Martin L Miller

List of Publications by Year in Descending Order

39 papers	15,026 citations	25 h-index	43 g-index
43 ext. papers	19,128 ext. citations	18.5 avg, IF	5.86 L-index

#	Paper	IF	Citations
39	Promises and challenges of adoptive T-cell therapies for solid tumours. *British Journal of Cancer*, **2021**, 124, 1759-1776	8.7	19
38	Copy number aberrations drive kinase rewiring, leading to genetic vulnerabilities in cancer. *Cell Reports*, **2021**, 35, 109155	10.6	0
37	Ovarian tumors orchestrate distinct cellular compositions. *Immunity*, **2021**, 54, 1107-1109	32.3	1
36	Unraveling tumor-immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. *Nature Genetics*, **2020**, 52, 582-593	36.3	64
35	Integrated Multi-Tumor Radio-Genomic Marker of Outcomes in Patients with High Serous Ovarian Carcinoma. *Cancers*, **2020**, 12,	6.6	7
34	Multi-site clonality analysis uncovers pervasive heterogeneity across melanoma metastases. *Nature Communications*, **2020**, 11, 4306	17.4	12
33	UVB-Induced Tumor Heterogeneity Diminishes Immune Response in Melanoma. *Cell*, **2019**, 179, 219-235.e21	56.2	143
32	Centriolar satellites are acentriolar assemblies of centrosomal proteins. *EMBO Journal*, **2019**, 38, e101082	11.3	26
31	Comprehensive Benchmarking and Integration of Tumor Microenvironment Cell Estimation Methods. *Cancer Research*, **2019**, 79, 6238-6246	10.1	38
30	Lack of detectable neoantigen depletion signals in the untreated cancer genome. *Nature Genetics*, **2019**, 51, 1741-1748	36.3	30
29	Mutational Analysis Identifies Therapeutic Biomarkers in Inflammatory Bowel Disease-Associated Colorectal Cancers. *Clinical Cancer Research*, **2018**, 24, 5133-5142	12.9	17
28	Heterogeneous Tumor-Immune Microenvironments among Differentially Growing Metastases in an Ovarian Cancer Patient. *Cell*, **2017**, 170, 927-938.e20	56.2	267
27	Integrin-α10 Dependency Identifies RAC and RICTOR as Therapeutic Targets in High-Grade Myxofibrosarcoma. *Cancer Discovery*, **2016**, 6, 1148-1165	24.4	40
26	MutationAligner: a resource of recurrent mutation hotspots in protein domains in cancer. *Nucleic Acids Research*, **2016**, 44, D986-91	20.1	11
25	Genomic Classification of Cutaneous Melanoma. *Cell*, **2015**, 161, 1681-96	56.2	1807
24	Cancer immunology. Mutational landscape determines sensitivity to PD-1 blockade in non-small cell lung cancer. *Science*, **2015**, 348, 124-8	33.3	5003
23	Pan-Cancer Analysis of Mutation Hotspots in Protein Domains. *Cell Systems*, **2015**, 1, 197-209	10.6	72

22	Friends not foes: CTLA-4 blockade and mTOR inhibition cooperate during CD8+ T cell priming to promote memory formation and metabolic readiness. *Journal of Immunology*, **2015**, 194, 2089-98	5.3	33
21	KinomeXplorer: an integrated platform for kinome biology studies. *Nature Methods*, **2014**, 11, 603-4	21.6	196
20	Spatial normalization of reverse phase protein array data. *PLoS ONE*, **2014**, 9, e97213	3.7	18
19	Cell-selective labeling using amino acid precursors for proteomic studies of multicellular environments. *Nature Methods*, **2013**, 10, 768-73	21.6	38
18	The Cancer Genome Atlas Pan-Cancer analysis project. *Nature Genetics*, **2013**, 45, 1113-20	36.3	3933
17	Emerging landscape of oncogenic signatures across human cancers. *Nature Genetics*, **2013**, 45, 1127-33	36.3	889
16	The SH2 domain interaction landscape. *Cell Reports*, **2013**, 3, 1293-305	10.6	89
15	Perturbation biology: inferring signaling networks in cellular systems. *PLoS Computational Biology*, **2013**, 9, e1003290	5	98
14	Drug synergy screen and network modeling in dedifferentiated liposarcoma identifies CDK4 and IGF1R as synergistic drug targets. *Science Signaling*, **2013**, 6, ra85	8.8	61
13	Meta-analysis of heterogeneous data sources for genome-scale identification of risk genes in complex phenotypes. *Genetic Epidemiology*, **2011**, 35, 318-32	2.6	28
12	Quantitative phosphoproteomics reveals widespread full phosphorylation site occupancy during mitosis. *Science Signaling*, **2010**, 3, ra3	8.8	1106
11	NetPhosBac - a predictor for Ser/Thr phosphorylation sites in bacterial proteins. *Proteomics*, **2009**, 9, 116-25	4.8	55
10	Transfection of small RNAs globally perturbs gene regulation by endogenous microRNAs. *Nature Biotechnology*, **2009**, 27, 549-55	44.5	393
9	Kinase-specific prediction of protein phosphorylation sites. *Methods in Molecular Biology*, **2009**, 527, 299-310, x	1.4	43
8	Motif decomposition of the phosphotyrosine proteome reveals a new N-terminal binding motif for SHIP2. *Molecular and Cellular Proteomics*, **2008**, 7, 181-92	7.6	13
7	Linear motif atlas for phosphorylation-dependent signaling. *Science Signaling*, **2008**, 1, ra2	8.8	342
6	NetPhosYeast: prediction of protein phosphorylation sites in yeast. *Bioinformatics*, **2007**, 23, 895-7	7.2	103
5	Characterization and location of secretory phospholipase A2 groups IIE, V, and X in the rat brain. *Journal of Neuroscience Research*, **2006**, 83, 874-82	4.4	21