

Jonathan J Keats

List of Publications by Year in descending order

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Version: 2024-02-01

72
papers

8,925
citations

109321

35
h-index

114465

63
g-index

81
all docs

81
docs citations

81
times ranked

11241
citing authors

#	ARTICLE	IF	CITATIONS
1	Unbiased cell surface proteomics identifies SEMA4A as an effective immunotherapy target for myeloma. <i>Blood</i> , 2022, 139, 2471-2482.	1.4	12
2	Structural variants shape the genomic landscape and clinical outcome of multiple myeloma. <i>Blood Cancer Journal</i> , 2022, 12, .	6.2	7
3	Perspectives on the Risk-Stratified Treatment of Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2022, 3, 273-284.	5.0	24
4	Daratumumab induces mechanisms of immune activation through CD38+ NK cell targeting. <i>Leukemia</i> , 2021, 35, 189-200.	7.2	56
5	The mevalonate pathway is an actionable vulnerability of t(4;14)-positive multiple myeloma. <i>Leukemia</i> , 2021, 35, 796-808.	7.2	19
6	Chromatin Accessibility Identifies Regulatory Elements Predictive of Gene Expression and Disease Outcome in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2021, 27, 3178-3189.	7.0	15
7	Venetoclax sensitivity in multiple myeloma is associated with B-cell gene expression. <i>Blood</i> , 2021, 137, 3604-3615.	1.4	44
8	Improving prognostic assignment in older adults with multiple myeloma using acquired genetic features, clonal hemopoiesis and telomere length. <i>Leukemia</i> , 2021, . .	7.2	8
9	Establishing community reference samples, data and call sets for benchmarking cancer mutation detection using whole-genome sequencing. <i>Nature Biotechnology</i> , 2021, 39, 1151-1160.	17.5	39
10	Plasma cell leukemia: A review of the molecular classification, diagnosis, and evidenced-based treatment. <i>Leukemia Research</i> , 2021, 111, 106687.	0.8	18
11	CD84 is a regulator of the immunosuppressive microenvironment in Multiple Myeloma. <i>JCI Insight</i> , 2021, 6, .	5.0	15
12	Genomic and Transcriptomic Analysis of Relapsed and Refractory Childhood Solid Tumors Reveals a Diverse Molecular Landscape and Mechanisms of Immune Evasion. <i>Cancer Research</i> , 2021, 81, 5818-5832.	0.9	10
13	Patient similarity network of newly diagnosed multiple myeloma identifies patient subgroups with distinct genetic features and clinical implications. <i>Science Advances</i> , 2021, 7, eabg9551.	10.3	49
14	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.	3.5	42
15	Transcriptional profiling of circulating tumor cells in multiple myeloma: a new model to understand disease dissemination. <i>Leukemia</i> , 2020, 34, 589-603.	7.2	41
16	MYC dysregulation in the progression of multiple myeloma. <i>Leukemia</i> , 2020, 34, 322-326.	7.2	108
17	Glucocorticoid receptor expression in multiple myeloma patients is a predictor of survival. <i>Leukemia and Lymphoma</i> , 2020, 61, 3493-3497.	1.3	4
18	Revealing the Impact of Structural Variants in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2020, 1, 258-273.	5.0	81

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19	Clonal hematopoiesis is associated with adverse outcomes in multiple myeloma patients undergoing transplant. <i>Nature Communications</i> , 2020, 11, 2996.	12.8	98
20	The CCND1 c.870G risk allele is enriched in individuals of African ancestry with plasma cell dyscrasias. <i>Blood Cancer Journal</i> , 2020, 10, 39.	6.2	4
21	c-MYC expression and maturity phenotypes are associated with outcome benefit from addition of ixazomib to lenalidomide+dexamethasone in myeloma. <i>European Journal of Haematology</i> , 2020, 105, 35-46.	2.2	8
22	Early Relapse Risk in Patients with Newly Diagnosed Multiple Myeloma Characterized by Next-generation Sequencing. <i>Clinical Cancer Research</i> , 2020, 26, 4832-4841.	7.0	33
23	MAGE-A inhibit apoptosis and promote proliferation in multiple myeloma through regulation of BIM and p21Cip1. <i>Oncotarget</i> , 2020, 11, 727-739.	1.8	12
24	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019, 33, 159-170.	7.2	313
25	Stability and uniqueness of clonal immunoglobulin CDR3 sequences for MRD tracking in multiple myeloma. <i>American Journal of Hematology</i> , 2019, 94, 1364-1373.	4.1	22
26	Multiple myeloma immunoglobulin lambda translocations portend poor prognosis. <i>Nature Communications</i> , 2019, 10, 1911.	12.8	109
27	Great Lakes Biorepository Research Network's Annual Biobanking Symposium: A Focus on Precision Medicine. <i>Biopreservation and Biobanking</i> , 2019, 17, 598-602.	1.0	0
28	MiR-16 regulates crosstalk in NF- κ B tolerogenic inflammatory signaling between myeloma cells and bone marrow macrophages. <i>JCI Insight</i> , 2019, 4, .	5.0	33
29	Copper 64 α -labeled daratumumab as a PET/CT imaging tracer for multiple myeloma. <i>Blood</i> , 2018, 131, 741-745.	1.4	54
30	Single cell dissection of plasma cell heterogeneity in symptomatic and asymptomatic myeloma. <i>Nature Medicine</i> , 2018, 24, 1867-1876.	30.7	179
31	Daratumumab induces CD38 internalization and impairs myeloma cell adhesion. <i>Oncolmunology</i> , 2018, 7, e1486948.	4.6	41
32	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , 2018, 132, 587-597.	1.4	335
33	RNA Polymerase I Inhibition with CX α 5461 as a Novel Therapeutic Strategy to Target <i>MYC</i> in Multiple Myeloma. <i>British Journal of Haematology</i> , 2017, 177, 80-94.	2.5	51
34	UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. <i>Cell Reports</i> , 2017, 21, 628-640.	6.4	106
35	Comprehensive molecular profiling of 718 Multiple Myelomas reveals significant differences in mutation frequencies between African and European descent cases. <i>PLoS Genetics</i> , 2017, 13, e1007087.	3.5	66
36	A Comparison of Clinical FISH and Sequencing Based FISH Estimates in Multiple Myeloma: An Mmrf Compass Analysis. <i>Blood</i> , 2016, 128, 374-374.	1.4	14

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37	Promiscuous MYC locus rearrangements hijack enhancers but mostly super-enhancers to dysregulate MYC expression in multiple myeloma. <i>Leukemia</i> , 2014, 28, 1725-1735.	7.2	221
38	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	16.8	847
39	Abstract 898: Expression of immunoglobulin and its receptor are major determinants of multiple myeloma patient sensitivity to proteasome inhibitors. , 2014, , .		1
40	Abstract 2375: A method to identify copy number aberrations (CNAs) from whole exome sequence (WES) data and its application to multiple myeloma cell lines and patient samples. , 2014, , .		0
41	Xbp1s-Negative Tumor B Cells and Pre-Plasmablasts Mediate Therapeutic Proteasome Inhibitor Resistance in Multiple Myeloma. <i>Cancer Cell</i> , 2013, 24, 289-304.	16.8	298
42	Interim Analysis Of The Mmrf Commpass Trial, a Longitudinal Study In Multiple Myeloma Relating Clinical Outcomes To Genomic and Immunophenotypic Profiles. <i>Blood</i> , 2013, 122, 532-532.	1.4	34
43	Abstract 5209: Characterization of an isogenic model system for KDM6A/UTX loss in multiple myeloma.. <i>Cancer Research</i> , 2013, 73, 5209-5209.	0.9	1
44	Abstract 806: RNA sequencing based prognostic indexes show a high degree of correlation with historic array based gene expression measurements in multiple myeloma.. , 2013, , .		0
45	Genomic analysis of marginal zone and lymphoplasmacytic lymphomas identified common and disease-specific abnormalities. <i>Modern Pathology</i> , 2012, 25, 651-660.	5.5	66
46	Whole-genome sequencing of multiple myeloma from diagnosis to plasma cell leukemia reveals genomic initiating events, evolution, and clonal tides. <i>Blood</i> , 2012, 120, 1060-1066.	1.4	357
47	Clonal competition with alternating dominance in multiple myeloma. <i>Blood</i> , 2012, 120, 1067-1076.	1.4	575
48	Abstract 4561: The MMRF CoMMpassSM Study: A prospective, longitudinal, multicenter observational study in newly diagnosed multiple myeloma patients to assess the relationship between patient outcomes, treatment regimens and molecular profiles. , 2012, , .		0
49	RNAi screen of the druggable genome identifies modulators of proteasome inhibitor sensitivity in myeloma including CDK5. <i>Blood</i> , 2011, 117, 3847-3857.	1.4	97
50	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.	27.8	1,288
51	Abstract 4838: Longitudinal assessment of high risk t(4;14) multiple myeloma using next generation whole genome sequencing. , 2011, , .		0
52	Classical and/or alternative NF- κ B pathway activation in multiple myeloma. <i>Blood</i> , 2010, 115, 3541-3552.	1.4	253
53	Abstract 4822: Analysis of somatic copy number alterations associated with poor prognosis and progression of multiple myeloma in African Americans. , 2010, , .		0
54	Spontaneous Remission in a Patient With t(4;14) Translocation Multiple Myeloma. <i>Journal of Clinical Oncology</i> , 2009, 27, e194-e197.	1.6	4

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55	Identification of Copy Number Abnormalities and Inactivating Mutations in Two Negative Regulators of Nuclear Factor- κ B Signaling Pathways in Waldenström's Macroglobulinemia. <i>Cancer Research</i> , 2009, 69, 3579-3588.	0.9	154
56	High-Resolution Genomic Analysis in Waldenström's Macroglobulinemia Identifies Disease-Specific and Common Abnormalities with Marginal Zone Lymphomas. <i>Clinical Lymphoma and Myeloma</i> , 2009, 9, 39-42.	1.4	32
57	Targeting NF- κ B Signaling in Multiple Myeloma. <i>Clinical Lymphoma and Myeloma</i> , 2009, 9, S14-S16.	1.4	1
58	Nonredundant and complementary functions of TRAF2 and TRAF3 in a ubiquitination cascade that activates NIK-dependent alternative NF- κ B signaling. <i>Nature Immunology</i> , 2008, 9, 1364-1370.	14.5	552
59	The selective Aurora B kinase inhibitor AZD1152 is a potential new treatment for multiple myeloma. <i>British Journal of Haematology</i> , 2008, 140, 295-302.	2.5	58
60	Aurora A kinase RNAi and small molecule inhibition of Aurora kinases with VE-465 induce apoptotic death in multiple myeloma cells. <i>Leukemia and Lymphoma</i> , 2008, 49, 559-569.	1.3	51
61	Loss of p53 Is a Marker of Progression in Plasma Cell Neoplasias and Is a Negative Prognostic Factor in Relapsed Disease.. <i>Blood</i> , 2008, 112, 1663-1663.	1.4	1
62	Promiscuous Mutations Activate the Noncanonical NF- κ B Pathway in Multiple Myeloma. <i>Cancer Cell</i> , 2007, 12, 131-144.	16.8	941
63	Multiple Myeloma (MM) Is Characterized by Genomic Instability Regardless of Ploidy Categories and Degree of Karyotypic Complexity Is an Important Prognostic Factor.. <i>Blood</i> , 2007, 110, 1476-1476.	1.4	0
64	Identification of Survival Critical Genomic Gains or Losses in Myeloma (MM) Using Array-Comparative Genomic Hybridization (aCGH).. <i>Blood</i> , 2007, 110, 2471-2471.	1.4	0
65	Ten years and counting: so what do we know about t(4;14)(p16;q32) multiple myeloma. <i>Leukemia and Lymphoma</i> , 2006, 47, 2289-2300.	1.3	90
66	Aurora Kinases as Therapeutic Targets in Multiple Myeloma.. <i>Blood</i> , 2006, 108, 847-847.	1.4	12
67	SSX Cancer Testis Antigens are Expressed in Most Multiple Myeloma Patients. <i>Journal of Immunotherapy</i> , 2005, 28, 564-575.	2.4	53
68	Overexpression of transcripts originating from the MMSET locus characterizes all t(4;14)(p16;q32)-positive multiple myeloma patients. <i>Blood</i> , 2005, 105, 4060-4069.	1.4	159
69	Receptor for hyaluronan-mediated motility correlates with centrosome abnormalities in multiple myeloma and maintains mitotic integrity. <i>Cancer Research</i> , 2005, 65, 850-60.	0.9	73
70	RHAMM expression and isoform balance predict aggressive disease and poor survival in multiple myeloma. <i>Blood</i> , 2004, 104, 1151-1158.	1.4	85
71	RHAMM Is a Centrosomal Protein That Interacts with Dynein and Maintains Spindle Pole Stability. <i>Molecular Biology of the Cell</i> , 2003, 14, 2262-2276.	2.1	167
72	In multiple myeloma, t(4;14)(p16;q32) is an adverse prognostic factor irrespective of FGFR3 expression. <i>Blood</i> , 2003, 101, 1520-1529.	1.4	356