Michael A Bauer

List of Publications by Year
in descending order

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66	1,819	516561 16	276775 41
papers	citations	h-index	g-index

68	68	68	2447
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. Blood, 2018, 132, 587-597.	0.6	335
2	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. Leukemia, 2019, 33, 159-170.	3.3	313
3	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. Nature Communications, 2017, 8, 268.	5.8	277
4	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. Blood, 2016, 128, 1735-1744.	0.6	170
5	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. Leukemia, 2019, 33, 1713-1722.	3.3	112
6	The level of deletion 17p and bi-allelic inactivation of TP53 has a significant impact on clinical outcome in multiple myeloma. Haematologica, 2017, 102, e364-e367.	1.7	57
7	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. Nature Communications, 2021, 12, 293.	5.8	54
8	Bi-allelic inactivation is more prevalent at relapse in multiple myeloma, identifying RB1 as an independent prognostic marker. Blood Cancer Journal, 2017, 7, e535-e535.	2.8	48
9	Microhomology-mediated end joining drives complex rearrangements and overexpression of MYC and PVT1 in multiple myeloma. Haematologica, 2020, 105, 1055-1066.	1.7	42
10	BRAF and DIS3 Mutations Associate with Adverse Outcome in a Long-term Follow-up of Patients with Multiple Myeloma. Clinical Cancer Research, 2020, 26, 2422-2432.	3.2	37
11	Bone marrow microenvironments that contribute to patient outcomes in newly diagnosed multiple myeloma: A cohort study of patients in the Total Therapy clinical trials. PLoS Medicine, 2020, 17, e1003323.	3.9	33
12	Usability survey of biomedical question answering systems. Human Genomics, 2012, 6, 17.	1.4	28
13	Kinase domain activation through gene rearrangement in multiple myeloma. Leukemia, 2018, 32, 2435-2444.	3.3	26
14	Chromothripsis as a pathogenic driver of multiple myeloma. Seminars in Cell and Developmental Biology, 2022, 123, 115-123.	2.3	22
15	Phenotypic plasticity in temperature stress resistance is triggered by photoperiod in a fly. Evolutionary Ecology, 2012, 26, 1067-1083.	0.5	20
16	The functional epigenetic landscape of aberrant gene expression in molecular subgroups of newly diagnosed multiple myeloma. Journal of Hematology and Oncology, 2020, 13, 108.	6.9	20
17	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. Haematologica, 2021, 106, 736-745.	1.7	20
18	Knowledge Building Insights on Biomarkers of Arsenic Toxicity to Keratinocytes and Melanocytes. Biomarker Insights, 2012, 7, BMI.S7799.	1.0	16

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19	Late Effects of 1H + 16O on Short-Term and Object Memory, Hippocampal Dendritic Morphology and Mutagenesis. Frontiers in Behavioral Neuroscience, 2020, 14, 96.	1.0	15
20	Towards the integration, annotation and association of historical microarray experiments with RNA-seq. BMC Bioinformatics, 2013, 14, S4.	1.2	14
21	Low-Level Environmental Heavy Metals are Associated with Obesity Among Postmenopausal Women in a Southern State. Exposure and Health, 2021, 13, 269-280.	2.8	14
22	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of TP53. Oncotarget, 2019, 10, 732-737.	0.8	13
23	The genomic landscape of plasma cells in systemic light chain amyloidosis. Blood, 2018, 132, 2775-2777.	0.6	12
24	NATbox: a network analysis toolbox in R. BMC Bioinformatics, 2009, 10, S14.	1.2	9
25	XLPM: efficient algorithm for the analysis of protein-protein contacts using chemical cross-linking mass spectrometry. BMC Bioinformatics, 2014, 15, S16.	1.2	8
26	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. Leukemia, 2021, , .	3.3	8
27	FiNGS: high quality somatic mutations using filters for next generation sequencing. BMC Bioinformatics, 2021, 22, 77.	1.2	7
28	High Risk Multiple Myeloma Demonstrates Marked Spatial Genomic Heterogeneity Between Focal Lesions and Random Bone Marrow; Implications for Targeted Therapy and Treatment Resistance. Blood, 2015, 126, 20-20.	0.6	7
29	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. Blood Cancer Journal, 2022, 12, .	2.8	7
30	Enhancing cancer clonality analysis with integrative genomics. BMC Bioinformatics, 2015, 16, S7.	1.2	6
31	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. Leukemia, 2022, 36, 591-595.	3.3	6
32	Revealing the inherent heterogeneity of human malignancies by variant consensus strategies coupled with cancer clonal analysis. BMC Bioinformatics, 2014, 15, S9.	1.2	5
33	Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregulate Gene Function By a Range of Mechanisms. Blood, 2019, 134, 3767-3767.	0.6	5
34	Highâ€risk transcriptional profiles in multiple myeloma are an acquired feature that can occur in any subtype and more frequently with each subsequent relapse. British Journal of Haematology, 2021, 195, 283-286.	1.2	4
35	Leveraging The Old With The New: Exploring and Integrating Historic Microarray Studies With Next Generation Sequencing For Multiple Myeloma. Blood, 2013, 122, 3122-3122.	0.6	4
36	Insights into high-risk multiple myeloma from an analysis of the role of PHF19 in cancer. Journal of Experimental and Clinical Cancer Research, 2021, 40, 380.	3.5	4

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37	Genome-Wide DNA Methylation Signatures Predict the Early Asymptomatic Doxorubicin-Induced Cardiotoxicity in Breast Cancer. Cancers, 2021, 13, 6291.	1.7	4
38	WikiHyperGlossary (WHG): an information literacy technology for chemistry documents. Journal of Cheminformatics, 2015, 7, 22.	2.8	3
39	Integrating External Resources with a Task-Based Programming Model. , 2017, , .		3
40	Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. Blood, 2018, 132, 1882-1882.	0.6	3
41	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. Blood, 2018, 132, 408-408.	0.6	3
42	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. Blood, 2017, 130, 65-65.	0.6	3
43	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. BMC Bioinformatics, 2020, 21, 144.	1.2	2
44	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. Blood, 2019, 134, 4333-4333.	0.6	2
45	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. Blood, 2019, 134, 4346-4346.	0.6	2
46	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278.	0.6	2
47	The Multiple Myeloma Genome Project: Development of a Molecular Segmentation Strategy for the Clinical Classification of Multiple Myeloma. Blood, 2016, 128, 196-196.	0.6	2
48	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) CoMMpassstudy. Blood, 2021, 138, 4117-4117.	0.6	2
49	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. Blood, 2020, 136, 8-9.	0.6	2
50	Leveraging the new with the old: providing a framework for the integration of historic microarray studies with next generation sequencing. BMC Bioinformatics, 2014, 15, S3.	1.2	1
51	A detailed exploration of using RNA-Seq data in established multiple myeloma gene expression profile microarray based risk scores. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e57-e58.	0.2	1
52	Comprehensive Genomic Profiling of Multiple Myeloma in the Course of Clinical Care Identifies Targetable and Prognostically Significant Genomic Alterations. Blood, 2015, 126, 369-369.	0.6	1
53	The Impact of Combination Chemotherapy and Tandem Stem Cell Transplant on Clonal Substructure and Mutational Pattern at Relapse of MM. Blood, 2015, 126, 372-372.	0.6	1
54	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. Blood, 2016, 128, 4416-4416.	0.6	1

#	Article	IF	Citations
55	Abstract 5324: Intragenic DNA-hypomethylation promotes overexpression ofITGB7in MF subgroup of multiple myeloma. , 2018, , .		1
56	Expression Signature of Myeloma Residual Cells Is Characterized By Genes Associated with Proliferation, Epigenetic Modification, and Stem Cell Maintenance. Blood, 2018, 132, 4465-4465.	0.6	1
57	Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. Blood, 2018, 132, 1906-1906.	0.6	1
58	ISDB: Interaction Sentence Database. BMC Research Notes, 2010, 3, 122.	0.6	0
59	Long-term Analysis Of Multiple Sequential Samples Reveals Patterns Of Progression In Smoldering Myeloma. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e59-e60.	0.2	0
60	Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. Blood, 2018, 132, 4457-4457.	0.6	0
61	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.	0.6	0
62	Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. Blood, 2018, 132, 3185-3185.	0.6	0
63	Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. Blood, 2018, 132, 4454-4454.	0.6	0
64	Example of a Scalable and Adaptable Approach for NGS Analyses Leveraging High-Performance Computing. , 2019, , 247-269.		0
65	Multiomic Mapping of Copy Number and Structural Variation on Chromosome 1 (Chr1) Highlights Multiple Recurrent Disease Drivers. Blood, 2021, 138, 721-721.	0.6	0
66	OrthoCARs: Engineered human IL-2/IL-2Rb orthogonal pairs selectively enhance CAR T cell antitumorefficacy. Blood, 2020, 136, 35-35.	0.6	0