

Cody Ashby

List of Publications by Year in descending order

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Version: 2024-02-01

67
papers

1,919
citations

430442

18
h-index

264894

42
g-index

73
all docs

73
docs citations

73
times ranked

2757
citing authors

#	ARTICLE	IF	CITATIONS
1	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019, 33, 159-170.	3.3	313
2	Spatial genomic heterogeneity in multiple myeloma revealed by multi-region sequencing. <i>Nature Communications</i> , 2017, 8, 268.	5.8	277
3	Bridger: a new framework for de novo transcriptome assembly using RNA-seq data. <i>Genome Biology</i> , 2015, 16, 30.	3.8	258
4	Clonal selection and double-hit events involving tumor suppressor genes underlie relapse in myeloma. <i>Blood</i> , 2016, 128, 1735-1744.	0.6	170
5	Combination of flow cytometry and functional imaging for monitoring of residual disease in myeloma. <i>Leukemia</i> , 2019, 33, 1713-1722.	3.3	112
6	Revealing the Impact of Structural Variants in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020, 1, 258-273.	2.6	81
7	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.	1.7	67
8	The level of deletion 17p and bi-allelic inactivation of <i>TP53</i> has a significant impact on clinical outcome in multiple myeloma. <i>Haematologica</i> , 2017, 102, e364-e367.	1.7	57
9	The molecular make up of smoldering myeloma highlights the evolutionary pathways leading to multiple myeloma. <i>Nature Communications</i> , 2021, 12, 293.	5.8	54
10	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-e535.	2.8	48
11	Microhomology-mediated end joining drives complex rearrangements and overexpression of <i>MYC</i> and <i>PVT1</i> in multiple myeloma. <i>Haematologica</i> , 2020, 105, 1055-1066.	1.7	42
12	Accelerated single cell seeding in relapsed multiple myeloma. <i>Nature Communications</i> , 2020, 11, 3617.	5.8	41
13	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.	3.3	39
14	<i>BRAF</i> and <i>DIS3</i> 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.	3.2	37
15	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.	3.9	33
16	Genomic analysis of primary plasma cell leukemia reveals complex structural alterations and high-risk mutational patterns. <i>Blood Cancer Journal</i> , 2020, 10, 70.	2.8	27
17	Chromothripsis as a pathogenic driver of multiple myeloma. <i>Seminars in Cell and Developmental Biology</i> , 2022, 123, 115-123.	2.3	22
18	Monitoring treatment response and disease progression in myeloma with circulating cell-free DNA. <i>European Journal of Haematology</i> , 2021, 106, 230-240.	1.1	21

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19	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.	6.9	20
20	Differential RNA splicing as a potentially important driver mechanism in multiple myeloma. <i>Haematologica</i> , 2021, 106, 736-745.	1.7	20
21	DNAP: A Pipeline for DNA-seq Data Analysis. <i>Scientific Reports</i> , 2018, 8, 6793.	1.6	14
22	Poor overall survival in hyperhaploid multiple myeloma is defined by double-hit bi-allelic inactivation of <i>TP53</i> . <i>Oncotarget</i> , 2019, 10, 732-737.	0.8	13
23	The genomic landscape of plasma cells in systemic light chain amyloidosis. <i>Blood</i> , 2018, 132, 2775-2777.	0.6	12
24	Mutations in <i>CRBN</i> and other cereblon pathway genes are infrequently associated with acquired resistance to immunomodulatory drugs. <i>Leukemia</i> , 2021, 35, 3017-3020.	3.3	11
25	TRIP13 modulates protein deubiquitination and accelerates tumor development and progression of B cell malignancies. <i>Journal of Clinical Investigation</i> , 2021, 131, .	3.9	10
26	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , 2021, .	3.3	8
27	Epigenomic translocation of H3K4me3 broad domains over oncogenes following hijacking of super-enhancers. <i>Genome Research</i> , 2022, 32, 1343-1354.	2.4	8
28	eMBI: Boosting Gene Expression-based Clustering for Cancer Subtypes. <i>Cancer Informatics</i> , 2014, 13s2, CIN.S13777.	0.9	7
29	FiNGS: high quality somatic mutations using filters for next generation sequencing. <i>BMC Bioinformatics</i> , 2021, 22, 77.	1.2	7
30	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. <i>Blood Cancer Journal</i> , 2022, 12, .	2.8	7
31	New enumeration algorithm for protein structure comparison and classification. <i>BMC Genomics</i> , 2013, 14, S1.	1.2	6
32	Enhancing cancer clonality analysis with integrative genomics. <i>BMC Bioinformatics</i> , 2015, 16, S7.	1.2	6
33	SPARCoC: A New Framework for Molecular Pattern Discovery and Cancer Gene Identification. <i>PLoS ONE</i> , 2015, 10, e0117135.	1.1	6
34	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> , 2022, 36, 591-595.	3.3	6
35	Molecular characterization and clinical outcome of B-cell precursor acute lymphoblastic leukemia with <i>IG-MYC</i> rearrangement. <i>Haematologica</i> , 2023, 108, 717-731.	1.7	6
36	Myeloma Genome Project Panel is a Comprehensive Targeted Genomics Panel for Molecular Profiling of Patients with Multiple Myeloma. <i>Clinical Cancer Research</i> , 2022, 28, 2854-2864.	3.2	6

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37	Chromoplexy and Chromothripsis Are Important Prognostically in Myeloma and Deregate Gene Function By a Range of Mechanisms. <i>Blood</i> , 2019, 134, 3767-3767.	0.6	5
38	Notch3 signaling between myeloma cells and osteocytes in the tumor niche promotes tumor growth and bone destruction. <i>Neoplasia</i> , 2022, 28, 100785.	2.3	5
39	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.	1.2	4
40	Baseline and on-Treatment Bone Marrow Microenvironments Predict Myeloma Patient Outcomes and Inform Potential Intervention Strategies. <i>Blood</i> , 2018, 132, 1882-1882.	0.6	3
41	Chromothripsis and Chromoplexy Are Associated with DNA Instability and Adverse Clinical Outcome in Multiple Myeloma. <i>Blood</i> , 2018, 132, 408-408.	0.6	3
42	TarPan: an easily adaptable targeted sequencing panel viewer for research and clinical use. <i>BMC Bioinformatics</i> , 2020, 21, 144.	1.2	2
43	The Mutational Landscape of Primary Plasma Cell Leukemia. <i>Blood</i> , 2018, 132, 114-114.	0.6	2
44	A High-Risk Multiple Myeloma Group Identified By Integrative Multi-Omics Segmentation of Newly Diagnosed Patients. <i>Blood</i> , 2018, 132, 3165-3165.	0.6	2
45	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.	0.6	2
46	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.	0.6	2
47	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. <i>Blood</i> , 2016, 128, 3278-3278.	0.6	2
48	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.	0.6	2
49	Multiple Myeloma with a Deletion of Chromosome 17p: TP53 Mutations Are Highly Prevalent and Negatively Affect Prognosis. <i>Blood</i> , 2016, 128, 3271-3271.	0.6	2
50	Influence of Aging Processes on the Biology and Outcome of Multiple Myeloma. <i>Blood</i> , 2020, 136, 8-9.	0.6	2
51	A detailed exploration of using RNA-Seq data in established multiple myeloma gene expression profile microarray based risk scores. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e57-e58.	0.2	1
52	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.	0.6	1
53	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. <i>Blood</i> , 2016, 128, 4416-4416.	0.6	1
54	Extracting Prognostic Molecular Information from PET-CT Imaging of Multiple Myeloma Using Radiomic Approaches. <i>Blood</i> , 2018, 132, 1906-1906.	0.6	1

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55	Epigenetic Deregulation of Telomere-Related Genes in Newly Diagnosed Multiple Myeloma Patients. <i>Cancers</i> , 2021, 13, 6348.	1.7	1
56	Long-term Analysis Of Multiple Sequential Samples Reveals Patterns Of Progression In Smoldering Myeloma. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e59-e60.	0.2	0
57	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.	0.6	0
58	Poor Overall Survival in Hyperhaploid Multiple Myeloma Is Defined By Double-Hit Bi-Allelic Inactivation of TP53. <i>Blood</i> , 2018, 132, 4441-4441.	0.6	0
59	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.	0.6	0
60	Global 3D-Epigenetic Dysregulation of Cyclin D1 and D2 Actively Controls Their Expression Pattern in Multiple Myeloma. <i>Blood</i> , 2018, 132, 3904-3904.	0.6	0
61	Combination of Flow Cytometry and Functional Imaging for Monitoring of Residual Disease in Myeloma. <i>Blood</i> , 2018, 132, 3185-3185.	0.6	0
62	Hotspot Mutations in SF3B1 Result in Increased Alternative Splicing in Multiple Myeloma and Activation of Key Cellular Pathways. <i>Blood</i> , 2018, 132, 4454-4454.	0.6	0
63	High Levels of APOBEC3B Gene Expression Contribute to Poor Prognosis in Multiple Myeloma Patients. <i>Blood</i> , 2018, 132, 3897-3897.	0.6	0
64	Proliferation and Molecular Risk Score of Low Risk Myeloma Cells Are Increased in High Risk Microenvironment Via Augmented Bioavailability of Growth Factors. <i>Blood</i> , 2018, 132, 1929-1929.	0.6	0
65	Example of a Scalable and Adaptable Approach for NGS Analyses Leveraging High-Performance Computing. , 2019, , 247-269.		0
66	The mTOR Component, Rictor, Is Regulated By the Microenvironment to Control Dormancy and Proliferative States in Myeloma Cells. <i>Blood</i> , 2019, 134, 4412-4412.	0.6	0
67	Mutations in <i>CRBN</i> 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.	0.6	0