

Martin L Miller

List of Publications by Year in descending order

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Version: 2024-02-01

35
papers

21,452
citations

218677

26
h-index

361022

35
g-index

43
all docs

43
docs citations

43
times ranked

37712
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational landscape determines sensitivity to PD-1 blockade in nonâ€“small cell lung cancer. <i>Science</i> , 2015, 348, 124-128.	12.6	6,756
2	The Cancer Genome Atlas Pan-Cancer analysis project. <i>Nature Genetics</i> , 2013, 45, 1113-1120.	21.4	6,265
3	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
4	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. <i>Science Signaling</i> , 2010, 3, ra3.	3.6	1,319
5	Emerging landscape of oncogenic signatures across human cancers. <i>Nature Genetics</i> , 2013, 45, 1127-1133.	21.4	1,190
6	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. <i>Nature Biotechnology</i> , 2009, 27, 549-555.	17.5	470
7	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	3.6	418
8	Heterogeneous Tumor-Immune Microenvironments among Differentially Growing Metastases in an Ovarian Cancer Patient. <i>Cell</i> , 2017, 170, 927-938.e20.	28.9	368
9	KinomeXplorer: an integrated platform for kinome biology studies. <i>Nature Methods</i> , 2014, 11, 603-604.	19.0	304
10	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. <i>Cell</i> , 2019, 179, 219-235.e21.	28.9	270
11	Unraveling tumorâ€™ immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593.	21.4	136
12	Perturbation Biology: Inferring Signaling Networks in Cellular Systems. <i>PLoS Computational Biology</i> , 2013, 9, e1003290.	3.2	128
13	NetPhosYeast: prediction of protein phosphorylation sites in yeast. <i>Bioinformatics</i> , 2007, 23, 895-897.	4.1	121
14	Comprehensive Benchmarking and Integration of Tumor Microenvironment Cell Estimation Methods. <i>Cancer Research</i> , 2019, 79, 6238-6246.	0.9	116
15	Promises and challenges of adoptive T-cell therapies for solid tumours. <i>British Journal of Cancer</i> , 2021, 124, 1759-1776.	6.4	113
16	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
17	Drug Synergy Screen and Network Modeling in Dedifferentiated Liposarcoma Identifies CDK4 and IGF1R as Synergistic Drug Targets. <i>Science Signaling</i> , 2013, 6, ra85.	3.6	97
18	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015, 1, 197-209.	6.2	94

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19	NetPhosBac – A predictor for Ser/Thr phosphorylation sites in bacterial proteins. <i>Proteomics</i> , 2009, 9, 116-125.	2.2	67
20	Integrin-10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. <i>Cancer Discovery</i> , 2016, 6, 1148-1165.	9.4	62
21	Lack of detectable neoantigen depletion signals in the untreated cancer genome. <i>Nature Genetics</i> , 2019, 51, 1741-1748.	21.4	59
22	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. <i>Nature Methods</i> , 2013, 10, 768-773.	19.0	55
23	Centriolar satellites are acentriolar assemblies of centrosomal proteins. <i>EMBO Journal</i> , 2019, 38, e101082.	7.8	55
24	Kinase-Specific Prediction of Protein Phosphorylation Sites. <i>Methods in Molecular Biology</i> , 2009, 527, 299-310.	0.9	52
25	Friends Not Foes: CTLA-4 Blockade and mTOR Inhibition Cooperate during CD8+ T Cell Priming To Promote Memory Formation and Metabolic Readiness. <i>Journal of Immunology</i> , 2015, 194, 2089-2098.	0.8	39
26	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. <i>Genetic Epidemiology</i> , 2011, 35, 318-332.	1.3	31
27	Characterization and location of secretory phospholipase A2 groups IIE, V, and X in the rat brain. <i>Journal of Neuroscience Research</i> , 2006, 83, 874-882.	2.9	26
28	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease-Associated Colorectal Cancers. <i>Clinical Cancer Research</i> , 2018, 24, 5133-5142.	7.0	26
29	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020, 11, 4306.	12.8	26
30	Integrated Multi-Tumor Radio-Genomic Marker of Outcomes in Patients with High Serous Ovarian Carcinoma. <i>Cancers</i> , 2020, 12, 3403.	3.7	24
31	Spatial Normalization of Reverse Phase Protein Array Data. <i>PLoS ONE</i> , 2014, 9, e97213.	2.5	23
32	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	14.5	21
33	Motif Decomposition of the Phosphotyrosine Proteome Reveals a New N-terminal Binding Motif for SHIP2. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 181-192.	3.8	15
34	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. <i>Cell Reports</i> , 2021, 35, 109155.	6.4	10
35	Ovarian tumors orchestrate distinct cellular compositions. <i>Immunity</i> , 2021, 54, 1107-1109.	14.3	9