

Mehmet Samur

List of Publications by Year in Descending Order

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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.

92
papers

1,879
citations

22
h-index

43
g-index

102
ext. papers

2,741
ext. citations

5.6
avg, IF

4.35
L-index

#	Paper	IF	Citations
92	Functional dissection of inherited non-coding variation influencing multiple myeloma risk.. <i>Nature Communications</i> , 2022 , 13, 151	17.4	0
91	Deciphering spatial genomic heterogeneity at a single cell resolution in multiple myeloma.. <i>Nature Communications</i> , 2022 , 13, 807	17.4	2
90	B Cell Transcriptional Coactivator POU2AF1 (BOB-1) Is an Early Transcription Factor Modulating the Protein Synthesis and Ribosomal Biogenesis in Multiple Myeloma: With Therapeutic Implication. <i>Blood</i> , 2021 , 138, 2670-2670	2.2	
89	IgM-MM is predominantly a pre-germinal center disorder and has a distinct genomic and transcriptomic signature from WM. <i>Blood</i> , 2021 , 138, 1980-1985	2.2	1
88	Defining Genomic Probability of Progression to Identify Low-Risk Smoldering Multiple Myeloma. <i>Blood</i> , 2021 , 138, 545-545	2.2	0
87	16p Deletion Involving BCMA Locus Is Frequent and Predominantly Observed with del17p. <i>Blood</i> , 2021 , 138, 1590-1590	2.2	
86	Dual BCL-2/BCL-XL Inhibitor Pelcitoclax (APG-1252) Overcomes Intrinsic and Acquired Resistance to Venetoclax in Multiple Myeloma Cells. <i>Blood</i> , 2021 , 138, 2655-2655	2.2	1
85	CCL20 induces colorectal cancer neoplastic epithelial cell proliferation, migration, and further CCL20 production through autocrine HGF-c-Met and MSP-MSPR signaling pathways. <i>Oncotarget</i> , 2021 , 12, 2323-2337	3.3	0
84	Clonal Hematopoiesis Is Frequent and Associated with Inferior Survival Irrespective of Transplantation Strategy in Patients with Newly Diagnosed Multiple Myeloma. <i>Blood</i> , 2021 , 138, 1127-1127	2.2	1
83	Aberrant CDK7 Activity Drives the Cell Cycle and Transcriptional Dysregulation to Support Multiple Myeloma Growth: An Attractive Molecular Vulnerability. <i>Blood</i> , 2021 , 138, 2687-2687	2.2	
82	Dysregulated APOBEC3G causes DNA damage and promotes genomic instability in multiple myeloma. <i>Blood Cancer Journal</i> , 2021 , 11, 166	7	2
81	Lysine Demethylase 5A is Required for MYC Driven Transcription in Multiple Myeloma. <i>Blood Cancer Discovery</i> , 2021 , 2, 370-387	7	4
80	Bortezomib induces anti-multiple myeloma immune response mediated by cGAS/STING pathway activation. <i>Blood Cancer Discovery</i> , 2021 , 2, 468-483	7	15
79	Integrated genomics and comprehensive validation reveal drivers of genomic evolution in esophageal adenocarcinoma. <i>Communications Biology</i> , 2021 , 4, 617	6.7	0
78	Identification of novel anti-tumor therapeutic target via proteomic characterization of ubiquitin receptor ADRM1/Rpn13. <i>Blood Cancer Journal</i> , 2021 , 11, 13	7	1
77	Biallelic loss of BCMA as a resistance mechanism to CAR T cell therapy in a patient with multiple myeloma. <i>Nature Communications</i> , 2021 , 12, 868	17.4	54
76	A large meta-analysis establishes the role of MRD negativity in long-term survival outcomes in patients with multiple myeloma. <i>Blood Advances</i> , 2020 , 4, 5988-5999	7.8	62

75	YWHAE/14-3-3 σ expression impacts the protein load, contributing to proteasome inhibitor sensitivity in multiple myeloma. <i>Blood</i> , 2020 , 136, 468-479	2.2	3
74	RNA Regulator of Lipogenesis (RROL) Is a Novel Lncrna Mediating Protein-Protein Interaction at Gene Regulatory Loci Driving Lipogenic Programs in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 20-21	2.2	
73	A Prospective Study and Identification of Genomewide Association Markers of Familial Predisposition to Plasma Cell Dyscrasias. <i>Blood</i> , 2020 , 136, 8-8	2.2	
72	Activation of the ERK Pathway Drives Acquired Resistance to Venetoclax in MM Cell Models. <i>Blood</i> , 2020 , 136, 21-22	2.2	0
71	TRAF2 Mediates Sensitivity to Immunomodulatory Drugs in the Bone Marrow Microenvironment. <i>Blood</i> , 2020 , 136, 31-31	2.2	
70	Exploring POU2AF1 (BOB-1) Dependency and Transcription Addiction in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 49-49	2.2	
69	Genomic and Transcriptomic Characterization of IgM Multiple Myeloma Identifies a Pre-Germinal Center Plasma Cell Disorder with Immature B-Cell Transcription-Factor Signature. <i>Blood</i> , 2020 , 136, 7-8	2.2	
68	Disruption of the m-SWI/SNF Complex Mediated By Recurrent Non-Coding Mutations in BCL7A Induces Tumor Cell Proliferation in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 40-40	2.2	0
67	Targeting MM at the Nexus between Cell Cycle and Transcriptional Regulation Via CDK7 Inhibition. <i>Blood</i> , 2020 , 136, 1-2	2.2	
66	Proteomic Characterization of Ubiquitin Receptor ADRM1/Rpn13. <i>Blood</i> , 2020 , 136, 39-39	2.2	
65	Enhancing the Immune Surveillance in Multiple Myeloma Via CDK4/6 Inhibition. <i>Blood</i> , 2020 , 136, 33-34	2.2	1
64	High-Dose Melphalan Significantly Increases Mutational Burden in Multiple Myeloma Cells at Relapse: Results from a Randomized Study in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 4-5	2.2	6
63	Biallelic Loss of BCMA Triggers Resistance to Anti-BCMA CAR T Cell Therapy in Multiple Myeloma. <i>Blood</i> , 2020 , 136, 14-14	2.2	7
62	Bortezomib Induces Anti-Multiple Myeloma Immune Response Mediated By Cgas/Sting Pathway Activation, Type I Interferon Secretion, and Immunogenic Cell Death: Clinical Application. <i>Blood</i> , 2020 , 136, 7-8	2.2	2
61	Genome-Wide Somatic Alterations in Multiple Myeloma Reveal a Superior Outcome Group. <i>Journal of Clinical Oncology</i> , 2020 , 38, 3107-3118	2.2	19
60	Targeting histone deacetylase 3 (HDAC3) in the bone marrow microenvironment inhibits multiple myeloma proliferation by modulating exosomes and IL-6 trans-signaling. <i>Leukemia</i> , 2020 , 34, 196-209	10.7	32
59	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019 , 10, 3835	17.4	94
58	Targeting MUC1-C Inhibits TWIST1 Signaling in Triple-Negative Breast Cancer. <i>Molecular Cancer Therapeutics</i> , 2019 , 18, 1744-1754	6.1	25

57	MUC1-C Activates the NuRD Complex to Drive Dedifferentiation of Triple-Negative Breast Cancer Cells. <i>Cancer Research</i> , 2019 , 79, 5711-5722	10.1	22
56	Deciphering the chronology of copy number alterations in Multiple Myeloma. <i>Blood Cancer Journal</i> , 2019 , 9, 39	7	25
55	A high-risk, Double-Hit, group of newly diagnosed myeloma identified by genomic analysis. <i>Leukemia</i> , 2019 , 33, 159-170	10.7	176
54	MUC1-C represses the RASSF1A tumor suppressor in human carcinoma cells. <i>Oncogene</i> , 2019 , 38, 7266-7277	7.7	11
53	Expanded Meta-Analyses Confirms the Association between MRD and Long-Term Survival Outcomes in Multiple Myeloma (MM). <i>Blood</i> , 2019 , 134, 4742-4742	2.2	3
52	HDAC8 Maintain Cytoskeleton Integrity Via Homologous Recombination and Represent a Novel Therapeutic Target in Multiple Myeloma. <i>Blood</i> , 2019 , 134, 4385-4385	2.2	
51	Loss-of-Function of Gabarap Impairs Bortezomib-Induced Anti-Tumor Immunity in Multiple Myeloma: Clinical Application. <i>Blood</i> , 2019 , 134, 134-134	2.2	2
50	Amplification and overexpression of E2 ubiquitin conjugase UBE2T promotes homologous recombination in multiple myeloma. <i>Blood Advances</i> , 2019 , 3, 3968-3972	7.8	8
49	Widespread intronic polyadenylation diversifies immune cell transcriptomes. <i>Nature Communications</i> , 2018 , 9, 1716	17.4	66
48	Long intergenic non-coding RNAs have an independent impact on survival in multiple myeloma. <i>Leukemia</i> , 2018 , 32, 2626-2635	10.7	31
47	Therapeutic vulnerability of multiple myeloma to MIR17PTi, a first-in-class inhibitor of pri-miR-17-92. <i>Blood</i> , 2018 , 132, 1050-1063	2.2	40
46	Genomic patterns of progression in smoldering multiple myeloma. <i>Nature Communications</i> , 2018 , 9, 3363	7.4	99
45	Identification of novel mutational drivers reveals oncogene dependencies in multiple myeloma. <i>Blood</i> , 2018 , 132, 587-597	2.2	196
44	Insights into the genomic landscape of MYD88 wild-type Waldenström macroglobulinemia. <i>Blood Advances</i> , 2018 , 2, 2937-2946	7.8	36
43	Functional Role of Linc-RNAs in Multiple Myeloma: Linc-MIR17HG Affects Fatty Acid Biosynthesis Via transcriptional Regulation of ACC1 with Potential Therapeutic Implications. <i>Blood</i> , 2018 , 132, 1925-1925	2.2	25
42	Dysregulation of Splicing in Multiple Myeloma: The Splicing Factor SRSF1 Supports MM Cell Proliferation Via Splicing Control. <i>Blood</i> , 2018 , 132, 4500-4500	2.2	1
41	Variable BCL2/BCL2L1 ratio in multiple myeloma with t(11;14). <i>Blood</i> , 2018 , 132, 2778-2780	2.2	10
40	Non-overlapping Control of Transcriptome by Promoter- and Super-Enhancer-Associated Dependencies in Multiple Myeloma. <i>Cell Reports</i> , 2018 , 25, 3693-3705.e6	10.6	11

39	Role of apurinic/aprimidinic nucleases in the regulation of homologous recombination in myeloma: mechanisms and translational significance. <i>Blood Cancer Journal</i> , 2018 , 8, 92	7	23
38	A multiple myeloma classification system that associates normal B-cell subset phenotypes with prognosis. <i>Blood Advances</i> , 2018 , 2, 2400-2411	7.8	3
37	Functional role and therapeutic targeting of p21-activated kinase 4 in multiple myeloma. <i>Blood</i> , 2017 , 129, 2233-2245	2.2	25
36	p53-related protein kinase confers poor prognosis and represents a novel therapeutic target in multiple myeloma. <i>Blood</i> , 2017 , 129, 1308-1319	2.2	26
35	Blockade of Deubiquitylating Enzyme USP1 Inhibits DNA Repair and Triggers Apoptosis in Multiple Myeloma Cells. <i>Clinical Cancer Research</i> , 2017 , 23, 4280-4289	12.9	44
34	Association of Minimal Residual Disease With Superior Survival Outcomes in Patients With Multiple Myeloma: A Meta-analysis. <i>JAMA Oncology</i> , 2017 , 3, 28-35	13.4	273
33	PAK4 Inhibition Impacts Growth and Survival, and Increases Sensitivity to DNA-Damaging Agents in Waldenstrom Macroglobulinemia. <i>Blood</i> , 2017 , 130, 648-648	2.2	
32	Mapping of the Multiple Myeloma Transcriptional Core Regulatory Circuitry Reveals TCF3 As a Novel Dependency and an Oncogenic Collaborator of MYC. <i>Blood</i> , 2017 , 130, 64-64	2.2	1
31	Stromal CCR6 drives tumor growth in a murine transplantable colon cancer through recruitment of tumor-promoting macrophages. <i>Oncotarget</i> , 2016 , 5, e1189052	7.2	36
30	Deficiency of IL-17A, but not the prototypical Th17 transcription factor ROR γ , decreases murine spontaneous intestinal tumorigenesis. <i>Cancer Immunology, Immunotherapy</i> , 2016 , 65, 13-24	7.4	10
29	The KDM3A-KLF2-IRF4 axis maintains myeloma cell survival. <i>Nature Communications</i> , 2016 , 7, 10258	17.4	61
28	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. <i>Blood</i> , 2016 , 128, 116-116	2.2	2
27	Whole Genome Sequencing of Unique Paired SMM/MGUS Progressing to MM Samples Reveals a Genomic Landscape with Diverse Evolutionary Pattern. <i>Blood</i> , 2016 , 128, 2088-2088	2.2	0
26	A Detailed Alternate Splicing Landscape in Multiple Myeloma with Significant Potential Biological and Clinical Implications. <i>Blood</i> , 2016 , 128, 356-356	2.2	1
25	Dysregulated Aid/Apobec Family Proteins Promote Genomic Instability in Multiple Myeloma. <i>Blood</i> , 2016 , 128, 803-803	2.2	1
24	Deubiquitylating Enzyme USP1 As Therapeutic Target in Multiple Myeloma. <i>Blood</i> , 2016 , 128, 3290-3290	2.2	2
23	Flap Structure-Specific Endonuclease 1 (FEN1) May be a Key Mediator of Genome Instability in Myeloma: A Cellular Vulnerability with Potential Therapeutic Significance. <i>Blood</i> , 2016 , 128, 4440-4440	2.2	
22	Lenalidomide Enhances Immune Checkpoint Blockade-Induced Immune Response in Multiple Myeloma. <i>Clinical Cancer Research</i> , 2015 , 21, 4607-18	12.9	214

21	Nuclease Activity Is Associated with Genomic Instability As Well As Survival in Myeloma; Underlying Mechanisms and Significance. <i>Blood</i> , 2015 , 126, 2420-2420	2.2	2
20	Identification of a Novel Long Intergenic Noncoding RNA - Linc00936, with Significant Impact on Multiple Myeloma Cell Growth Via mTOR Pathway Inhibition. <i>Blood</i> , 2015 , 126, 504-504	2.2	2
19	Functional and Clinical Impact of Splicing Factor Dysregulation in Multiple Myeloma. <i>Blood</i> , 2015 , 126, 726-726	2.2	1
18	The Fusion Gene Landscape in Multiple Myeloma, with Clinical Impact. <i>Blood</i> , 2015 , 126, 835-835	2.2	1
17	Functional and Genomic Signatures of Homologous Recombination (HR) Predict for Clinical Outcome in Multiple Myeloma (MM). <i>Blood</i> , 2015 , 126, 3626-3626	2.2	
16	Apurinic/Apyrimidinic Endonuclease 1 Induced Genomic Instability Causes T-Cell Acute Lymphoblastic Leukemia in Zebrafish. <i>Blood</i> , 2015 , 126, 1431-1431	2.2	
15	Dysregulated Nucleotide Excision Repair (NER) Is a New Target in Multiple Myeloma. <i>Blood</i> , 2015 , 126, 4187-4187	2.2	
14	Discovery and Characterization of Promoter and Super-Enhancer-Associated Dependencies through E2F and BET Bromodomains in Multiple Myeloma. <i>Blood</i> , 2015 , 126, 838-838	2.2	
13	Differential and limited expression of mutant alleles in multiple myeloma. <i>Blood</i> , 2014 , 124, 3110-7	2.2	42
12	Heteroclitic XBP1 peptides evoke tumor-specific memory cytotoxic T lymphocytes against breast cancer, colon cancer, and pancreatic cancer cells. <i>Onc Immunology</i> , 2014 , 3, e970914	7.2	18
11	LSD1 Impairs the Epithelial-Mesenchymal Transition (EMT) and Osteoclastogenesis Potency in Multiple Myeloma and Synergistically Induces Cytotoxicity with HDAC Inhibitors. <i>Blood</i> , 2014 , 124, 3410-3410	2.2	4
10	Targeting Aberrant Non-Homologous End Joining in Multiple Myeloma: Role of the Classical and Alternative Pathways in Genomic Instability. <i>Blood</i> , 2014 , 124, 3417-3417	2.2	1
9	Alternative Splicing Is a Frequent Event and Impacts Clinical Outcome in Myeloma: A Large RNA-Seq Data Analysis of Newly-Diagnosed Myeloma Patients. <i>Blood</i> , 2014 , 124, 638-638	2.2	1
8	Frequent Igh Fusion Transcripts with Clinical Impact in Multiple Myeloma. <i>Blood</i> , 2014 , 124, 721-721	2.2	1
7	Nucleotide Excision Repair (NER) Is Frequently Impaired and Affects Outcome in Multiple Myeloma (MM). <i>Blood</i> , 2014 , 124, 2055-2055	2.2	
6	Bone Marrow Microenvironment Regulates Alternative Splicing Events in Myeloma Cells through Downregulation of RNA Binding Protein Fox2. <i>Blood</i> , 2014 , 124, 4714-4714	2.2	
5	Long Intergenic Non-Coding RNAs (lincRNA) Impacts Biology and Clinical Outcome in Multiple Myeloma. <i>Blood</i> , 2014 , 124, 642-642	2.2	
4	Differential and Limited Expression of Mutant Alleles in Multiple Myeloma. <i>Blood</i> , 2014 , 124, 2007-2007	2.2	

- 3 Aberrant Non-Homologous End Joining in Multiple Myeloma: A Role in Genomic Instability and As Potential Prognostic Marker.. *Blood*, **2012**, 120, 2932-2932 2.2 3
- 2 Studying Evolution of Multiple Myeloma with CanEvolve. *Blood*, **2011**, 118, 2886-2886 2.2
- 1 Multiple Myeloma DREAM Challenge Reveals Epigenetic RegulatorPHF19As Marker of Aggressive Disease 2