Michael D Mclellan

List of Publications by Citations

100 papers	81,707 citations	76 h-index	110 g-index
110 ext. papers	99,007 ext. citations	25.3 avg, IF	8.93 L-index

#	Paper	IF	Citations
100	Comprehensive molecular portraits of human breast tumours. *Nature*, **2012**, 490, 61-70	50.4	8025
99	A map of human genome variation from population-scale sequencing. *Nature*, **2010**, 467, 1061-73	50.4	6142
98	An integrated map of genetic variation from 1,092 human genomes. *Nature*, **2012**, 491, 56-65	50.4	6049
97	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. *Nature*, **2008**, 455, 1061-8	50.4	5669
96	Integrated genomic analyses of ovarian carcinoma. *Nature*, **2011**, 474, 609-15	50.4	5210
95	Comprehensive molecular characterization of gastric adenocarcinoma. *Nature*, **2014**, 513, 202-9	50.4	3659
94	Comprehensive molecular profiling of lung adenocarcinoma. *Nature*, **2014**, 511, 543-50	50.4	3310
93	Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. *New England Journal of Medicine*, **2013**, 368, 2059-74	59.2	3137
92	VarScan 2: somatic mutation and copy number alteration discovery in cancer by exome sequencing. *Genome Research*, **2012**, 22, 568-76	9.7	2895
91	Mutational landscape and significance across 12 major cancer types. *Nature*, **2013**, 502, 333-339	50.4	2803
90	Integrated genomic characterization of endometrial carcinoma. *Nature*, **2013**, 497, 67-73	50.4	2800
89	Somatic mutations affect key pathways in lung adenocarcinoma. *Nature*, **2008**, 455, 1069-75	50.4	2280
88	Recurring mutations found by sequencing an acute myeloid leukemia genome. *New England Journal of Medicine*, **2009**, 361, 1058-66	59.2	1765
87	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. *Nature*, **2012**, 481, 506-10	50.4	1511
86	DNMT3A mutations in acute myeloid leukemia. *New England Journal of Medicine*, **2010**, 363, 2424-33	59.2	1486
85	The origin and evolution of mutations in acute myeloid leukemia. *Cell*, **2012**, 150, 264-78	56.2	1143
84	Age-related mutations associated with clonal hematopoietic expansion and malignancies. *Nature Medicine*, **2014**, 20, 1472-8	50.5	1125

83	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
82	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. *Nature*, **2008**, 456, 66-72	50.4	1064
81	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. *Nature Methods*, **2009**, 6, 677-81	21.6	1062
80	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. *Cell*, **2015**, 163, 506-19	56.2	1055
79	Proteogenomics connects somatic mutations to signalling in breast cancer. *Nature*, **2016**, 534, 55-62	50.4	938
78	Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. *Cell*, **2014**, 158, 929-944	56.2	935
77	Genome remodelling in a basal-like breast cancer metastasis and xenograft. *Nature*, **2010**, 464, 999-1005	50.4	935
76	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. *Bioinformatics*, **2009**, 25, 2283-5	7.2	890
75	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. *Cell*, **2018**, 173, 291-304.e6	56.2	888
74	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
73	Whole-genome analysis informs breast cancer response to aromatase inhibition. *Nature*, **2012**, 486, 353-60	50.4	793
72	Clonal architecture of secondary acute myeloid leukemia. *New England Journal of Medicine*, **2012**, 366, 1090-8	59.2	582
71	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
70	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. *Nature Genetics*, **2015**, 47, 106-14	36.3	547
69	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
68	Recurrent DNMT3A mutations in patients with myelodysplastic syndromes. *Leukemia*, **2011**, 25, 1153-8	10.7	419
67	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. *Nature Genetics*, **2011**, 44, 53-7	36.3	408
66	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405

65	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
64	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. *Cell Reports*, **2018**, 23, 181-193.e7	10.6	366
63	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342
62	MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. *Bioinformatics*, **2014**, 30, 1015-6	7.2	341
61	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
60	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
59	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. *Nature Genetics*, **2004**, 36, 1268-74	36.3	308
58	C-terminal truncations in human 3'-5'DNA exonuclease TREX1 cause autosomal dominant retinal vasculopathy with cerebral leukodystrophy. *Nature Genetics*, **2007**, 39, 1068-70	36.3	307
57	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
56	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. *Cancer Cell*, **2018**, 33, 706-720.e9	24.3	275
55	SMN2 splice modulators enhance U1-pre-mRNA association and rescue SMA mice. *Nature Chemical Biology*, **2015**, 11, 511-7	11.7	253
54	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. *Cell Reports*, **2017**, 18, 2780-2794	10.6	247
53	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
52	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
51	Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. *Leukemia*, **2013**, 27, 1275-82	10.7	219
50	Acquired copy number alterations in adult acute myeloid leukemia genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2009**, 106, 12950-5	11.5	209
49	Integrated analysis of germline and somatic variants in ovarian cancer. *Nature Communications*, **2014**, 5, 3156	17.4	199
48	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. *Cell Reports*, **2018**, 23, 282-296.e4	10.6	188

47	Novel MEK1 mutation identified by mutational analysis of epidermal growth factor receptor signaling pathway genes in lung adenocarcinoma. *Cancer Research*, **2008**, 68, 5524-8	10.1	185
46	Patterns and functional implications of rare germline variants across 12 cancer types. *Nature Communications*, **2015**, 6, 10086	17.4	170
45	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
44	Somatic mutations and germline sequence variants in the expressed tyrosine kinase genes of patients with de novo acute myeloid leukemia. *Blood*, **2008**, 111, 4797-808	2.2	166
43	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. *Cell Systems*, **2018**, 6, 282-300.e2	10.6	159
42	Clinical and molecular delineation of the 17q21.31 microdeletion syndrome. *Journal of Medical Genetics*, **2008**, 45, 710-20	5.8	156
41	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
40	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. *Cell Reports*, **2018**, 23, 297-312.e12	10.6	147
39	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
38	Identification of a novel TP53 cancer susceptibility mutation through whole-genome sequencing of a patient with therapy-related AML. *JAMA - Journal of the American Medical Association*, **2011**, 305, 1568-76	27.4	125
37	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
36	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
35	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. *Nature Communications*, **2013**, 4, 2730	17.4	91
34	Protein-structure-guided discovery of functional mutations across 19 cancer types. *Nature Genetics*, **2016**, 48, 827-37	36.3	88
33	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. *Cell Systems*, **2018**, 7, 422-437.e7	10.6	85
32	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. *Journal of Clinical Investigation*, **2011**, 121, 1445-55	15.9	82
31	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. *Molecular and Cellular Proteomics*, **2016**, 15, 1060-71	7.6	80
30	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. *Nature Communications*, **2017**, 8, 14864	17.4	78

29	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. *Genome Research*, **2013**, 23, 431-9	9.7	77
28	Distinct patterns of mutations occurring in de novo AML versus AML arising in the setting of severe congenital neutropenia. *Blood*, **2007**, 110, 1648-55	2.2	77
27	Identification of somatic JAK1 mutations in patients with acute myeloid leukemia. *Blood*, **2008**, 111, 4809-12	9.1	75
26	Mutational analysis of EGFR and related signaling pathway genes in lung adenocarcinomas identifies a novel somatic kinase domain mutation in FGFR4. *PLoS ONE*, **2007**, 2, e426	3.7	73
25	Reduced PU.1 expression causes myeloid progenitor expansion and increased leukemia penetrance in mice expressing PML-RARalpha. *Proceedings of the National Academy of Sciences of the United States of America*, **2005**, 102, 12513-8	11.5	73
24	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
23	PolyScan: an automatic indel and SNP detection approach to the analysis of human resequencing data. *Genome Research*, **2007**, 17, 659-66	9.7	66
22	Systematic discovery of complex insertions and deletions in human cancers. *Nature Medicine*, **2016**, 22, 97-104	50.5	62
21	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. *Nature*, **2005**, 434, 724-31	50.4	61
20	Genome Modeling System: A Knowledge Management Platform for Genomics. *PLoS Computational Biology*, **2015**, 11, e1004274	5	59
19	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	26.6	56
18	A pilot study of high-throughput, sequence-based mutational profiling of primary human acute myeloid leukemia cell genomes. *Proceedings of the National Academy of Sciences of the United States of America*, **2003**, 100, 14275-80	11.5	50
17	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. *Bioinformatics*, **2010**, 26, 464-9	7.2	49
16	Re-sequencing expands our understanding of the phenotypic impact of variants at GWAS loci. *PLoS Genetics*, **2014**, 10, e1004147	6	42
15	Breast Cancer Neoantigens Can Induce CD8 T-Cell Responses and Antitumor Immunity. *Cancer Immunology Research*, **2017**, 5, 516-523	12.5	40
14	Clonal evolution revealed by whole genome sequencing in a case of primary myelofibrosis transformed to secondary acute myeloid leukemia. *Leukemia*, **2015**, 29, 869-76	10.7	38
13	Low frequency of telomerase RNA mutations among children with aplastic anemia or myelodysplastic syndrome. *Journal of Pediatric Hematology/Oncology*, **2006**, 28, 450-3	1.2	25
12	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. *Blood*, **2014**, 124, 3887-95	2.2	18

List of Publications

11	BreakTrans: uncovering the genomic architecture of gene fusions. *Genome Biology*, **2013**, 14, R87	18.3	18
10	Clinical outcomes and differential effects of PI3K pathway mutation in obese versus non-obese patients with cervical cancer. *Oncotarget*, **2018**, 9, 4061-4073	3.3	10
9	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
8	Optimized polyepitope neoantigen DNA vaccines elicit neoantigen-specific immune responses in preclinical models and in clinical translation. *Genome Medicine*, **2021**, 13, 56	14.4	9
7	BreakPoint Surveyor: a pipeline for structural variant visualization. *Bioinformatics*, **2017**, 33, 3121-3122	7.2	5
6	Pan-cancer analysis of somatic mutations across 21 neuroendocrine tumor types. *Cell Research*, **2018**, 28, 601-604	24.7	3
5	Clonal Evolution Revealed by Whole Genome Sequencing in a Case of Primary Myelofibrosis Transformed to Secondary Acute Myeloid Leukemia. *Blood*, **2012**, 120, 706-706	2.2	1
4	HPV-EM: an accurate HPV detection and genotyping EM algorithm. *Scientific Reports*, **2020**, 10, 14340	4.9	0
3	Somatic mutational profile of Merkel cell carcinoma treated with immune checkpoint blockade: Preliminary results from a planned multiplatform analysis.. *Journal of Clinical Oncology*, **2019**, 37, e21064-e21064	2.2	
2	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. *Blood*, **2009**, 114, 3965-3965	2.2	
1	Personalized DNA neoantigen vaccine in combination with plasmid IL-12 for the treatment of a patient with anaplastic astrocytoma.. *Journal of Clinical Oncology*, **2021**, 39, e14561-e14561	2.2	