

Martin L Miller

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8694606/publications.pdf>

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	Promises and challenges of adoptive T-cell therapies for solid tumours. <i>British Journal of Cancer</i> , 2021, 124, 1759-1776.	6.4	113
2	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. <i>Cell Reports</i> , 2021, 35, 109155.	6.4	10
3	Ovarian tumors orchestrate distinct cellular compositions. <i>Immunity</i> , 2021, 54, 1107-1109.	14.3	9
4	Integrated Multi-Tumor Radio-Genomic Marker of Outcomes in Patients with High Serous Ovarian Carcinoma. <i>Cancers</i> , 2020, 12, 3403.	3.7	24
5	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. <i>Nature Communications</i> , 2020, 11, 4306.	12.8	26
6	Unraveling tumor-immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. <i>Nature Genetics</i> , 2020, 52, 582-593.	21.4	136
7	Comprehensive Benchmarking and Integration of Tumor Microenvironment Cell Estimation Methods. <i>Cancer Research</i> , 2019, 79, 6238-6246.	0.9	116
8	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. <i>Cell</i> , 2019, 179, 219-235.e21.	28.9	270
9	Centriolar satellites are acentriolar assemblies of centrosomal proteins. <i>EMBO Journal</i> , 2019, 38, e101082.	7.8	55
10	Lack of detectable neoantigen depletion signals in the untreated cancer genome. <i>Nature Genetics</i> , 2019, 51, 1741-1748.	21.4	59
11	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease-Associated Colorectal Cancers. <i>Clinical Cancer Research</i> , 2018, 24, 5133-5142.	7.0	26
12	Heterogeneous Tumor-Immune Microenvironments among Differentially Growing Metastases in an Ovarian Cancer Patient. <i>Cell</i> , 2017, 170, 927-938.e20.	28.9	368
13	Integrin- β 10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. <i>Cancer Discovery</i> , 2016, 6, 1148-1165.	9.4	62
14	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. <i>Nucleic Acids Research</i> , 2016, 44, D986-D991.	14.5	21
15	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
16	Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015, 161, 1681-1696.	28.9	2,562
17	Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. <i>Science</i> , 2015, 348, 124-128.	12.6	6,756
18	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. <i>Cell Systems</i> , 2015, 1, 197-209.	6.2	94

#	ARTICLE	IF	CITATIONS
19	Spatial Normalization of Reverse Phase Protein Array Data. PLoS ONE, 2014, 9, e97213.	2.5	23
20	KinomeXplorer: an integrated platform for kinome biology studies. Nature Methods, 2014, 11, 603-604.	19.0	304
21	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. Nature Methods, 2013, 10, 768-773.	19.0	55
22	The Cancer Genome Atlas Pan-Cancer analysis project. Nature Genetics, 2013, 45, 1113-1120.	21.4	6,265
23	Emerging landscape of oncogenic signatures across human cancers. Nature Genetics, 2013, 45, 1127-1133.	21.4	1,190
24	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	6.4	110
25	Perturbation Biology: Inferring Signaling Networks in Cellular Systems. PLoS Computational Biology, 2013, 9, e1003290.	3.2	128
26	Drug Synergy Screen and Network Modeling in Dedifferentiated Liposarcoma Identifies CDK4 and IGF1R as Synergistic Drug Targets. Science Signaling, 2013, 6, ra85.	3.6	97
27	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. Genetic Epidemiology, 2011, 35, 318-332.	1.3	31
28	Quantitative Phosphoproteomics Reveals Widespread Full Phosphorylation Site Occupancy During Mitosis. Science Signaling, 2010, 3, ra3.	3.6	1,319
29	NetPhosBac – A predictor for Ser/Thr phosphorylation sites in bacterial proteins. Proteomics, 2009, 9, 116-125.	2.2	67
30	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. Nature Biotechnology, 2009, 27, 549-555.	17.5	470
31	Kinase-Specific Prediction of Protein Phosphorylation Sites. Methods in Molecular Biology, 2009, 527, 299-310.	0.9	52
32	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	3.6	418
33	Motif Decomposition of the Phosphotyrosine Proteome Reveals a New N-terminal Binding Motif for SHIP2. Molecular and Cellular Proteomics, 2008, 7, 181-192.	3.8	15
34	NetPhosYeast: prediction of protein phosphorylation sites in yeast. Bioinformatics, 2007, 23, 895-897.	4.1	121
35	Characterization and location of secretory phospholipase A2 groups IIE, V, and X in the rat brain. Journal of Neuroscience Research, 2006, 83, 874-882.	2.9	26