Michael D Mclellan

List of Publications by Year
in descending order

102	109,838	7672 79	31191 106
papers	citations	h-index	g-index

110	110	110	129626
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Stem cell architecture drives myelodysplastic syndrome progression and predicts response to venetoclax-based therapy. Nature Medicine, 2022, 28, 557-567.	15.2	26
2	Optimized polyepitope neoantigen DNA vaccines elicit neoantigen-specific immune responses in preclinical models and in clinical translation. Genome Medicine, 2021, 13, 56.	3.6	34
3	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.	0.8	0
4	HPV transcript expression affects cervical cancer response to chemoradiation. JCI Insight, 2021, 6, .	2.3	12
5	HPV-EM: an accurate HPV detection and genotyping EM algorithm. Scientific Reports, 2020, 10, 14340.	1.6	3
6	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
7	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.	0.8	0
8	Pan-cancer analysis of somatic mutations across 21 neuroendocrine tumor types. Cell Research, 2018, 28, 601-604.	5.7	4
9	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
10	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
11	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
12	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
13	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	13.5	272
14	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	13.5	1,417
15	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
16	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	2.9	333
17	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
18	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205

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19	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	2.9	523
20	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	2.9	683
21	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. Cell Reports, 2018, 23, 172-180.e3.	2.9	119
22	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
23	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
24	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
25	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	2.9	177
26	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
27	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	2.9	284
28	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.	7.7	400
29	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
30	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	7.7	396
31	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-Î² Superfamily. Cell Systems, 2018, 7, 422-437.e7.	2.9	134
32	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
33	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	7.7	623
34	Clinical outcomes and differential effects of PI3K pathway mutation in obese versus non-obese patients with cervical cancer. Oncotarget, 2018, 9, 4061-4073.	0.8	14
35	Breast Cancer Neoantigens Can Induce CD8+ T-Cell Responses and Antitumor Immunity. Cancer Immunology Research, 2017, 5, 516-523.	1.6	74
36	Proteogenomic integration reveals therapeutic targets in breast cancer xenografts. Nature Communications, 2017, 8, 14864.	5.8	112

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37	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	2.9	416
38	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	13.5	738
39	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	1.8	5
40	Proteogenomics connects somatic mutations to signalling in breast cancer. Nature, 2016, 534, 55-62.	13.7	1,384
41	Protein-structure-guided discovery of functional mutations across 19 cancer types. Nature Genetics, 2016, 48, 827-837.	9.4	128
42	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	15.2	93
43	An Analysis of the Sensitivity of Proteogenomic Mapping of Somatic Mutations and Novel Splicing Events in Cancer. Molecular and Cellular Proteomics, 2016, 15, 1060-1071.	2.5	104
44	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.5	83
45	SMN2 splice modulators enhance U1â€“pre-mRNA association and rescue SMA mice. Nature Chemical Biology, 2015, 11, 511-517.	3.9	341
46	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	5.8	243
47	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	13.5	1,485
48	Pan-cancer network analysis identifies combinations of rare somatic mutations across pathways and protein complexes. Nature Genetics, 2015, 47, 106-114.	9.4	830
49	Clonal evolution revealed by whole genome sequencing in a case of primary myelofibrosis transformed to secondary acute myeloid leukemia. Leukemia, 2015, 29, 869-876.	3.3	44
50	Re-sequencing Expands Our Understanding of the Phenotypic Impact of Variants at GWAS Loci. PLoS Genetics, 2014, 10, e1004147.	1.5	50
51	Integrated analysis of germline and somatic variants in ovarian cancer. Nature Communications, 2014, 5, 3156.	5.8	253
52	MSIsensor: microsatellite instability detection using paired tumor-normal sequence data. Bioinformatics, 2014, 30, 1015-1016.	1.8	599
53	Age-related mutations associated with clonal hematopoietic expansion and malignancies. Nature Medicine, 2014, 20, 1472-1478.	15.2	1,533
54	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055

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55	Comprehensive molecular profiling of lung adenocarcinoma. Nature, 2014, 511, 543-550.	13.7	4,572
56	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
57	Caspase-9 is required for normal hematopoietic development and protection from alkylator-induced DNA damage in mice. Blood, 2014, 124, 3887-3895.	0.6	20
58	Identification of a pan-cancer oncogenic microRNA superfamily anchored by a central core seed motif. Nature Communications, 2013, 4, 2730.	5.8	104
59	Mutational landscape and significance across 12 major cancer types. Nature, 2013, 502, 333-339.	13.7	3,695
60	BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87.	13.9	25
61	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
62	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
63	Clonal diversity of recurrently mutated genes in myelodysplastic syndromes. Leukemia, 2013, 27, 1275-1282.	3.3	260
64	Somatic neurofibromatosis type 1 (NF1) inactivation characterizes NF1-associated pilocytic astrocytoma. Genome Research, 2013, 23, 431-439.	2.4	99
65	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	13.7	922
66	An integrated map of genetic variation from 1,092 human genomes. Nature, 2012, 491, 56-65.	13.7	7,199
67	Recurrent mutations in the U2AF1 splicing factor in myelodysplastic syndromes. Nature Genetics, 2012, 44, 53-57.	9.4	513
68	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	13.7	10,282
69	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	13.9	688
70	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	13.7	1,795
71	VarScan 2: Somatic mutation and copy number alteration discovery in cancer by exome sequencing. Genome Research, 2012, 22, 568-576.	2.4	4,086
72	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	13.5	1,365

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73	Clonal Evolution Revealed by Whole Genome Sequencing in a Case of Primary Myelofibrosis Transformed to Secondary Acute Myeloid Leukemia. Blood, 2012, 120, 706-706.	0.6	1
74	Integrated genomic analyses of ovarian carcinoma. Nature, 2011, 474, 609-615.	13.7	6,541
75	Recurrent DNMT3A mutations in patients with myelodysplastic syndromes. Leukemia, 2011, 25, 1153-1158.	3.3	483
76	Identification of a Novel <emph type="ital">TP53</emph> Cancer Susceptibility Mutation Through Whole-Genome Sequencing of a Patient With Therapy-Related AML. JAMA - Journal of the American Medical Association, 2011, 305, 1568.	3.8	146
77	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	3.9	91
78	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	13.7	1,077
79	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
80	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. Bioinformatics, 2010, 26, 464-469.	1.8	59
81	DNMT3AMutations in Acute Myeloid Leukemia. New England Journal of Medicine, 2010, 363, 2424-2433.	13.9	1,777
82	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	1.8	1,193
83	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	9.0	1,322
84	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	13.9	2,009
85	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, 12950-12955.	3.3	231
86	DNA Sequencing of a Murine Acute Promyelocytic Leukemia (APL) Genome Using Next Generation Technology.. Blood, 2009, 114, 3965-3965.	0.6	0
87	Comprehensive genomic characterization defines human glioblastoma genes and core pathways. Nature, 2008, 455, 1061-1068.	13.7	6,879
88	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	13.7	2,694
89	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	13.7	1,275
90	Identification of somatic JAK1 mutations in patients with acute myeloid leukemia. Blood, 2008, 111, 4809-4812.	0.6	84

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91	Novel MEK1 Mutation Identified by Mutational Analysis of Epidermal Growth Factor Receptor Signaling Pathway Genes in Lung Adenocarcinoma. Cancer Research, 2008, 68, 5524-5528.	0.4	206
92	Clinical and molecular delineation of the 17q21.31 microdeletion syndrome. Journal of Medical Genetics, 2008, 45, 710-720.	1.5	191
93	Somatic mutations and germline sequence variants in the expressed tyrosine kinase genes of patients with de novo acute myeloid leukemia. Blood, 2008, 111, 4797-4808.	0.6	198
94	PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data. Genome Research, 2007, 17, 659-666.	2.4	76
95	Distinct patterns of mutations occurring in de novo AML versus AML arising in the setting of severe congenital neutropenia. Blood, 2007, 110, 1648-1655.	0.6	88
96	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.	1.1	77
97	C-terminal truncations in human 3â€²-5â€² DNA exonuclease TREX1 cause autosomal dominant retinal vasculopathy with cerebral leukodystrophy. Nature Genetics, 2007, 39, 1068-1070.	9.4	366
98	Low Frequency of Telomerase RNA Mutations Among Children With Aplastic Anemia or Myelodysplastic Syndrome. Journal of Pediatric Hematology/Oncology, 2006, 28, 450-453.	0.3	27
99	Generation and annotation of the DNA sequences of human chromosomes 2 and 4. Nature, 2005, 434, 724-731.	13.7	85
100	Reduced PU.1 expression causes myeloid progenitor expansion and increased leukemia penetrance in mice expressing PML-RARÂ. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 12513-12518.	3.3	81
101	Comparison of genome degradation in Paratyphi A and Typhi, human-restricted serovars of Salmonella enterica that cause typhoid. Nature Genetics, 2004, 36, 1268-1274.	9.4	367
102	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, 14275-14280.	3.3	55