

Cody Ashby

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

1,111
citations

15
h-index

33
g-index

73
ext. papers

1,555
ext. citations

5.8
avg. IF

3.75
L-index

#	Paper	IF	Citations
61	Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. <i>Genome Biology</i> , 2015 , 16, 30	18.3	190
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	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> , 2019 , 104, 1440-1450	6.6	39
53	Loss of heterozygosity as a marker of homologous repair deficiency in multiple myeloma: a role for PARP inhibition?. <i>Leukemia</i> , 2018 , 32, 1561-1566	10.7	29
52	Revealing the impact of structural variants in multiple myeloma. <i>Blood Cancer Discovery</i> , 2020 , 1, 258-273		28
51	Microhomology-mediated end joining drives complex rearrangements and overexpression of and in multiple myeloma. <i>Haematologica</i> , 2020 , 105, 1055-1066	6.6	22
50	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
49	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
48	Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. <i>Blood Cancer Journal</i> , 2020 , 10, 70	7	16
47	Accelerated single cell seeding in relapsed multiple myeloma. <i>Nature Communications</i> , 2020 , 11, 3617	17.4	16
46	DNAP: A Pipeline for DNA-seq Data Analysis. <i>Scientific Reports</i> , 2018 , 8, 6793	4.9	11
45	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

44	The genomic landscape of plasma cells in systemic light chain amyloidosis. <i>Blood</i> , 2018 , 132, 2775-2777	2.2	10
43	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
42	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. <i>Haematologica</i> , 2021 , 106, 736-745	6.6	7
41	eMBI: Boosting Gene Expression-based Clustering for Cancer Subtypes. <i>Cancer Informatics</i> , 2014 , 13, 105-12	2.4	5
40	SPARCoC: a new framework for molecular pattern discovery and cancer gene identification. <i>PLoS ONE</i> , 2015 , 10, e0117135	3.7	5
39	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
38	Monitoring treatment response and disease progression in myeloma with circulating cell-free DNA. <i>European Journal of Haematology</i> , 2021 , 106, 230-240	3.8	5
37	New enumeration algorithm for protein structure comparison and classification. <i>BMC Genomics</i> , 2013 , 14 Suppl 2, S1	4.5	4
36	Enhancing cancer clonality analysis with integrative genomics. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 13, S7	3.6	3
35	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
34	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
33	Mutations in CRBN and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. <i>Leukemia</i> , 2021 , 35, 3017-3020	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	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
30	The Mutational Landscape of Primary Plasma Cell Leukemia. <i>Blood</i> , 2018 , 132, 114-114	2.2	2
29	A High-Risk Multiple Myeloma Group Identified By Integrative Multi-Omics Segmentation of Newly Diagnosed Patients. <i>Blood</i> , 2018 , 132, 3165-3165	2.2	2
28	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
27	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

26	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
25	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
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	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , 2020 , 136, 8-9	2.2	1
22	Long-Term Follow-up Identifies Double Hit and Key Mutations As Impacting Progression Free and Overall Survival in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 110-110	2.2	1
21	Revealing the impact of recurrent and rare structural variants in multiple myeloma		1
20	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
19	Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , 2021 ,	7.5	1
18	TRIP13 modulates protein deubiquitination and accelerates tumor development and progression of B cell malignancies. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	1
17	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. <i>BMC Bioinformatics</i> , 2020 , 21, 144	3.6	1
16	FiNGS: high quality somatic mutations using filters for next generation sequencing. <i>BMC Bioinformatics</i> , 2021 , 22, 77	3.6	1
15	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , 2016 , 128, 4416-4416	2.2	0
14	Notch3 signaling between myeloma cells and osteocytes in the tumor niche promotes tumor growth and bone destruction.. <i>Neoplasia</i> , 2022 , 28, 100785	6.4	0
13	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> , 2020 , 136, 6-7	2.2	
12	Global Expression Changes of Malignant Plasma Cells over Time Reveals the Evolutionary Development of Signatures of Aggressive Clinical Behavior. <i>Blood</i> , 2018 , 132, 4457-4457	2.2	
11	Poor Overall Survival in Hyperhaploid Multiple Myeloma Is Defined By Double-Hit Bi-Allelic Inactivation of TP53. <i>Blood</i> , 2018 , 132, 4441-4441	2.2	
10	Mutations and Copy Number Changes Predict Progression from Smoldering Myeloma to Symptomatic Myeloma in the Era of Novel IMWG Criteria. <i>Blood</i> , 2018 , 132, 4456-4456	2.2	
9	Global 3D-Epigenetic Dysregulation of Cyclin D1 and D2 Actively Controls Their Expression Pattern in Multiple Myeloma. <i>Blood</i> , 2018 , 132, 3904-3904	2.2	

- 8 Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. *Blood*, **2018**, 132, 3185-3185 2.2
- 7 Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. *Blood*, **2018**, 132, 1906-1906 2.2
- 6 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
- 5 High Levels of APOBEC3B Gene Expression Contribute to Poor Prognosis in Multiple Myeloma Patients. *Blood*, **2018**, 132, 3897-3897 2.2
- 4 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
- 3 Example of a Scalable and Adaptable Approach for NGS Analyses Leveraging High-Performance Computing **2019**, 247-269
- 2 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
- 1 Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. *Blood*, **2016**, 128, 3271-3271 2.2