Caleb K Stein

List of Publications by Year
in descending order

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34 papers	339 citations	1306789 7 h-index	887659 17 g-index
34 all docs	34 docs citations	34 times ranked	910 citing authors

#	Article	IF	Citations
1	MYC dysregulation in the progression of multiple myeloma. Leukemia, 2020, 34, 322-326.	3.3	108
2	Removing batch effects from purified plasma cell gene expression microarrays with modified ComBat. BMC Bioinformatics, 2015, 16, 63.	1.2	73
3	Tumor Burden Limits Bispecific Antibody Efficacy through T-cell Exhaustion Averted by Concurrent Cytotoxic Therapy. Blood Cancer Discovery, 2021, 2, 354-369.	2.6	37
4	The varied distribution and impact of RAS codon and other key DNA alterations across the translocation cyclin D subgroups in multiple myeloma. Oncotarget, 2017, 8, 27854-27867.	0.8	25
5	Identification of PIKfyve kinase as a target in multiple myeloma. Haematologica, 2020, 105, 1641-1649.	1.7	25
6	Monosomic Loss of MIR15A/MIR16-1 Is a Driver of Multiple Myeloma Proliferation and Disease Progression. Blood Cancer Discovery, 2020, 1, 68-81.	2.6	24
7	The Clinical Impact of Macrofocal Disease in Multiple Myeloma Differs Between Presentation and Relapse. Blood, 2016, 128, 4431-4431.	0.6	8
8	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
9	Chimeric Antigen Receptor T Cell Therapy Pipeline at a Glance: A Retrospective and Systematic Analysis from Clinicaltrials.Gov. Blood, 2019, 134, 5629-5629.	0.6	5
10	Higher Expressions of PTH Receptor Type 1 and/or 2 in Bone Marrow Is Associated to Longer Survival in Newly Diagnosed Myeloma Patients Enrolled in Total Therapy 3. Blood, 2014, 124, 3409-3409.	0.6	5
11	Characterization of the Mutational Landscape of Multiple Myeloma Using Comprehensive Genomic Profiling. Blood, 2014, 124, 3418-3418.	0.6	3
12	Transcriptional Plasticity Compensates for Ikaros and Aiolos Proteasomal Degradation and Mediates Resistance to IMiDs in Multiple Myeloma (MM). Blood, 2017, 130, 63-63.	0.6	3
13	The Composition and Clinical Impact of Focal Lesions and Their Impact on the Microenvironment in Myeloma. Blood, 2015, 126, 1806-1806.	0.6	2
14	Extensive Regional Intra-Clonal Heterogeneity in Multiple Myeloma - Implications for Diagnostics, Risk Stratification and Targeted Treatment. Blood, 2016, 128, 3278-3278.	0.6	2
15	Inhibition of the Epigenetic Modifier EZH2 Upregulates Cell Cycle Control Genes to Inhibit Myeloma Cell Growth and Overcome High-Risk Disease Features. Blood, 2016, 128, 3289-3289.	0.6	2
16	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
17	Modified Combat Removes Batch Effects from Myeloma Cell GEPâ€“derived Risk Scores and Molecular Subgroup Assignment. Blood, 2014, 124, 3355-3355.	0.6	1
18	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

#	Article	IF	Citations
19	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
20	Stem Cell-like Characteristics of MM Plasma Cells Vary By ROS Levels: Implications for Targeted Therapy. Blood, 2015, 126, 1820-1820.	0.6	1
21	Defining the Impact of Tandem Autologous Stem Cell Transplantation in Multiple Myeloma: A Case-Match Analysis in the Total Therapy Trials. Blood, 2015, 126, 3182-3182.	0.6	1
22	Identification of Biomarkers Associated with MAF-Mediated Resistance to Proteasome Inhibitors in t(14;16) Multiple Myeloma. Blood, 2015, 126, 3020-3020.	0.6	1
23	A Survey of Fusion Genes in Myeloma Identifies Kinase Domain Activation Which Could be Targeted with Available Treatments. Blood, 2016, 128, 117-117.	0.6	1
24	High Risk Myeloma Is Characterized By the Bi-Allelic Inactivation of CDKN2C and RB1. Blood, 2016, 128, 4416-4416.	0.6	1
25	Sustained Growth of Primary Myeloma Cells in Coculture with Whole Donor Bone Marrow Is Associated with Induced Secretion of the Microenvironmental Mediator of Cytokinesis, Hemicentin-1. Blood, 2014, 124, 3403-3403.	0.6	0
26	Identifying a Gene Expression (GEP)-Based Model Predicting for Progression from AMM to Cmm Requiring Therapy in S0120 Patients Treated at Mirt. Blood, 2014, 124, 2078-2078.	0.6	0
27	Low-Dose 28-Day Metronomically Scheduled Therapy (METRO) for Newly Diagnosed High-Risk Multiple Myeloma: A Pilot Study. Blood, 2014, 124, 5770-5770.	0.6	0
28	Defining Risk of MGUS and AMM Progression to Myeloma By Ig Heavy-Chain FISH. Blood, 2014, 124, 3408-3408.	0.6	0
29	Molecular Subtyping and Risk Stratification for the Classification of Myeloma. Blood, 2015, 126, 4173-4173.	0.6	0
30	Identifying Targets for Therapy in High Risk t(4;14) Myeloma Using Multi-Level Molecular and Phenotypic Analysis of Isogenic MMSET and MMSET Knock out Cell Lines. Blood, 2015, 126, 1792-1792.	0.6	0
31	47 Genes Define Myeloma Cell Acquired Resistance to Bortezomib and Have Profound Prognostic Implications in Multiple Myeloma. Blood, 2015, 126, 499-499.	0.6	0
32	The Mutational and Signaling Landscape of Multiple Myeloma Varies Dependent upon Translocation Cyclin D (TC) Subgroup. Blood, 2016, 128, 4441-4441.	0.6	0
33	Integrative Analysis of FISH, Transcriptomics and Mutational Status Predicts Responsiveness to Novel Agents in Multiple Myeloma. Blood, 2019, 134, 574-574.	0.6	0
34	Disrupting Ectopic Super-Enhancers to Treat Multiple Myeloma. Blood, 2021, 138, 1593-1593.	0.6	0