

# Brian A Walker

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/6518511/brian-a-walker-publications-by-citations.pdf>  
**Version:** 2024-04-10

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.  
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

218 papers	7,860 citations	44 h-index	87 g-index
242 ext. papers	9,500 ext. citations	5.6 avg, IF	5.45 L-index

#	Paper	IF	Citations
218	The genetic architecture of multiple myeloma. <i>Nature Reviews Cancer</i> , <b>2012</b> , 12, 335-48	31.3	607
217	The chicken B locus is a minimal essential major histocompatibility complex. <i>Nature</i> , <b>1999</b> , 401, 923-5	50.4	493
216	Mutational Spectrum, Copy Number Changes, and Outcome: Results of a Sequencing Study of Patients With Newly Diagnosed Myeloma. <i>Journal of Clinical Oncology</i> , <b>2015</b> , 33, 3911-20	2.2	348
215	A genetic variation map for chicken with 2.8 million single-nucleotide polymorphisms. <i>Nature</i> , <b>2004</b> , 432, 717-22	50.4	341
214	A compendium of myeloma-associated chromosomal copy number abnormalities and their prognostic value. <i>Blood</i> , <b>2010</b> , 116, e56-65	2.2	263
213	A novel prognostic model in myeloma based on co-segregating adverse FISH lesions and the ISS: analysis of patients treated in the MRC Myeloma IX trial. <i>Leukemia</i> , <b>2012</b> , 26, 349-55	10.7	236
212	Intracloal heterogeneity is a critical early event in the development of myeloma and precedes the development of clinical symptoms. <i>Leukemia</i> , <b>2014</b> , 28, 384-390	10.7	202
211	Intracloal heterogeneity and distinct molecular mechanisms characterize the development of t(4;14) and t(11;14) myeloma. <i>Blood</i> , <b>2012</b> , 120, 1077-86	2.2	200
210	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , <b>2018</b> , 132, 587-597	2.2	196
209	Aberrant global methylation patterns affect the molecular pathogenesis and prognosis of multiple myeloma. <i>Blood</i> , <b>2011</b> , 117, 553-62	2.2	182
208	APOBEC family mutational signatures are associated with poor prognosis translocations in multiple myeloma. <i>Nature Communications</i> , <b>2015</b> , 6, 6997	17.4	176
207	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , <b>2019</b> , 33, 159-170	10.7	176
206	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. <i>Nature Communications</i> , <b>2017</b> , 8, 268	17.4	170
205	Integration of global SNP-based mapping and expression arrays reveals key regions, mechanisms, and genes important in the pathogenesis of multiple myeloma. <i>Blood</i> , <b>2006</b> , 108, 1733-43	2.2	163
204	Single-cell genetic analysis reveals the composition of initiating clones and phylogenetic patterns of branching and parallel evolution in myeloma. <i>Leukemia</i> , <b>2014</b> , 28, 1705-15	10.7	162
203	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. <i>Blood</i> , <b>2016</b> , 128, 1735-44	2.2	129
202	Global methylation analysis identifies prognostically important epigenetically inactivated tumor suppressor genes in multiple myeloma. <i>Blood</i> , <b>2013</b> , 122, 219-26	2.2	128

201	Common variation at 3p22.1 and 7p15.3 influences multiple myeloma risk. <i>Nature Genetics</i> , <b>2011</b> , 44, 58-61	36.3	122
200	Mapping of chromosome 1p deletions in myeloma identifies FAM46C at 1p12 and CDKN2C at 1p32.3 as being genes in regions associated with adverse survival. <i>Clinical Cancer Research</i> , <b>2011</b> , 17, 7776-84	12.9	122
199	Gene mapping and expression analysis of 16q loss of heterozygosity identifies WWOX and CYLD as being important in determining clinical outcome in multiple myeloma. <i>Blood</i> , <b>2007</b> , 110, 3291-300	2.2	121
198	Low expression of hexokinase-2 is associated with false-negative FDG-positron emission tomography in multiple myeloma. <i>Blood</i> , <b>2017</b> , 130, 30-34	2.2	120
197	Common variation at 3q26.2, 6p21.33, 17p11.2 and 22q13.1 influences multiple myeloma risk. <i>Nature Genetics</i> , <b>2013</b> , 45, 1221-1225	36.3	119
196	Translocations at 8q24 juxtapose MYC with genes that harbor superenhancers resulting in overexpression and poor prognosis in myeloma patients. <i>Blood Cancer Journal</i> , <b>2014</b> , 4, e191	7	114
195	Homozygous deletion mapping in myeloma samples identifies genes and an expression signature relevant to pathogenesis and outcome. <i>Clinical Cancer Research</i> , <b>2010</b> , 16, 1856-64	12.9	109
194	Prediction of outcome in newly diagnosed myeloma: a meta-analysis of the molecular profiles of 1905 trial patients. <i>Leukemia</i> , <b>2018</b> , 32, 102-110	10.7	108
193	Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. <i>Nature Communications</i> , <b>2016</b> , 7, 12050	17.4	101
192	Characterization of IGH locus breakpoints in multiple myeloma indicates a subset of translocations appear to occur in pregerminal center B cells. <i>Blood</i> , <b>2013</b> , 121, 3413-9	2.2	101
191	MMSET deregulation affects cell cycle progression and adhesion regulons in t(4;14) myeloma plasma cells. <i>Haematologica</i> , <b>2009</b> , 94, 78-86	6.6	94
190	XBP1s levels are implicated in the biology and outcome of myeloma mediating different clinical outcomes to thalidomide-based treatments. <i>Blood</i> , <b>2010</b> , 116, 250-3	2.2	92
189	Genetic factors underlying the risk of thalidomide-related neuropathy in patients with multiple myeloma. <i>Journal of Clinical Oncology</i> , <b>2011</b> , 29, 797-804	2.2	84
188	The CCND1 c.870G>A polymorphism is a risk factor for t(11;14)(q13;q32) multiple myeloma. <i>Nature Genetics</i> , <b>2013</b> , 45, 522-525	36.3	79
187	EAPH-05. MOLECULAR PROFILING AND IDENTIFICATION OF TARGETED THERAPIES FOR CHILDREN AND YOUNG ADULTS WITH PRIMARY CENTRAL NERVOUS SYSTEM TUMOURS IN THE UNITED KINGDOM. <i>Neuro-Oncology</i> , <b>2018</b> , 20, i66-i66	1	78
186	487. Severity and Clinical Outcomes of Clostridium difficile Infection Based on Toxin B Assay Results. <i>Open Forum Infectious Diseases</i> , <b>2018</b> , 5, S180-S181	1	78
185	Cancer-selective targeting of the NF- $\kappa$ B survival pathway with GADD45/MKK7 inhibitors. <i>Cancer Cell</i> , <b>2014</b> , 26, 495-508	24.3	77
184	Deletions of CDKN2C in multiple myeloma: biological and clinical implications. <i>Clinical Cancer Research</i> , <b>2008</b> , 14, 6033-41	12.9	77

183	The dominantly expressed class I molecule of the chicken MHC is explained by coevolution with the polymorphic peptide transporter (TAP) genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2011</b> , 108, 8396-401	11.5	72
182	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. <i>Leukemia</i> , <b>2019</b> , 33, 1713-1722	10.7	66
181	Overexpression of EZH2 in multiple myeloma is associated with poor prognosis and dysregulation of cell cycle control. <i>Blood Cancer Journal</i> , <b>2017</b> , 7, e549	7	60
180	Identification of multiple risk loci and regulatory mechanisms influencing susceptibility to multiple myeloma. <i>Nature Communications</i> , <b>2018</b> , 9, 3707	17.4	57
179	The Spectrum and Clinical Impact of Epigenetic Modifier Mutations in Myeloma. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 5783-5794	12.9	56
178	The reconstruction of transcriptional networks reveals critical genes with implications for clinical outcome of multiple myeloma. <i>Clinical Cancer Research</i> , <b>2011</b> , 17, 7402-12	12.9	53
177	The clinical impact and molecular biology of del(17p) in multiple myeloma treated with conventional or thalidomide-based therapy. <i>Genes Chromosomes and Cancer</i> , <b>2011</b> , 50, 765-74	5	52
176	Coexistent hyperdiploidy does not abrogate poor prognosis in myeloma with adverse cytogenetics and may precede IGH translocations. <i>Blood</i> , <b>2015</b> , 125, 831-40	2.2	48
175	The level of deletion 17p and bi-allelic inactivation of has a significant impact on clinical outcome in multiple myeloma. <i>Haematologica</i> , <b>2017</b> , 102, e364-e367	6.6	44
174	Improved risk stratification in myeloma using a microRNA-based classifier. <i>British Journal of Haematology</i> , <b>2013</b> , 162, 348-59	4.5	44
173	The presence of large focal lesions is a strong independent prognostic factor in multiple myeloma. <i>Blood</i> , <b>2018</b> , 132, 59-66	2.2	43
172	The spectrum of somatic mutations in monoclonal gammopathy of undetermined significance indicates a less complex genomic landscape than that in multiple myeloma. <i>Haematologica</i> , <b>2017</b> , 102, 1617-1625	6.6	42
171	Bi-allelic inactivation is more prevalent at relapse in multiple myeloma, identifying RB1 as an independent prognostic marker. <i>Blood Cancer Journal</i> , <b>2017</b> , 7, e535	7	39
170	Clonal evolution in myeloma: the impact of maintenance lenalidomide and depth of response on the genetics and sub-clonal structure of relapsed disease in uniformly treated newly diagnosed patients. <i>Haematologica</i> , <b>2019</b> , 104, 1440-1450	6.6	39
169	Aminopeptidase inhibition as a targeted treatment strategy in myeloma. <i>Molecular Cancer Therapeutics</i> , <b>2009</b> , 8, 762-70	6.1	39
168	High-resolution genomic profiling in hairy cell leukemia-variant compared with typical hairy cell leukemia. <i>Leukemia</i> , <b>2011</b> , 25, 1189-92	10.7	37
167	Integrated analysis of microRNAs, transcription factors and target genes expression discloses a specific molecular architecture of hyperdiploid multiple myeloma. <i>Oncotarget</i> , <b>2015</b> , 6, 19132-47	3.3	37
166	Genes with a spike expression are clustered in chromosome (sub)bands and spike (sub)bands have a powerful prognostic value in patients with multiple myeloma. <i>Haematologica</i> , <b>2012</b> , 97, 622-30	6.6	34

165	Gender disparities in the tumor genetics and clinical outcome of multiple myeloma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , <b>2011</b> , 20, 1703-7	4	33
164	Chicken TAP genes differ from their human orthologues in locus organisation, size, sequence features and polymorphism. <i>Immunogenetics</i> , <b>2005</b> , 57, 232-47	3.2	33
163	MMSET is the key molecular target in t(4;14) myeloma. <i>Blood Cancer Journal</i> , <b>2013</b> , 3, e114	7	32
162	Inherited genetic susceptibility to monoclonal gammopathy of unknown significance. <i>Blood</i> , <b>2014</b> , 123, 2513-7; quiz 2593	2.2	31
161	A TC classification-based predictor for multiple myeloma using multiplexed real-time quantitative PCR. <i>Leukemia</i> , <b>2013</b> , 27, 1754-7	10.7	31
160	Inactivating Mutations Are Enriched in Advanced Breast Cancer and Contribute to Endocrine Therapy Resistance. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 608-622	12.9	31
159	Long-term outcomes after autologous stem cell transplantation for multiple myeloma. <i>Blood Advances</i> , <b>2020</b> , 4, 422-431	7.8	30
158	Loss of heterozygosity as a marker of homologous repair deficiency in multiple myeloma: a role for PARP inhibition?. <i>Leukemia</i> , <b>2018</b> , 32, 1561-1566	10.7	29
157	Treatment to suppression of focal lesions on positron emission tomography-computed tomography is a therapeutic goal in newly diagnosed multiple myeloma. <i>Haematologica</i> , <b>2018</b> , 103, 1047-1053	6.6	29
156	Understanding next generation sequencing in oncology: A guide for oncologists. <i>Critical Reviews in Oncology/Hematology</i> , <b>2015</b> , 96, 463-74	7	28
155	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , <b>2020</b> , 34, 1866-1874	10.7	27
154	Comprehensive translocation and clonality detection in lymphoproliferative disorders by next-generation sequencing. <i>Haematologica</i> , <b>2017</b> , 102, e57-e60	6.6	26
153	A molecular diagnostic approach able to detect the recurrent genetic prognostic factors typical of presenting myeloma. <i>Genes Chromosomes and Cancer</i> , <b>2015</b> , 54, 91-8	5	26
152	A gene expression-based predictor for myeloma patients at high risk of developing bone disease on bisphosphonate treatment. <i>Clinical Cancer Research</i> , <b>2011</b> , 17, 6347-55	12.9	25
151	A modified method for whole exome resequencing from minimal amounts of starting DNA. <i>PLoS ONE</i> , <b>2012</b> , 7, e32617	3.7	24
150	High expression levels of the mammalian target of rapamycin inhibitor DEPTOR are predictive of response to thalidomide in myeloma. <i>Leukemia and Lymphoma</i> , <b>2010</b> , 51, 2126-9	1.9	23
149	The 7p15.3 (rs4487645) association for multiple myeloma shows strong allele-specific regulation of the MYC-interacting gene CDCA7L in malignant plasma cells. <i>Haematologica</i> , <b>2015</b> , 100, e110-3	6.6	22
148	Microhomology-mediated end joining drives complex rearrangements and overexpression of and in multiple myeloma. <i>Haematologica</i> , <b>2020</b> , 105, 1055-1066	6.6	22

147	The prognostic value of the depth of response in multiple myeloma depends on the time of assessment, risk status and molecular subtype. <i>Haematologica</i> , <b>2017</b> , 102, e313-e316	6.6	21
146	A tailored molecular profiling programme for children with cancer to identify clinically actionable genetic alterations. <i>European Journal of Cancer</i> , <b>2019</b> , 121, 224-235	7.5	21
145	Genomewide profiling of copy-number alteration in monoclonal gammopathy of undetermined significance. <i>European Journal of Haematology</i> , <b>2016</b> , 97, 568-575	3.8	20
144	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. <i>Nature Communications</i> , <b>2021</b> , 12, 293	17.4	20
143	The varied distribution and impact of RAS codon and other key DNA alterations across the translocation cyclin D subgroups in multiple myeloma. <i>Oncotarget</i> , <b>2017</b> , 8, 27854-27867	3.3	19
142	Genetic correlation between multiple myeloma and chronic lymphocytic leukaemia provides evidence for shared aetiology. <i>Blood Cancer Journal</i> , <b>2018</b> , 9, 1	7	18
141	and Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 2422-2432	12.9	17
140	An acquired high-risk chromosome instability phenotype in multiple myeloma: Jumping 1q Syndrome. <i>Blood Cancer Journal</i> , <b>2019</b> , 9, 62	7	17
139	Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. <i>Blood Cancer Journal</i> , <b>2020</b> , 10, 70	7	16
138	Investigating the feasibility of tumour molecular profiling in gastrointestinal malignancies in routine clinical practice. <i>Annals of Oncology</i> , <b>2018</b> , 29, 230-236	10.3	16
137	Use of single nucleotide polymorphism-based mapping arrays to detect copy number changes and loss of heterozygosity in multiple myeloma. <i>Clinical Lymphoma and Myeloma</i> , <b>2006</b> , 7, 186-91		16
136	Whole-genome sequencing reveals progressive versus stable myeloma precursor conditions as two distinct entities. <i>Nature Communications</i> , <b>2021</b> , 12, 1861	17.4	16
135	Kinase domain activation through gene rearrangement in multiple myeloma. <i>Leukemia</i> , <b>2018</b> , 32, 2435-2447	16.7	15
134	Neutral tumor evolution in myeloma is associated with poor prognosis. <i>Blood</i> , <b>2017</b> , 130, 1639-1643	2.2	14
133	MAFb protein confers intrinsic resistance to proteasome inhibitors in multiple myeloma. <i>BMC Cancer</i> , <b>2018</b> , 18, 724	4.8	13
132	Biology and treatment of myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , <b>2014</b> , 14 Suppl, S65-70	2	13
131	Daratumumab and dexamethasone is safe and effective for triple refractory myeloma patients: final results of the IFM 2014-04 (Etoile du Nord) trial. <i>British Journal of Haematology</i> , <b>2019</b> , 187, 319-327	4.5	12
130	Development of a targeted sequencing approach to identify prognostic, predictive and diagnostic markers in paediatric solid tumours. <i>Oncotarget</i> , <b>2017</b> , 8, 112036-112050	3.3	12

129	Impact of Genes Highly Correlated with MMSET Myeloma on the Survival of Non-MMSET Myeloma Patients. <i>Clinical Cancer Research</i> , <b>2016</b> , 22, 4039-44	12.9	11
128	Molecular profiling of colorectal pulmonary metastases and primary tumours: implications for targeted treatment. <i>Oncotarget</i> , <b>2017</b> , 8, 64999-65008	3.3	11
127	Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. <i>PLoS Medicine</i> , <b>2020</b> , 17, e1003323	11.6	10
126	The genomic landscape of plasma cells in systemic light chain amyloidosis. <i>Blood</i> , <b>2018</b> , 132, 2775-2777	2.2	10
125	Search for rare protein altering variants influencing susceptibility to multiple myeloma. <i>Oncotarget</i> , <b>2017</b> , 8, 36203-36210	3.3	9
124	Assessing the effect of obesity-related traits on multiple myeloma using a Mendelian randomisation approach. <i>Blood Cancer Journal</i> , <b>2017</b> , 7, e573	7	8
123	The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. <i>Journal of Hematology and Oncology</i> , <b>2020</b> , 13, 108	22.4	8
122	The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. <i>Blood</i> , <b>2016</b> , 128, 4431-4431	2.2	7
121	The combination of HDAC and aminopeptidase inhibitors is highly synergistic in myeloma and leads to disruption of the NFB signalling pathway. <i>Oncotarget</i> , <b>2015</b> , 6, 17314-27	3.3	7
120	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. <i>Haematologica</i> , <b>2021</b> , 106, 736-745	6.6	7
119	Knick-knack PADIMAC. <i>Blood</i> , <b>2018</b> , 132, 2110-2111	2.2	7
118	Identification of a novel t(7;14) translocation in multiple myeloma resulting in overexpression of EGFR. <i>Genes Chromosomes and Cancer</i> , <b>2013</b> , 52, 817-22	5	6
117	Transcriptome-wide association study of multiple myeloma identifies candidate susceptibility genes. <i>Human Genomics</i> , <b>2019</b> , 13, 37	6.8	5
116	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of. <i>Oncotarget</i> , <b>2019</b> , 10, 732-737	3.3	5
115	Monitoring treatment response and disease progression in myeloma with circulating cell-free DNA. <i>European Journal of Haematology</i> , <b>2021</b> , 106, 230-240	3.8	5
114	A novel functional role for MMSET in RNA processing based on the link between the REIIBP isoform and its interaction with the SMN complex. <i>PLoS ONE</i> , <b>2014</b> , 9, e99493	3.7	4
113	Whole Exome Sequencing in Multiple Myeloma to Identify Somatic Single Nucleotide Variants and Key Translocations Involving Immunoglobulin Loci and MYC. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1792, 71-95	1.4	4
112	A gene expression based predictor for high risk myeloma treated with intensive therapy and autologous stem cell rescue. <i>Leukemia and Lymphoma</i> , <b>2015</b> , 56, 594-601	1.9	3



111	Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregulate Gene Function By a Range of Mechanisms. <i>Blood</i> , <b>2019</b> , 134, 3767-3767	2.2	3
110	Defining Myeloma Patients at High Risk of Developing Bone Disease While on Bisphosphonate Treatment. <i>Blood</i> , <b>2010</b> , 116, 782-782	2.2	3
109	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , <b>2021</b> ,	10.7	3
108	PHF19 inhibition as a therapeutic target in multiple myeloma. <i>Current Research in Translational Medicine</i> , <b>2021</b> , 69, 103290	3.7	3
107	A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. <i>Blood Advances</i> , <b>2018</b> , 2, 2400-2411	7.8	3
106	Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. <i>Leukemia</i> , <b>2021</b> , 35, 3017-3020	10.7	3
105	Plasma cells expression from smouldering myeloma to myeloma reveals the importance of the PRC2 complex, cell cycle progression, and the divergent evolutionary pathways within the different molecular subgroups. <i>Leukemia</i> , <b>2021</b> ,	10.7	3
104	The Chromosome 13 Conundrum in Multiple Myeloma. <i>Blood Cancer Discovery</i> , <b>2020</b> , 1, 16-17	7	2
103	Complete Genome Sequences of Four Isolates of Vancomycin-Resistant <i>Enterococcus faecium</i> with the Gene and Two Daptomycin Resistance Mutations, Obtained from Two Inpatients with Prolonged Bacteremia. <i>Microbiology Resource Announcements</i> , <b>2020</b> , 9,	1.3	2
102	Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. <i>Blood</i> , <b>2018</b> , 132, 1882-1882	2.2	2
101	The Mutational Landscape of Primary Plasma Cell Leukemia. <i>Blood</i> , <b>2018</b> , 132, 114-114	2.2	2
100	A High-Risk Multiple Myeloma Group Identified By Integrative Multi-Omics Segmentation of Newly Diagnosed Patients. <i>Blood</i> , <b>2018</b> , 132, 3165-3165	2.2	2
99	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. <i>Blood</i> , <b>2018</b> , 132, 408-408	2.2	2
98	Analysis of the Sub-Clonal Structure of Smoldering Myeloma over Time Provides a New Means of Disease Monitoring and Highlights Evolutionary Trajectories Leading to Myeloma. <i>Blood</i> , <b>2019</b> , 134, 4333-4333 <sup>2</sup>	2.2	2
97	The Spectrum of Exomic Mutation in Elderly Myeloma Differs Substantially from Patients at Younger Ages Consistent with a Different Evolutionary Trajectory to Full Blown Disease Based on Age of Onset. <i>Blood</i> , <b>2019</b> , 134, 4346-4346	2.2	2
96	Mutant KRAS Enhances Stress Granules and Resistance to Proteasome Inhibition Via 15-d-PGJ2 in Multiple Myeloma. <i>Blood</i> , <b>2019</b> , 134, 4383-4383	2.2	2
95	EARLY Results of TOTAL Therapy 7 (TT7): High Response Rates of NEWLY Diagnosed High Risk Myeloma to Daratumumab. <i>Blood</i> , <b>2019</b> , 134, 4569-4569	2.2	2
94	Whole-Genome Sequencing Reveals Evidence of Two Biologically and Clinically Distinct Entities: Progressive Versus Stable Myeloma Precursor Disease. <i>Blood</i> , <b>2020</b> , 136, 47-48	2.2	2



93	Genetic Variations Associated with Overall and Progression-Free Survival in Multiple Myeloma Patients Treated with Thalidomide Combinations.. <i>Blood</i> , <b>2009</b> , 114, 426-426	2.2	2
92	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. <i>Blood</i> , <b>2016</b> , 128, 3278-3278	2.2	2
91	Inhibition of the Epigenetic Modifier EZH2 Upregulates Cell Cycle Control Genes to Inhibit Myeloma Cell Growth and Overcome High-Risk Disease Features. <i>Blood</i> , <b>2016</b> , 128, 3289-3289	2.2	2
90	The Impact of Maintenance Lenalidomide on the Mutational Status of the Myeloma Clone at Relapse in the NCRI Myeloma XI Trial for Newly Diagnosed Multiple Myeloma Patients (NDMM). <i>Blood</i> , <b>2016</b> , 128, 4412-4412	2.2	2
89	MYC Rearrangements in Multiple Myeloma Are Complex, Can Involve More Than Five Different Chromosomes, and Correlate with Increased Expression of MYC and a Distinct Downstream Gene Expression Pattern. <i>Blood</i> , <b>2017</b> , 130, 65-65	2.2	2
88	Multiple Myeloma DREAM Challenge Reveals Epigenetic Regulator PHF19 As Marker of Aggressive Disease		2
87	Translocations and Jumping Rearrangements at 8q24 Result in over-Expression of MYC and are Key Drivers of Disease Progression. <i>Blood</i> , <b>2016</b> , 128, 115-115	2.2	2
86	Two Cases of Vancomycin-Resistant Bacteremia With Development of Daptomycin-Resistant Phenotype and its Detection Using Oxford Nanopore Sequencing. <i>Open Forum Infectious Diseases</i> , <b>2020</b> , 7, ofaa180	1	2
85	Cryopreservation Preserves Cell-Type Composition and Gene Expression Profiles in Bone Marrow Aspirates From Multiple Myeloma Patients. <i>Frontiers in Genetics</i> , <b>2021</b> , 12, 663487	4.5	2
84	High-risk transcriptional profiles in multiple myeloma are an acquired feature that can occur in any subtype and more frequently with each subsequent relapse. <i>British Journal of Haematology</i> , <b>2021</b> , 195, 283-286	4.5	2
83	Intron retention-induced neoantigen load correlates with unfavorable prognosis in multiple myeloma. <i>Oncogene</i> , <b>2021</b> , 40, 6130-6138	9.2	2
82	Perspectives on the Risk-Stratified Treatment of Multiple Myeloma. <i>Blood Cancer Discovery</i> , OF1-OF12	7	2
81	Draft Genome Sequences of 48 Vancomycin-Resistant Enterococcus faecium Strains Isolated from Inpatients with Bacteremia and Urinary Tract Infection. <i>Microbiology Resource Announcements</i> , <b>2019</b> , 8,	1.3	1
80	A Rapid and Robust Protocol for Reduced Representation Bisulfite Sequencing in Multiple Myeloma. <i>Methods in Molecular Biology</i> , <b>2018</b> , 1792, 179-191	1.4	1
79	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , <b>2020</b> , 136, 8-9	2.2	1
78	Paradoxical sex-specific patterns of autoantibody response to SARS-CoV-2 infection.. <i>Journal of Translational Medicine</i> , <b>2021</b> , 19, 524	8.5	1
77	Deep Immunoprofiling of the Bone Marrow Microenvironmental Changes Underlying the Multistep Progression of Multiple Myeloma. <i>Blood</i> , <b>2018</b> , 132, 243-243	2.2	1
76	Long-Term Follow-up Identifies Double Hit and Key Mutations As Impacting Progression Free and Overall Survival in Multiple Myeloma. <i>Blood</i> , <b>2018</b> , 132, 110-110	2.2	1

75	Fine Mapping and Expression Analysis of Chromosome 1 with the Aim of Defining Critically Deregulated Genes Important in the Pathogenesis of Myeloma.. <i>Blood</i> , <b>2006</b> , 108, 112-112	2.2	1
74	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.. <i>Blood</i> , <b>2007</b> , 110, 395-395	2.2	1
73	Hypermethylation Is A Key Feature of the Transition of Multiple Myeloma to Plasma Cell Leukemia. <i>Blood</i> , <b>2010</b> , 116, 535-535	2.2	1
72	Concurrent Amplification of MYC and 1q21 in Multiple Myeloma: Focal and Segmental Jumping Translocations of MYC. <i>Blood</i> , <b>2016</b> , 128, 3266-3266	2.2	1
71	Loss of heterozygosity in multiple myeloma: A role for PARP inhibition?. <i>Journal of Clinical Oncology</i> , <b>2017</b> , 35, 8026-8026	2.2	1
70	Insights into high-risk multiple myeloma from an analysis of the role of PHF19 in cancer. <i>Journal of Experimental and Clinical Cancer Research</i> , <b>2021</b> , 40, 380	12.8	1
69	Expression Signature of Myeloma Residual Cells Is Characterized By Genes Associated with Proliferation, Epigenetic Modification, and Stem Cell Maintenance. <i>Blood</i> , <b>2018</b> , 132, 4465-4465	2.2	1
68	Long-Term Outcome of Total Therapy Regimens: Impact of Molecular Subgroups. <i>Blood</i> , <b>2019</b> , 134, 3309-3309	2.2	1
67	Diagnostic Evidence GAuge of Single cells (DEGAS): A flexible deep-transfer learning framework for prioritizing cells in relation to disease		1
66	Whole genome sequencing provides evidence of two biologically and clinically distinct entities of asymptomatic monoclonal gammopathies: progressive versus stable myeloma precursor condition		1
65	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. <i>Blood</i> , <b>2016</b> , 128, 196-196	2.2	1
64	Inhibition of HDACs and Aminopeptidases Is Highly Synergistic in Myeloma Cells Resulting in Cell Death Via the Upregulation of BIRC3, a Key Mediator of NF-KappaB Signalling.. <i>Blood</i> , <b>2009</b> , 114, 607-607	2.2	1
63	Defining High Risk Myeloma Using Co-Segregating FISH Variables; Results of MRC Myeloma IX. <i>Blood</i> , <b>2010</b> , 116, 1907-1907	2.2	1
62	Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , <b>2021</b> ,	7.5	1
61	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 144	3.6	1
60	Diagnostic Evidence GAuge of Single cells (DEGAS): a flexible deep transfer learning framework for prioritizing cells in relation to disease.. <i>Genome Medicine</i> , <b>2022</b> , 14, 11	14.4	0
59	An Acquired High-Risk Chromosome Instability Phenotype in Multiple Myeloma: Jumping 1q Syndrome. <i>Blood</i> , <b>2018</b> , 132, 4489-4489	2.2	0
58	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , <b>2016</b> , 128, 4416-4416	2.2	0

57	MYC Translocations In Multiple Myeloma Involve Recruitment Of Enhancer Elements Resulting In Over-Expression and Decreased Overall Survival. <i>Blood</i> , <b>2013</b> , 122, 274-274	2.2	O
56	Chromosomal 1q21 abnormalities in multiple myeloma: a review of translational, clinical research, and therapeutic strategies. <i>Expert Review of Hematology</i> , <b>2021</b> , 1-16	2.8	O
55	B-cell malignancies: capture-sequencing strategies for identification of gene rearrangements and translocations into immunoglobulin gene loci. <i>Blood and Lymphatic Cancer: Targets and Therapy</i> , <b>2014</b> , 107	2.6	
54	Mutations in CRBN and Other Cereblon Pathway Genes Are Only Associated with Acquired Resistance to Immunomodulatory Drugs in a Subset of Patients and Cell Line Models. <i>Blood</i> , <b>2020</b> , 136, 6-7	2.2	
53	Impact of Etiological Cytogenetic Abnormalities on Immunoparesis and Progression-Free and Overall Survival in Newly Diagnosed Multiple Myeloma. <i>Blood</i> , <b>2020</b> , 136, 6-6	2.2	
52	Gene Expression Reveals Two Distinct Biological Groups within T-Cell Prolymphocytic Leukaemia.. <i>Blood</i> , <b>2005</b> , 106, 4366-4366	2.2	
51	Insights into the Basis of Chromosomal Imbalances during the Clonal Evolution of Multiple Myeloma Using SNP Array Analysis.. <i>Blood</i> , <b>2005</b> , 106, 621-621	2.2	
50	Development of a Panel of 3,500 SNP Based Functional Genetic Variants Relevant to the Etiology and Outcome in Multiple Myeloma.. <i>Blood</i> , <b>2005</b> , 106, 620-620	2.2	
49	Ultra-Rapid, High-Throughput Molecular Diagnostics in Hemato-Oncology.. <i>Blood</i> , <b>2005</b> , 106, 3270-3270	2.2	
48	Identification of Collaborating Oncogeneic Events Leading to Disease Progression in Myeloma Cases with a t(4;14) and t(11;14) Using SNP and Gene Expression Arrays.. <i>Blood</i> , <b>2005</b> , 106, 1542-1542	2.2	
47	Status of Chromosome 13 in Multiple Myeloma: Integrated Approach Using SNP Mapping Array and Gene Expression Array.. <i>Blood</i> , <b>2005</b> , 106, 1563-1563	2.2	
46	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.. <i>Blood</i> , <b>2006</b> , 108, 110-110	2.2	
45	Sub-Classification of Hyperdiploid Myeloma Using Global Gene Expression Profiling and SNP-Based Mapping Arrays.. <i>Blood</i> , <b>2006</b> , 108, 3390-3390	2.2	
44	Genome-Wide Identification of Gene Expression Networks Affected by Genomic Changes in Multiple Myeloma.. <i>Blood</i> , <b>2007</b> , 110, 2494-2494	2.2	
43	Mutation and Methylation Analysis of WWOX and CYLD on 16q; Potential Tumor Suppressor Genes in Myeloma.. <i>Blood</i> , <b>2007</b> , 110, 2473-2473	2.2	
42	Screening of Homozygous Deletions Identifies Key Deregulated Genes and Pathways in Multiple Myeloma.. <i>Blood</i> , <b>2007</b> , 110, 2474-2474	2.2	
41	An Integrated Pharmacogenomic Strategy for the Definition of Thalidomide Response Signatures in Presenting Cases of Multiple Myeloma.. <i>Blood</i> , <b>2007</b> , 110, 2493-2493	2.2	
40	Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. <i>Blood</i> , <b>2018</b> , 132, 4457-4457	2.2	

- 39 Poor Overall Survival in Hyperhaploid Multiple Myeloma Is Defined By Double-Hit Bi-Allelic Inactivation of TP53. *Blood*, **2018**, 132, 4441-4441 2.2
- 38 Sequential Improvements in the Outcome of Autologous Stem Cell Transplantation for Multiple Myeloma over Time. *Blood*, **2018**, 132, 3168-3168 2.2
- 37 Myeloma Patient-Derived Bone Marrow Serum Negatively Regulates Natural Killer Cell Activity. *Blood*, **2018**, 132, 4468-4468 2.2
- 36 Mutations and Copy Number Changes Predict Progression from Smoldering Myeloma to Symptomatic Myeloma in the Era of Novel IMWG Criteria. *Blood*, **2018**, 132, 4456-4456 2.2
- 35 Global 3D-Epigenetic Dysregulation of Cyclin D1 and D2 Actively Controls Their Expression Pattern in Multiple Myeloma. *Blood*, **2018**, 132, 3904-3904 2.2
- 34 Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. *Blood*, **2018**, 132, 3185-3185 2.2
- 33 Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. *Blood*, **2018**, 132, 1906-1906 2.2
- 32 Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. *Blood*, **2018**, 132, 4454-4454 2.2
- 31 High Levels of APOBEC3B Gene Expression Contribute to Poor Prognosis in Multiple Myeloma Patients. *Blood*, **2018**, 132, 3897-3897 2.2
- 30 Mutant KRAS and Brafs Upregulate Stress Granules and Mediate Drug Resistance, Which Can be Modulated By Cox2 Inhibition in Multiple Myeloma. *Blood*, **2018**, 132, 3166-3166 2.2
- 29 Characterization of the Immune Impact of Daratumumab By Mass Cytometry in Multiple Myeloma. *Blood*, **2018**, 132, 4466-4466 2.2
- 28 Proliferation and Molecular Risk Score of Low Risk Myeloma Cells Are Increased in High Risk Microenvironment Via Augmented Bioavailability of Growth Factors. *Blood*, **2018**, 132, 1929-1929 2.2
- 27 Aberrant Epigenomic Regulatory Networks in Multiple Myeloma and Strategies for Their Targeted Reversal. *RNA Technologies*, **2019**, 543-572 0.2
- 26 The mTOR Component, Rictor, Is Regulated By the Microenvironment to Control Dormancy and Proliferative States in Myeloma Cells. *Blood*, **2019**, 134, 4412-4412 2.2
- 25 The Role of PHF19 As a Promoter of Tumorigenicity and Therapeutic Target in Multiple Myeloma. *Blood*, **2019**, 134, 508-508 2.2
- 24 Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. *Blood*, **2019**, 134, 4370-4370 2.2
- 23 Molecular Subgroups of Hyperdiploidy and Their Prognostic Relevance - an Analysis of 1,036 Myeloma Trial Patients. *Blood*, **2015**, 126, 2983-2983 2.2
- 22 Specific Identification of High Risk Disease Using Molecular Profiling By Mymap (Myeloma MLPA and translocation PCR) of 1,036 Cases. *Blood*, **2015**, 126, 2981-2981 2.2

21	The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. <i>Blood</i> , <b>2016</b> , 128, 4441-4441	2.2
20	The Metabolic Phenotype of Myeloma Plasma Cells Differs Between Active and Residual Disease States. <i>Blood</i> , <b>2016</b> , 128, 4438-4438	2.2
19	Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. <i>Blood</i> , <b>2016</b> , 128, 3271-3271	2.2
18	The Impact of Constitutional Copy Number Variants in Myeloma. <i>Blood</i> , <b>2008</b> , 112, 496-496	2.2
17	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling Identifies Kinase Pathway Alterations.. <i>Blood</i> , <b>2008</b> , 112, 1694-1694	2.2
16	High Resolution Genomic Profiling Using Single Nucleotide Polymorphism Microarrays Identifies Multiple Novel Genomic Minimally Deleted Regions in Multiple Myeloma. <i>Blood</i> , <b>2008</b> , 112, 625-625	2.2
15	High Resolution Genomic Profiling Using Single Nucleotide Polymorphism Microarrays Reveals Novel Genomic Lesions in Hairy Cell Leukaemia and Hairy-Cell Leukaemia Variant. <i>Blood</i> , <b>2008</b> , 112, 3136 <sup>2,2</sup> -3136	2.2
14	XBPI Expression Is An Important Prognostic Factor for Newly Diagnosed Myeloma Patients.. <i>Blood</i> , <b>2008</b> , 112, 1686-1686	2.2
13	Homozygous Deletions Can Be Used to Define a Cell Death Specific Gene Expression Signature Able to Predict Outcome in Myeloma. <i>Blood</i> , <b>2008</b> , 112, 2725-2725	2.2
12	Genome-Wide Profiling of DNA Copy Number Variation in CLL Cases Lacking 17p- (TP53) or 11q- (ATM) Abnormalities Selected from the CLL4 Study. <i>Blood</i> , <b>2008</b> , 112, 3140-3140	2.2
11	Gene Expression Profiling Classifies Splenic Marginal Zone Lymphoma and Hairy Cell Leukemia-Variant as Related Diseases That Are Distinct From Typical Hairy Cell Leukemia.. <i>Blood</i> , <b>2009</b> , 114, 3467-3467	2.2
10	Global Methylation Array Analysis of Multiple Myeloma Samples Indicate An Alteration of Epigenetics During the Transition From MGUS to Myeloma and An Increased Frequency of Gene Methylation in t(4;14) Myeloma.. <i>Blood</i> , <b>2009</b> , 114, 121-121	2.2
9	Molecular Characterization of Human Multiple Myeloma Cell Lines by Genome-Wide Profiling.. <i>Blood</i> , <b>2009</b> , 114, 1793-1793	2.2
8	UTX, a Histone Demethylase, Is Inactivated through Homozygous Deletion, Mutation, and DNA Methylation in Multiple Myeloma.. <i>Blood</i> , <b>2009</b> , 114, 1798-1798	2.2
7	Expression Profile and up-Regulation of Telomere-Associated Proteins In Multiple Myeloma. <i>Blood</i> , <b>2010</b> , 116, 4050-4050	2.2
6	Whole Genome Sequencing Illuminates the Genetic and Biological Features Underlying the Transition of SMM to MM. <i>Blood</i> , <b>2011</b> , 118, 296-296	2.2
5	A Novel Mouse Model of Multiple Myeloma Representative of Human Disease and Its Use in Preclinical Therapeutic Assessment. <i>Blood</i> , <b>2011</b> , 118, 2907-2907	2.2
4	Exome Sequencing of the t(4;14) and t(11;14) Translocation Specific Subgroups of MM. <i>Blood</i> , <b>2011</b> , 118, 1817-1817	2.2

- 3 Base-Pair Resolution Mapping of IGH Translocations in Multiple Myeloma Using Targeted Capture and Massively Parallel Sequencing. *Blood*, **2012**, 120, 3490-3490 2.2
- 2 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
- 1 What Is Genomic High-Risk Myeloma?. *Hemato*, **2022**, 3, 287-297 0.2