David C Johnson

List of Publications by Year in Descending Order

56 papers	2,922 citations	24 h-index	54 g-index
57 ext. papers	3,414 ext. citations	7.4 avg, IF	4 L-index

#	Paper	IF	Citations
56	Predicting ultrahigh risk multiple myeloma by molecular profiling: an analysis of newly diagnosed transplant eligible myeloma XI trial patients. *Leukemia*, **2020**, 34, 3091-3096	10.7	13
55	The coordinated action of VCP/p97 and GCN2 regulates cancer cell metabolism and proteostasis during nutrient limitation. *Oncogene*, **2019**, 38, 3216-3231	9.2	23
54	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. *Human Genomics*, **2019**, 13, 37	6.8	5
53	Regions of homozygosity as risk factors for multiple myeloma. *Annals of Human Genetics*, **2019**, 83, 231-238	2.2	1
52	Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. *Leukemia*, **2018**, 32, 102-110	10.7	108
51	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. *Blood Cancer Journal*, **2018**, 9, 1	7	18
50	Subclonal copy number is associated with prognosis in multiple myeloma. *Blood*, **2018**, 132, 2465-2469	2.2	21
49	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. *Nature Communications*, **2018**, 9, 3707	17.4	57
48	Genome-wide association analysis of chronic lymphocytic leukaemia, Hodgkin lymphoma and multiple myeloma identifies pleiotropic risk loci. *Scientific Reports*, **2017**, 7, 41071	4.9	27
47	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. *Blood Cancer Journal*, **2017**, 7, e573	7	8
46	Genome-wide association study of immunoglobulin light chain amyloidosis in three patient cohorts: comparison with myeloma. *Leukemia*, **2017**, 31, 1735-1742	10.7	32
45	Neutral tumor evolution in myeloma is associated with poor prognosis. *Blood*, **2017**, 130, 1639-1643	2.2	14
44	Genetic Predisposition to Multiple Myeloma at 5q15 Is Mediated by an ELL2 Enhancer Polymorphism. *Cell Reports*, **2017**, 20, 2556-2564	10.6	15
43	Search for rare protein altering variants influencing susceptibility to multiple myeloma. *Oncotarget*, **2017**, 8, 36203-36210	3.3	9
42	Multiple myeloma risk variant at 7p15.3 creates an IRF4-binding site and interferes with CDCA7L expression. *Nature Communications*, **2016**, 7, 13656	17.4	26
41	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. *Nature Communications*, **2016**, 7, 12050	17.4	101
40	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. *Clinical Cancer Research*, **2016**, 22, 5783-5794	12.9	56

39	Genetic factors influencing the risk of multiple myeloma bone disease. *Leukemia*, **2016**, 30, 883-8	10.7	11
38	Genome-wide association study identifies variation at 6q25.1 associated with survival in multiple myeloma. *Nature Communications*, **2016**, 7, 10290	17.4	26
37	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. *Nature Communications*, **2015**, 6, 6997	17.4	176
36	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. *Journal of Clinical Oncology*, **2015**, 33, 3911-20	2.2	348
35	Implementation of genome-wide complex trait analysis to quantify the heritability in multiple myeloma. *Scientific Reports*, **2015**, 5, 12473	4.9	16
34	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, e110-3	6.6	22
33	Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. *Leukemia*, **2014**, 28, 1705-15	10.7	162
32	Inherited genetic susceptibility to multiple myeloma. *Leukemia*, **2014**, 28, 518-24	10.7	54
31	Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. *Blood*, **2014**, 123, 2513-7; quiz 2593	2.2	31
30	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	7	114
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	10.7	202
28	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. *Nature Genetics*, **2013**, 45, 1221-1225	36.3	119
27	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. *Nature Genetics*, **2013**, 45, 522-525	36.3	79
26	Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. *Blood*, **2013**, 121, 3413-9	2.2	101
25	MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. *Blood*, **2013**, 122, 274-274	2.2	0
24	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	2.2	
23	Intraclonal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. *Blood*, **2012**, 120, 1077-86	2.2	200
22	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. *Nature Genetics*, **2011**, 44, 58-61	36.3	122

21	Homozygous deletion mapping in myeloma samples identifies genes and an expression signature relevant to pathogenesis and outcome. *Clinical Cancer Research*, **2010**, 16, 1856-64	12.9	109
20	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. *Blood*, **2010**, 116, e56-65	2.2	263
19	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. *Blood*, **2010**, 116, 782-782	2.2	3
18	Expression Profile and up-Regulation of Telomere-Associated Proteins In Multiple Myeloma. *Blood*, **2010**, 116, 4050-4050	2.2	
17	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. *Blood*, **2009**, 114, 426-426	2.2	2
16	Genetic associations with thalidomide mediated venous thrombotic events in myeloma identified using targeted genotyping. *Blood*, **2008**, 112, 4924-34	2.2	59
15	Genetic Variation in ADME Genes Is Associated with Thalidomide Related Peripheral Neuropathy in Multiple Myeloma Patients.. *Blood*, **2008**, 112, 1675-1675	2.2	1
14	The Impact of Constitutional Copy Number Variants in Myeloma. *Blood*, **2008**, 112, 496-496	2.2	
13	Analytical Approaches for the BOAC SNP Panel Association with Progression Free Survival in Myeloma. *Blood*, **2008**, 112, 2715-2715	2.2	
12	XBP1 Expression Is An Important Prognostic Factor for Newly Diagnosed Myeloma Patients.. *Blood*, **2008**, 112, 1686-1686	2.2	
11	Large Scale Evaluation of Genetic Variation and the Risk of Multiple Myeloma.. *Blood*, **2008**, 112, 1679-1679	2.2	
10	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	2.2	1
9	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. *Blood*, **2007**, 110, 2473-2473	2.2	
8	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. *Blood*, **2007**, 110, 2474-2474	2.2	
7	An Integrated Pharmacogenomic Strategy for the Definition of Thalidomide Response Signatures in Presenting Cases of Multiple Myeloma.. *Blood*, **2007**, 110, 2493-2493	2.2	
6	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, 1733-43	2.2	163
5	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	2.2	1
4	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	2.2	

3	The Genetic Contribution to the Aetiology of Thalidomide Associated VTE.. *Blood*, **2006**, 108, 246-246	2.2
2	Sub-Classification of Hyperdiploid Myeloma Using Global Gene Expression Profiling and SNP-Based Mapping Arrays.. *Blood*, **2006**, 108, 3390-3390	2.2
1	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	2.2