

John D Shaughnessy Jr

List of Publications by Year in descending order

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144
papers

17,783
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docs citations

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times ranked

14818
citing authors

#	ARTICLE	IF	CITATIONS
1	Genetic Analysis of Multiple Myeloma Identifies Cytogenetic Alterations Implicated in Disease Complexity and Progression. <i>Cancers</i> , 2021, 13, 517.	1.7	12
2	TRIP13 modulates protein deubiquitination and accelerates tumor development and progression of B cell malignancies. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	10
3	NEK2 Inhibition Enhances the Efficacy of PD-1/PD-L1 Blockade in Multiple Myeloma. <i>Blood</i> , 2021, 138, 2671-2671.	0.6	2
4	N-Cadherin Stabilizes β -Catenin and Promotes β -Catenin/TCF Transcriptional Activation and Cell Adhesion-Mediated Drug Resistance in Multiple Myeloma. <i>Blood</i> , 2021, 138, 1572-1572.	0.6	0
5	Bispecific CAR-T Cells Targeting Both BCMA and CD24: A Potentially Treatment Approach for Multiple Myeloma. <i>Blood</i> , 2021, 138, 2802-2802.	0.6	4
6	Gene Expression Profiling Reveals Aberrant T-cell Marker Expression on Tumor Cells of Waldenström's Macroglobulinemia. <i>Clinical Cancer Research</i> , 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. <i>Blood</i> , 2016, 128, 5613-5613.	0.6	9
8	Mutation Burden in Multiple Myeloma Is Captured By Gene Expression Profiles. <i>Blood</i> , 2016, 128, 4450-4450.	0.6	0
9	Allelic mutations in noncoding genomic sequences construct novel transcription factor binding sites that promote gene overexpression. <i>Genes Chromosomes and Cancer</i> , 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. <i>BMC Medical Genomics</i> , 2014, 7, 25.	0.7	29
11	Clinical, genomic, and imaging predictors of myeloma progression from asymptomatic monoclonal gammopathies (SWOG S0120). <i>Blood</i> , 2014, 123, 78-85.	0.6	173
12	CYR61/CCN1 overexpression in the myeloma microenvironment is associated with superior survival and reduced bone disease. <i>Blood</i> , 2014, 124, 2051-2060.	0.6	26
13	TRIM13 (RFP2) downregulation decreases tumour cell growth in multiple myeloma through inhibition of NF- κ B pathway and proteasome activity. <i>British Journal of Haematology</i> , 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. <i>PLoS ONE</i> , 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. <i>American Journal of Clinical Pathology</i> , 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> . <i>Clinical Cancer Research</i> , 2012, 18, 5499-5506.	3.2	19
18	Developing and Validating Continuous Genomic Signatures in Randomized Clinical Trials for Predictive Medicine. <i>Clinical Cancer Research</i> , 2012, 18, 6065-6073.	3.2	54

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19	Highly activated and expanded natural killer cells for multiple myeloma immunotherapy. <i>Haematologica</i> , 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. <i>Blood</i> , 2012, 119, 503-512.	0.6	57
21	Proteasome Inhibitors and Bone Disease. <i>Seminars in Hematology</i> , 2012, 49, 243-248.	1.8	26
22	Proteasome Inhibitors: Introduction. <i>Seminars in Hematology</i> , 2012, 49, 193-195.	1.8	0
23	Prediction of cytogenetic abnormalities with gene expression profiles. <i>Blood</i> , 2012, 119, e148-e150.	0.6	36
24	Gene Expression Profiling (GEP) in MGUS and AMM: Predictors of Progression.. <i>Blood</i> , 2012, 120, 2933-2933.	0.6	0
25	Prospective Evaluation of Operating Characteristics of Prostate Cancer Detection Biomarkers. <i>Journal of Urology</i> , 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. <i>International Journal of Hematology</i> , 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. <i>Blood</i> , 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. <i>BMC Genomics</i> , 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. <i>Stem Cells</i> , 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. <i>Cancer</i> , 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. <i>Haematologica</i> , 2011, 96, 87-95.	1.7	188
32	Reply to J. Mehta. <i>Journal of Clinical Oncology</i> , 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. <i>Blood</i> , 2011, 118, 808-808.	0.6	1
34	Inducible Heme Oxygenase 1 (HMOX1) Promotes Osteoblastogenesis, and Inhibits Osteoclastogenesis and Myeloma-Induced Bone Disease. <i>Blood</i> , 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,. <i>Blood</i> , 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). <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 2010, 115, 61-70.	0.6	79
40	The sumoylation pathway is dysregulated in multiple myeloma and is associated with adverse patient outcome. <i>Blood</i> , 2010, 115, 2827-2834.	0.6	106
41	Superior results of Total Therapy 3 (2003-33) in gene expression profilingâ€“defined low-risk multiple myeloma confirmed in subsequent trial 2006-66 with VRD maintenance. <i>Blood</i> , 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. <i>Blood</i> , 2010, 116, 1220-1227.	0.6	100
43	Characterization of Wnt/ β -catenin signalling in osteoclasts in multiple myeloma. <i>British Journal of Haematology</i> , 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. <i>Nature Biotechnology</i> , 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. <i>Journal of Clinical Oncology</i> , 2010, 28, 3023-3027.	0.8	39
46	Clinical, Immunophenotypic, and Genetic Characterization of Small Lymphocyteâ€“Like Plasma Cell Myeloma. <i>American Journal of Clinical Pathology</i> , 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> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 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. <i>PLoS ONE</i> , 2010, 5, e15233.	1.1	38
49	Combinatorial efficacy of anti-CS1 monoclonal antibody elotuzumab (HuLuc63) and bortezomib against multiple myeloma. <i>Molecular Cancer Therapeutics</i> , 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. <i>Journal of Clinical Oncology</i> , 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. <i>European Journal of Haematology</i> , 2009, 82, 354-363.	1.1	32
52	Immunoglobulin isotypes in multiple myeloma: laboratory correlates and prognostic implications in total therapy protocols. <i>British Journal of Haematology</i> , 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 high-risk gene expression profile. <i>British Journal of Haematology</i> , 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. <i>British Journal of Haematology</i> , 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. <i>British Journal of Haematology</i> , 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. <i>Journal of Bone and Mineral Research</i> , 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. <i>Clinical Lymphoma and Myeloma</i> , 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. <i>Blood</i> , 2009, 114, 2068-2076.	0.6	463
60	The role of Dickkopf-1 in bone development, homeostasis, and disease. <i>Blood</i> , 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. <i>Blood</i> , 2009, 113, 4614-4626.	0.6	150
62	Bortezomib induces osteoblast differentiation via Wnt-independent activation of β -catenin/TCF signaling. <i>Blood</i> , 2009, 113, 4319-4330.	0.6	132
63	Inhibition of aurora kinases for tailored risk-adapted treatment of multiple myeloma. <i>Blood</i> , 2009, 113, 4331-4340.	0.6	97
64	RAR α 2 expression is associated with disease progression and plays a crucial role in efficacy of ATRA treatment in myeloma. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 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.. <i>Blood</i> , 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.. <i>Blood</i> , 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. <i>Statistics in Medicine</i> , 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. <i>Cancer</i> , 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. <i>Genes Chromosomes and Cancer</i> , 2008, 47, 573-590.	1.5	79

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73	An unexpected addiction. <i>Nature</i> , 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. <i>British Journal of Haematology</i> , 2008, 140, 625-634.	1.2	156
75	Infusion of haplo-identical killer immunoglobulin-like receptor ligand mismatched NK cells for relapsed myeloma in the setting of autologous stem cell transplantation. <i>British Journal of Haematology</i> , 2008, 143, 641-653.	1.2	175
76	Duration of Survival in Patients with Myeloma Treated with Thalidomide. <i>New England Journal of Medicine</i> , 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. <i>Bone</i> , 2008, 42, 669-680.	1.4	147
78	CS1, a Potential New Therapeutic Antibody Target for the Treatment of Multiple Myeloma. <i>Clinical Cancer Research</i> , 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. <i>Clinical Cancer Research</i> , 2008, 14, 4821-4829.	3.2	44
80	Ellipticine derivative NSC 338258 represents a potential new antineoplastic agent for the treatment of multiple myeloma. <i>Molecular Cancer Therapeutics</i> , 2008, 7, 500-509.	1.9	15
81	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. <i>Blood</i> , 2008, 111, 968-969.	0.6	66
82	Bortezomib down-regulates the cell-surface expression of HLA class I and enhances natural killer cell-mediated lysis of myeloma. <i>Blood</i> , 2008, 111, 1309-1317.	0.6	159
83	Overexpression and involvement in migration by the metastasis-associated phosphatase PRL-3 in human myeloma cells. <i>Blood</i> , 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. <i>Blood</i> , 2008, 112, 4235-4246.	0.6	124
85	Wnt3a signaling within bone inhibits multiple myeloma bone disease and tumor growth. <i>Blood</i> , 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. <i>Blood</i> , 2008, 112, 196-207.	0.6	223
87	First thalidomide clinical trial in multiple myeloma: a decade. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 2008, 112, 3122-3125.	0.6	90
90	Going with the flow, and beyond, in myeloma. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 2008, 112, 2701-2701.	0.6	0
95	Proteomic Profiling of Multiple Myeloma: Correlation of Protein and Gene Expression Data.. <i>Blood</i> , 2008, 112, 1705-1705.	0.6	0
96	Molecular Indicators of High-Risk Disease.. <i>Blood</i> , 2008, 112, sci-6-sci-6.	0.6	0
97	Bortezomib Induces Osteoblast Differentiation Via Wnt-Independent Activation of Beta-catenin/TCF Signaling. <i>Blood</i> , 2008, 112, 846-846.	0.6	0
98	Thalidomide induces limb deformities by perturbing the Bmp/Dkk1/Wnt signaling pathway. <i>FASEB Journal</i> , 2007, 21, 1410-1421.	0.2	118
99	Heparanase Enhances Syndecan-1 Shedding. <i>Journal of Biological Chemistry</i> , 2007, 282, 13326-13333.	1.6	237
100	Dickkopf Homolog 1 Mediates Endothelin-1-Stimulated New Bone Formation. <i>Molecular Endocrinology</i> , 2007, 21, 486-498.	3.7	169
101	Magnetic Resonance Imaging in Multiple Myeloma: Diagnostic and Clinical Implications. <i>Journal of Clinical Oncology</i> , 2007, 25, 1121-1128.	0.8	369
102	Frequent and specific immunity to the embryonal stem cell-associated antigen SOX2 in patients with monoclonal gammopathy. <i>Journal of Experimental Medicine</i> , 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. <i>Clinical Cancer Research</i> , 2007, 13, 7073-7079.	3.2	99
104	Gene-expression signature of benign monoclonal gammopathy evident in multiple myeloma is linked to good prognosis. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 2007, 109, 4995-5001.	0.6	139
107	Gene expression profiling and correlation with outcome in clinical trials of the proteasome inhibitor bortezomib. <i>Blood</i> , 2007, 109, 3177-3188.	0.6	379
108	Antibody-based inhibition of DKK1 suppresses tumor-induced bone resorption and multiple myeloma growth in vivo. <i>Blood</i> , 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. <i>Blood</i> , 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. <i>Blood</i> , 2007, 110, 827-832.	0.6	167
111	The syndecan-1 heparan sulfate proteoglycan is a viable target for myeloma therapy. <i>Blood</i> , 2007, 110, 2041-2048.	0.6	122
112	Dickkopf-1 (DKK1) is a widely expressed and potent tumor-associated antigen in multiple myeloma. <i>Blood</i> , 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 smoldering disease. <i>British Journal of Haematology</i> , 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. <i>British Journal of Haematology</i> , 2007, 137, 530-536.	1.2	44
115	Incorporating bortezomib into upfront treatment for multiple myeloma: early results of total therapy 3. <i>British Journal of Haematology</i> , 2007, 138, 176-185.	1.2	304
116	Establishment and exploitation of hyperdiploid and non-hyperdiploid human myeloma cell lines. <i>British Journal of Haematology</i> , 2007, 138, 802-811.	1.2	27
117	Frequent Engagement of the Classical and Alternative NF- κ B Pathways by Diverse Genetic Abnormalities in Multiple Myeloma. <i>Cancer Cell</i> , 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.. <i>Blood</i> , 2007, 110, 656-656.	0.6	1
119	Identification of Novel Transcriptional Consequences of Activation and Inactivation of TP53 in Multiple Myeloma.. <i>Blood</i> , 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. <i>Blood</i> , 2006, 108, 1724-1732.	0.6	417
121	The molecular classification of multiple myeloma. <i>Blood</i> , 2006, 108, 2020-2028.	0.6	997
122	Using Genomics to Identify High-Risk Myeloma after Autologous Stem Cell Transplantation. <i>Biology of Blood and Marrow Transplantation</i> , 2006, 12, 77-80.	2.0	20
123	Long-term outcome results of the first tandem autotransplant trial for multiple myeloma. <i>British Journal of Haematology</i> , 2006, 135, 158-164.	1.2	155
124	High-resolution genomic profiles define distinct clinico-pathogenetic subgroups of multiple myeloma patients. <i>Cancer Cell</i> , 2006, 9, 313-325.	7.7	404
125	Role of osteoblast suppression in multiple myeloma. <i>Journal of Cellular Biochemistry</i> , 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.. <i>Blood</i> , 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