036 63 h-index	16791 127 g-index
145 all docs	145 docs citations	145 times ranked	16219 citing authors

#	Article	IF	Citations
1	Genetic Analysis of Multiple Myeloma Identifies Cytogenetic Alterations Implicated in Disease Complexity and Progression. Cancers, 2021, 13, 517.	1.7	12
2	TRIP13 modulates protein deubiquitination and accelerates tumor development and progression of B cell malignancies. Journal of Clinical Investigation, 2021, 131, .	3.9	10
3	NEK2 Inhibition Enhances the Efficacy of PD-1/PD-L1 Blockade in Multiple Myeloma. Blood, 2021, 138, 2671-2671.	0.6	2
4	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
5	Bispecific CAR-T Cells Targeting Both BCMA and CD24: A Potentially Treatment Approach for Multiple Myeloma. Blood, 2021, 138, 2802-2802.	0.6	4
6	Gene Expression Profiling Reveals Aberrant T-cell Marker Expression on Tumor Cells of WaldenstrÃ¶m's Macroglobulinemia. Clinical Cancer Research, 2019, 25, 201-209.	3.2	9
7	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
8	Mutation Burden in Multiple Myeloma Is Captured By Gene Expression Profiles. Blood, 2016, 128, 4450-4450.	0.6	0
9	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
10	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
11	Clinical, genomic, and imaging predictors of myeloma progression from asymptomatic monoclonal gammopathies (SWOG S0120). Blood, 2014, 123, 78-85.	0.6	173
12	CYR61/CCN1 overexpression in the myeloma microenvironment is associated with superior survival and reduced bone disease. Blood, 2014, 124, 2051-2060.	0.6	26
13	<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
14	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
15	Gene Expression Signature in MGUS and Multiple Myeloma. , 2013, , 17-41.		0
16	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
17	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
18	Developing and Validating Continuous Genomic Signatures in Randomized Clinical Trials for Predictive Medicine. Clinical Cancer Research, 2012, 18, 6065-6073.	3.2	54

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19	Highly activated and expanded natural killer cells for multiple myeloma immunotherapy. Haematologica, 2012, 97, 1348-1356.	1.7	97
20	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
21	Proteasome Inhibitors and Bone Disease. Seminars in Hematology, 2012, 49, 243-248.	1.8	26
22	Proteasome Inhibitors: Introduction. Seminars in Hematology, 2012, 49, 193-195.	1.8	0
23	Prediction of cytogenetic abnormalities with gene expression profiles. Blood, 2012, 119, e148-e150.	0.6	36
24	Gene Expression Profiling (GEP) in MGUS and AMM: Predictors of Progression.. Blood, 2012, 120, 2933-2933.	0.6	0
25	Prospective Evaluation of Operating Characteristics of Prostate Cancer Detection Biomarkers. Journal of Urology, 2011, 185, 104-110.	0.2	27
26	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
27	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
28	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
29	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
30	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
31	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
32	Reply to J. Mehta. Journal of Clinical Oncology, 2011, 29, e125-e126.	0.8	0
33	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
34	Inducible Heme Oxygenase 1 (HMOX1) Promotes Osteoblastogenesis, and Inhibits Osteoclastogenesis and Myeloma-Induced Bone Disease. Blood, 2011, 118, 627-627.	0.6	3
35	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
36	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

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37	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
38	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
39	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
40	The sumoylation pathway is dysregulated in multiple myeloma and is associated with adverse patient outcome. Blood, 2010, 115, 2827-2834.	0.6	106
41	Superior results of Total Therapy 3 (2003-33) in gene expression profilingâ€œdefined low-risk multiple myeloma confirmed in subsequent trial 2006-66 with VRD maintenance. Blood, 2010, 115, 4168-4173.	0.6	196
42	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
43	Characterization of Wnt/Î²â€catenin signalling in osteoclasts in multiple myeloma. British Journal of Haematology, 2010, 148, 726-738.	1.2	55
44	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
45	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
46	Clinical, Immunophenotypic, and Genetic Characterization of Small Lymphocyteâ€œLike Plasma Cell Myeloma. American Journal of Clinical Pathology, 2010, 133, 265-270.	0.4	42
47	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
48	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
49	Combinatorial efficacy of anti-CS1 monoclonal antibody elotuzumab (HuLuc63) and bortezomib against multiple myeloma. Molecular Cancer Therapeutics, 2009, 8, 2616-2624.	1.9	161
50	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
51	High expression of <i>BCL3</i> in human myeloma cells is associated with increased proliferation and inferior prognosis. European Journal of Haematology, 2009, 82, 354-363.	1.1	32
52	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
53	Cytogenetic abnormalities in multiple myeloma: poor prognosis linked to concomitant detection in random and focal lesion bone marrow samples and associated with highâ€risk gene expression profile. British Journal of Haematology, 2009, 145, 637-641.	1.2	7
54	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

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55	<i>TP53</i> 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
56	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
57	Interphase FISH of Chromosome 1 and 13 in Newly Diagnosed Myeloma and the Disease Prognosis. , 2009, , .		1
58	New Insights into the Molecular Basis of Multiple Myeloma Pathogenesis and Prognosis. Clinical Lymphoma and Myeloma, 2009, 9, S10-S11.	1.4	0
59	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
60	The role of Dickkopf-1 in bone development, homeostasis, and disease. Blood, 2009, 113, 517-525.	0.6	350
61	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
62	Bortezomib induces osteoblast differentiation via Wnt-independent activation of Î²-catenin/TCF signaling. Blood, 2009, 113, 4319-4330.	0.6	132
63	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. Blood, 2009, 113, 4331-4340.	0.6	97
64	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
65	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
66	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
67	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
68	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
69	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
70	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
71	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
72	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

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73	An unexpected addiction. Nature, 2008, 454, 172-173.	13.7	7
74	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
75	Infusion of haploâ€identical killer immunoglobulinâ€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
76	Duration of Survival in Patients with Myeloma Treated with Thalidomide. New England Journal of Medicine, 2008, 359, 210-212.	13.9	12
77	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
78	CS1, a Potential New Therapeutic Antibody Target for the Treatment of Multiple Myeloma. Clinical Cancer Research, 2008, 14, 2775-2784.	3.2	491
79	Tumor Cell Gene Expression Changes Following Short-term <i>In vivo</i> Exposure to Single Agent Chemotherapeutics are Related to Survival in Multiple Myeloma. Clinical Cancer Research, 2008, 14, 4821-4829.	3.2	44
80	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
81	High-risk myeloma: a gene expressionâ€“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
82	Bortezomib down-regulates the cell-surface expression of HLA class I and enhances natural killer cellâ€“mediated lysis of myeloma. Blood, 2008, 111, 1309-1317.	0.6	159
83	Overexpression and involvement in migration by the metastasis-associated phosphatase PRL-3 in human myeloma cells. Blood, 2008, 111, 806-815.	0.6	90
84	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
85	Wnt3a signaling within bone inhibits multiple myeloma bone disease and tumor growth. Blood, 2008, 112, 374-382.	0.6	87
86	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
87	First thalidomide clinical trial in multiple myeloma: a decade. Blood, 2008, 112, 1035-1038.	0.6	47
88	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
89	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
90	Going with the flow, and beyond, in myeloma. Blood, 2008, 112, 3917-3918.	0.6	2

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91	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
92	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
93	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
94	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
95	Proteomic Profiling of Multiple Myeloma: Correlation of Protein and Gene Expression Data.. Blood, 2008, 112, 1705-1705.	0.6	0
96	Molecular Indicators of High-Risk Disease.. Blood, 2008, 112, sci-6-sci-6.	0.6	0
97	Bortezomib Induces Osteoblast Differentiation Via Wnt-Independent Activation of Beta-catenin/TCF Signaling. Blood, 2008, 112, 846-846.	0.6	0
98	Thalidomide induces limb deformities by perturbing the Bmp/Dkkl/Wnt signaling pathway. FASEB Journal, 2007, 21, 1410-1421.	0.2	118
99	Heparanase Enhances Syndecan-1 Shedding. Journal of Biological Chemistry, 2007, 282, 13326-13333.	1.6	237
100	Dickkopf Homolog 1 Mediates Endothelin-1-Stimulated New Bone Formation. Molecular Endocrinology, 2007, 21, 486-498.	3.7	169
101	Magnetic Resonance Imaging in Multiple Myeloma: Diagnostic and Clinical Implications. Journal of Clinical Oncology, 2007, 25, 1121-1128.	0.8	369
102	Frequent and specific immunity to the embryonal stem cellâ€"associated antigen SOX2 in patients with monoclonal gammopathy. Journal of Experimental Medicine, 2007, 204, 831-840.	4.2	175
103	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
104	Gene-expression signature of benign monoclonal gammopathy evident in multiple myeloma is linked to good prognosis. Blood, 2007, 109, 1692-1700.	0.6	328
105	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
106	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
107	Gene expression profiling and correlation with outcome in clinical trials of the proteasome inhibitor bortezomib. Blood, 2007, 109, 3177-3188.	0.6	379
108	Antibody-based inhibition of DKK1 suppresses tumor-induced bone resorption and multiple myeloma growth in vivo. Blood, 2007, 109, 2106-2111.	0.6	414

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109	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
110	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
111	The syndecan-1 heparan sulfate proteoglycan is a viable target for myeloma therapy. Blood, 2007, 110, 2041-2048.	0.6	122
112	Dickkopf-1 (DKK1) is a widely expressed and potent tumor-associated antigen in multiple myeloma. Blood, 2007, 110, 1587-1594.	0.6	115
113	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
114	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
115	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
116	Establishment and exploitation of hyperdiploid and nonâ€hyperdiploid human myeloma cell lines. British Journal of Haematology, 2007, 138, 802-811.	1.2	27
117	Frequent Engagement of the Classical and Alternative NF-Î°B Pathways by Diverse Genetic Abnormalities in Multiple Myeloma. Cancer Cell, 2007, 12, 115-130.	7.7	899
118	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
119	Identification of Novel Transcriptional Consequences of Activation and Inactivation of TP53 in Multiple Myeloma.. Blood, 2007, 110, 393-393.	0.6	20
120	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
121	The molecular classification of multiple myeloma. Blood, 2006, 108, 2020-2028.	0.6	997
122	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
123	Long-term outcome results of the first tandem autotransplant trial for multiple myeloma. British Journal of Haematology, 2006, 135, 158-164.	1.2	155
124	High-resolution genomic profiles define distinct clinico-pathogenetic subgroups of multiple myeloma patients. Cancer Cell, 2006, 9, 313-325.	7.7	404
125	Role of osteoblast suppression in multiple myeloma. Journal of Cellular Biochemistry, 2006, 98, 1-13.	1.2	28
126	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

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127	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
128	JNK Regulates DKK1 Expression in Multiple Myeloma Cells.. Blood, 2006, 108, 3411-3411.	0.6	0
129	Clinical use of genomics in multiple myeloma. Clinical Advances in Hematology and Oncology, 2006, 4, 419-21.	0.3	1
130	Dkk1 Transgenic Mice for the Study of Bone Lesions in Human Multiple Myeloma.. Blood, 2005, 106, 2505-2505.	0.6	0
131	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
132	Genetics and Cytogenetics of Multiple Myeloma. Cancer Research, 2004, 64, 1546-1558.	0.4	642
133	Expression of PAX5 in CD20-positive multiple myeloma assessed by immunohistochemistry and oligonucleotide microarray. Modern Pathology, 2004, 17, 1217-1222.	2.9	43
134	Global Gene Expression Profiling in the Study of Multiple Myeloma. International Journal of Hematology, 2003, 77, 213-225.	0.7	15
135	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
136	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
137	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
138	CGO: utilizing and integrating gene expression microarray data in clinical research and data management. Bioinformatics, 2002, 18, 327-328.	1.8	10
139	Integrating cytogenetics and gene expression profiling in the molecular analysis of Multiple Myeloma. International Journal of Hematology, 2002, 76, 59-64.	0.7	7
140	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
141	Evi27 encodes a novel membrane protein with homology to the IL17 receptor. Oncogene, 2000, 19, 2098-2109.	2.6	64
142	Leukaemia disease genes: large-scale cloning and pathway predictions. Nature Genetics, 1999, 23, 348-353.	9.4	221
143	Cooperative activation of Hoxa and Pbx1-related genes in murine myeloid leukaemias. Nature Genetics, 1996, 12, 149-153.	9.4	287
144	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