

Michael A Bauer

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

61
papers

1,057
citations

13
h-index

32
g-index

68
ext. papers

1,492
ext. citations

5
avg, IF

3.58
L-index

#	Paper	IF	Citations
61	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , 2018 , 132, 587-597	2.2	196
60	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019 , 33, 159-170	10.7	176
59	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. <i>Nature Communications</i> , 2017 , 8, 268	17.4	170
58	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. <i>Blood</i> , 2016 , 128, 1735-44	2.2	129
57	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. <i>Leukemia</i> , 2019 , 33, 1713-1722	10.7	66
56	The level of deletion 17p and bi-allelic inactivation of has a significant impact on clinical outcome in multiple myeloma. <i>Haematologica</i> , 2017 , 102, e364-e367	6.6	44
55	Bi-allelic inactivation is more prevalent at relapse in multiple myeloma, identifying RB1 as an independent prognostic marker. <i>Blood Cancer Journal</i> , 2017 , 7, e535	7	39
54	Microhomology-mediated end joining drives complex rearrangements and overexpression of and in multiple myeloma. <i>Haematologica</i> , 2020 , 105, 1055-1066	6.6	22
53	Usability survey of biomedical question answering systems. <i>Human Genomics</i> , 2012 , 6, 17	6.8	20
52	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. <i>Nature Communications</i> , 2021 , 12, 293	17.4	20
51	and Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , 2020 , 26, 2422-2432	12.9	17
50	Phenotypic plasticity in temperature stress resistance is triggered by photoperiod in a fly. <i>Evolutionary Ecology</i> , 2012 , 26, 1067-1083	1.8	16
49	Kinase domain activation through gene rearrangement in multiple myeloma. <i>Leukemia</i> , 2018 , 32, 2435-2444	10.7	15
48	Towards the integration, annotation and association of historical microarray experiments with RNA-seq. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 14, S4	3.6	12
47	Knowledge building insights on biomarkers of arsenic toxicity to keratinocytes and melanocytes. <i>Biomarker Insights</i> , 2012 , 7, 127-41	3.5	11
46	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> , 2020 , 17, e1003323	11.6	10
45	The genomic landscape of plasma cells in systemic light chain amyloidosis. <i>Blood</i> , 2018 , 132, 2775-2777	2.2	10

44	The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. <i>Journal of Hematology and Oncology</i> , 2020 , 13, 108	22.4	8
43	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. <i>Haematologica</i> , 2021 , 106, 736-745	6.6	7
42	Late Effects of H + O on Short-Term and Object Memory, Hippocampal Dendritic Morphology and Mutagenesis. <i>Frontiers in Behavioral Neuroscience</i> , 2020 , 14, 96	3.5	6
41	XLPM: efficient algorithm for the analysis of protein-protein contacts using chemical cross-linking mass spectrometry. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 11, S16	3.6	5
40	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of. <i>Oncotarget</i> , 2019 , 10, 732-737	3.3	5
39	NATbox: a network analysis toolbox in R. <i>BMC Bioinformatics</i> , 2009 , 10 Suppl 11, S14	3.6	4
38	High Risk Multiple Myeloma Demonstrates Marked Spatial Genomic Heterogeneity Between Focal Lesions and Random Bone Marrow; Implications for Targeted Therapy and Treatment Resistance. <i>Blood</i> , 2015 , 126, 20-20	2.2	4
37	Low-Level Environmental Heavy Metals are Associated with Obesity Among Postmenopausal Women in a Southern State. <i>Exposure and Health</i> , 2021 , 13, 269-280	8.8	4
36	Revealing the inherent heterogeneity of human malignancies by variant consensus strategies coupled with cancer clonal analysis. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 11, S9	3.6	3
35	Enhancing cancer clonality analysis with integrative genomics. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 13, S7	3.6	3
34	Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregulate Gene Function By a Range of Mechanisms. <i>Blood</i> , 2019 , 134, 3767-3767	2.2	3
33	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , 2021 ,	10.7	3
32	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> , 2021 ,	10.7	3
31	Integrating External Resources with a Task-Based Programming Model 2017 ,		2
30	Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. <i>Blood</i> , 2018 , 132, 1882-1882	2.2	2
29	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 408-408	2.2	2
28	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> , 2019 , 134, 4333-4333 ²	2.2	2
27	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> , 2019 , 134, 4346-4346	2.2	2

26	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. <i>Blood</i> , 2016 , 128, 3278-3278	2.2	2
25	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> , 2017 , 130, 65-65	2.2	2
24	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> , 2021 , 195, 283-286	4.5	2
23	WikiHyperGlossary (WHG): an information literacy technology for chemistry documents. <i>Journal of Cheminformatics</i> , 2015 , 7, 22	8.6	1
22	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , 2020 , 136, 8-9	2.2	1
21	Comprehensive Genomic Profiling of Multiple Myeloma in the Course of Clinical Care Identifies Targetable and Prognostically Significant Genomic Alterations. <i>Blood</i> , 2015 , 126, 369-369	2.2	1
20	The Impact of Combination Chemotherapy and Tandem Stem Cell Transplant on Clonal Substructure and Mutational Pattern at Relapse of MM. <i>Blood</i> , 2015 , 126, 372-372	2.2	1
19	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> , 2021 , 40, 380	12.8	1
18	Expression Signature of Myeloma Residual Cells Is Characterized By Genes Associated with Proliferation, Epigenetic Modification, and Stem Cell Maintenance. <i>Blood</i> , 2018 , 132, 4465-4465	2.2	1
17	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. <i>Blood</i> , 2016 , 128, 196-196	2.2	1
16	Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , 2021 ,	7.5	1
15	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. <i>BMC Bioinformatics</i> , 2020 , 21, 144	3.6	1
14	FiNGS: high quality somatic mutations using filters for next generation sequencing. <i>BMC Bioinformatics</i> , 2021 , 22, 77	3.6	1
13	Leveraging the new with the old: providing a framework for the integration of historic microarray studies with next generation sequencing. <i>BMC Bioinformatics</i> , 2014 , 15 Suppl 11, S3	3.6	0
12	Hispanic or Latin American Ancestry Is Associated with a Similar Genomic Profile and a Trend Toward Inferior Outcomes in Newly Diagnosed Multiple Myeloma As Compared to Non-Hispanic White Patients in the Multiple Myeloma Research Foundation (MMRF) CoMMpasstudy. <i>Blood</i> , 2021 , 138, 4117-4117	2.2	0
11	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , 2016 , 128, 4416-4416	2.2	0
10	ISDB: Interaction Sentence Database. <i>BMC Research Notes</i> , 2010 , 3, 122	2.3	
9	OrthoCARs: Engineered human IL-2/IL-2Rb orthogonal pairs selectively enhance CAR T cell antitumorefficacy. <i>Blood</i> , 2020 , 136, 35-35	2.2	

- 8 Multiomic Mapping of Copy Number and Structural Variation on Chromosome 1 (Chr1) Highlights Multiple Recurrent Disease Drivers. *Blood*, **2021**, 138, 721-721 2.2
- 7 Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. *Blood*, **2018**, 132, 4457-4457 2.2
- 6 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
- 5 Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. *Blood*, **2018**, 132, 3185-3185 2.2
- 4 Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. *Blood*, **2018**, 132, 1906-1906 2.2
- 3 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
- 2 Example of a Scalable and Adaptable Approach for NGS Analyses Leveraging High-Performance Computing **2019**, 247-269
- 1 Leveraging The Old With The New: Exploring and Integrating Historic Microarray Studies With Next Generation Sequencing For Multiple Myeloma. *Blood*, **2013**, 122, 3122-3122 2.2