David C Johnson

List of Publications by Year
in descending order

56 papers	3,729 citations	201385 27 h-index	223531 46 g-index
57 all docs	57 docs citations	57 times ranked	5452 citing authors

#	Article	IF	Citations
1	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.	0.8	463
2	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. Blood, 2010, 116, e56-e65.	0.6	315
3	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. Nature Communications, 2015, 6, 6997.	5.8	261
4	Intraclonal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. Leukemia, 2014, 28, 384-390.	3.3	252
5	Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. Blood, 2012, 120, 1077-1086.	0.6	231
6	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.	3.3	207
7	Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. Leukemia, 2018, 32, 102-110.	3.3	177
8	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.	0.6	176
9	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. Nature Communications, 2016, 7, 12050.	5.8	146
10	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. Nature Genetics, 2013, 45, 1221-1225.	9.4	143
11	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.	2.8	142
12	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. Nature Genetics, 2012, 44, 58-61.	9.4	137
13	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.	0.6	128
14	Homozygous Deletion Mapping in Myeloma Samples Identifies Genes and an Expression Signature Relevant to Pathogenesis and Outcome. Clinical Cancer Research, 2010, 16, 1856-1864.	3.2	124
15	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. Nature Genetics, 2013, 45, 522-525.	9.4	91
16	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. Nature Communications, 2018, 9, 3707.	5.8	86
17	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. Clinical Cancer Research, 2016, 22, 5783-5794.	3.2	81
18	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. Blood, 2008, 112, 4924-4934.	0.6	65

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19	Inherited genetic susceptibility to multiple myeloma. Leukemia, 2014, 28, 518-524.	3.3	60
20	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. Blood Cancer Journal, 2019, 9, 1.	2.8	40
21	The coordinated action of VCP/p97 and GCN2 regulates cancer cell metabolism and proteostasis during nutrient limitation. Oncogene, 2019, 38, 3216-3231.	2.6	33
22	Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. Blood, 2014, 123, 2513-2517.	0.6	32
23	Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. Nature Communications, 2016, 7, 13656.	5.8	32
24	Genome-wide association study of immunoglobulin light chain amyloidosis in three patient cohorts: comparison with myeloma. Leukemia, 2017, 31, 1735-1742.	3.3	32
25	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. Nature Communications, 2016, 7, 10290.	5.8	31
26	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. Scientific Reports, 2017, 7, 41071.	1.6	31
27	Subclonal TP53 copy number is associated with prognosis in multiple myeloma. Blood, 2018, 132, 2465-2469.	0.6	29
28	The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. Haematologica, 2015, 100, e110-e113.	1.7	27
29	Predicting ultrahigh risk multiple myeloma by molecular profiling: an analysis of newly diagnosed transplant eligible myeloma XI trial patients. Leukemia, 2020, 34, 3091-3096.	3.3	26
30	Neutral tumor evolution in myeloma is associated with poor prognosis. Blood, 2017, 130, 1639-1643.	0.6	20
31	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. Cell Reports, 2017, 20, 2556-2564.	2.9	17
32	Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. Scientific Reports, 2015, 5, 12473.	1.6	16
33	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. Human Genomics, 2019, 13, 37.	1.4	14
34	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. Blood Cancer Journal, 2017, 7, e573-e573.	2.8	12
35	Genetic factors influencing the risk of multiple myeloma bone disease. Leukemia, 2016, 30, 883-888.	3.3	11
36	Search for rare protein altering variants influencing susceptibility to multiple myeloma. Oncotarget, 2017, 8, 36203-36210.	0.8	11

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37	The Genetic Contribution to the Aetiology of Thalidomide Associated VTE.. Blood, 2006, 108, 246-246.	0.6	9
38	Genetic Variation in ADME Genes Is Associated with Thalidomide Related Peripheral Neuropathy in Multiple Myeloma Patients.. Blood, 2008, 112, 1675-1675.	0.6	3
39	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. Blood, 2010, 116, 782-782.	0.6	3
40	Regions of homozygosity as risk factors for multiple myeloma. Annals of Human Genetics, 2019, 83, 231-238.	0.3	2
41	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.	0.6	2
42	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. Blood, 2009, 114, 426-426.	0.6	2
43	MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. Blood, 2013, 122, 274-274.	0.6	2
44	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.	0.6	1
45	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.	0.6	1
46	The Impact of Constitutional Copy Number Variants in Myeloma. Blood, 2008, 112, 496-496.	0.6	1
47	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.	0.6	0
48	Sub-Classification of Hyperdiploid Myeloma Using Global Gene Expression Profiling and SNP-Based Mapping Arrays.. Blood, 2006, 108, 3390-3390.	0.6	0
49	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. Blood, 2007, 110, 2473-2473.	0.6	0
50	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. Blood, 2007, 110, 2474-2474.	0.6	0
51	An Integrated Pharmacogenomic Strategy for the Definition of Thalidomide Response Signatures in Presenting Cases of Multiple Myeloma.. Blood, 2007, 110, 2493-2493.	0.6	0
52	Analytical Approaches for the BOAC SNP Panel Association with Progression Free Survival in Myeloma. Blood, 2008, 112, 2715-2715.	0.6	0
53	XBP1 Expression Is An Important Prognostic Factor for Newly Diagnosed Myeloma Patients.. Blood, 2008, 112, 1686-1686.	0.6	0
54	Large Scale Evaluation of Genetic Variation and the Risk of Multiple Myeloma.. Blood, 2008, 112, 1679-1679.	0.6	0

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55	Expression Profile and up-Regulation of Telomere-Associated Proteins In Multiple Myeloma. Blood, 2010, 116, 4050-4050.	0.6	0
56	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.	0.6	0