Michael R Stratton

List of Publications by Year
in descending order

113 papers	90,249 citations	3515 90 h-index	22102 113 g-index
134 all docs	134 docs citations	134 times ranked	79903 citing authors

#	Article	IF	Citations
1	Mutations of the BRAF gene in human cancer. Nature, 2002, 417, 949-954.	13.7	9,374
2	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
3	Identification of the breast cancer susceptibility gene BRCA2. Nature, 1995, 378, 789-792.	13.7	3,230
4	The cancer genome. Nature, 2009, 458, 719-724.	13.7	2,904
5	A census of human cancer genes. Nature Reviews Cancer, 2004, 4, 177-183.	12.8	2,868
6	Patterns of somatic mutation in human cancer genomes. Nature, 2007, 446, 153-158.	13.7	2,802
7	Genomics of Drug Sensitivity in Cancer (GDSC): a resource for therapeutic biomarker discovery in cancer cells. Nucleic Acids Research, 2012, 41, D955-D961.	6.5	2,363
8	Systematic identification of genomic markers of drug sensitivity in cancer cells. Nature, 2012, 483, 570-575.	13.7	2,173
9	International network of cancer genome projects. Nature, 2010, 464, 993-998.	13.7	2,114
10	The repertoire of mutational signatures in human cancer. Nature, 2020, 578, 94-101.	13.7	2,104
11	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. Nucleic Acids Research, 2015, 43, D805-D811.	6.5	2,096
12	Massive Genomic Rearrangement Acquired in a Single Catastrophic Event during Cancer Development. Cell, 2011, 144, 27-40.	13.5	2,020
13	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
14	Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. Science, 1994, 265, 2088-2090.	6.0	1,725
15	Prospective Derivation of a Living Organoid Biobank of Colorectal Cancer Patients. Cell, 2015, 161, 933-945.	13.5	1,710
16	Mutational Processes Molding the Genomes of 21 Breast Cancers. Cell, 2012, 149, 979-993.	13.5	1,673
17	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	0.6	1,562
18	The landscape of cancer genes and mutational processes in breast cancer. Nature, 2012, 486, 400-404.	13.7	1,535

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19	A comprehensive catalogue of somatic mutations from a human cancer genome. Nature, 2010, 463, 191-196.	13.7	1,519
20	A Landscape of Pharmacogenomic Interactions in Cancer. Cell, 2016, 166, 740-754.	13.5	1,518
21	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	6.0	1,431
22	Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. Nature Genetics, 2015, 47, 505-511.	9.4	1,372
23	The Life History of 21 Breast Cancers. Cell, 2012, 149, 994-1007.	13.5	1,249
24	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. Nature, 2010, 467, 1109-1113.	13.7	1,200
25	JAK2Exon 12 Mutations in Polycythemia Vera and Idiopathic Erythrocytosis. New England Journal of Medicine, 2007, 356, 459-468.	13.9	1,173
26	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. Nature, 2011, 469, 539-542.	13.7	1,127
27	Deciphering Signatures of Mutational Processes Operative in Human Cancer. Cell Reports, 2013, 3, 246-259.	2.9	1,087
28	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	13.5	1,085
29	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. Nature, 2010, 463, 360-363.	13.7	1,062
30	A small-cell lung cancer genome with complex signatures of tobacco exposure. Nature, 2010, 463, 184-190.	13.7	972
31	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
32	Clock-like mutational processes in human somatic cells. Nature Genetics, 2015, 47, 1402-1407.	9.4	837
33	Somatic mutant clones colonize the human esophagus with age. Science, 2018, 362, 911-917.	6.0	805
34	Complex landscapes of somatic rearrangement in human breast cancer genomes. Nature, 2009, 462, 1005-1010.	13.7	776
35	Tissue-specific mutation accumulation in human adult stem cells during life. Nature, 2016, 538, 260-264.	13.7	759
36	Intragenic ERBB2 kinase mutations in tumours. Nature, 2004, 431, 525-526.	13.7	757

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37	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. Nature Genetics, 2008, 40, 722-729.	9.4	736
38	Somatic mutations of the histone H3K27 demethylase gene UTX in human cancer. Nature Genetics, 2009, 41, 521-523.	9.4	734
39	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	15.2	711
40	Signatures of mutation and selection in the cancer genome. Nature, 2010, 463, 893-898.	13.7	661
41	Exploring the Genomes of Cancer Cells: Progress and Promise. Science, 2011, 331, 1553-1558.	6.0	606
42	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	7.7	534
43	Timing, rates and spectra of human germline mutation. Nature Genetics, 2016, 48, 126-133.	9.4	502
44	A census of amplified and overexpressed human cancer genes. Nature Reviews Cancer, 2010, 10, 59-64.	12.8	480
45	The landscape of somatic mutation in normal colorectal epithelial cells. Nature, 2019, 574, 532-537.	13.7	468
46	Somatic Mutations of the Protein Kinase Gene Family in Human Lung Cancer. Cancer Research, 2005, 65, 7591-7595.	0.4	429
47	Population dynamics of normal human blood inferred from somatic mutations. Nature, 2018, 561, 473-478.	13.7	427
48	Intra-tumour diversification in colorectal cancer at the single-cell level. Nature, 2018, 556, 457-462.	13.7	406
49	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. Cell, 2016, 167, 1145-1149.	13.5	404
50	Mutational signatures: the patterns of somatic mutations hidden in cancer genomes. Current Opinion in Genetics and Development, 2014, 24, 52-60.	1.5	393
51	Loss of the Mismatch Repair Protein MSH6 in Human Glioblastomas Is Associated with Tumor Progression during Temozolomide Treatment. Clinical Cancer Research, 2007, 13, 2038-2045.	3.2	384
52	A Hypermutation Phenotype and Somatic MSH6 Mutations in Recurrent Human Malignant Gliomas after Alkylator Chemotherapy. Cancer Research, 2006, 66, 3987-3991.	0.4	383
53	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. Molecular Cancer Therapeutics, 2006, 5, 2606-2612.	1.9	374
54	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348

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55	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	13.7	338
56	Tobacco smoking and somatic mutations in human bronchial epithelium. Nature, 2020, 578, 266-272.	13.7	336
57	DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis. ELife, 2013, 2, e00534.	2.8	322
58	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 13081-13086.	3.3	320
59	High-Resolution Analysis of DNA Copy Number Using Oligonucleotide Microarrays. Genome Research, 2004, 14, 287-295.	2.4	319
60	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. Nature Genetics, 2005, 37, 590-592.	9.4	318
61	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
62	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	13.7	315
63	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. Cell, 2019, 176, 1282-1294.e20.	13.5	298
64	Alcohol and endogenous aldehydes damage chromosomes and mutate stem cells. Nature, 2018, 553, 171-177.	13.7	284
65	Genomics and the Continuum of Cancer Care. New England Journal of Medicine, 2011, 364, 340-350.	13.9	282
66	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. Nature, 2014, 508, 98-102.	13.7	261
67	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. Nature Genetics, 2014, 46, 487-491.	9.4	254
68	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	13.7	254
69	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. Nature, 2019, 574, 538-542.	13.7	251
70	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. Nature Genetics, 2021, 53, 1698-1711.	9.4	238
71	The topography of mutational processes in breast cancer genomes. Nature Communications, 2016, 7, 11383.	5.8	235
72	Genome-Wide Mutational Signatures of Aristolochic Acid and Its Application as a Screening Tool. Science Translational Medicine, 2013, 5, 197ra101.	5.8	233

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73	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
74	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	13.7	211
75	The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. Nature Communications, 2018, 9, 3667.	5.8	208
76	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	6.0	195
77	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. Genome Research, 2007, 17, 1296-1303.	2.4	180
78	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	13.7	180
79	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. Nature Communications, 2017, 8, 15936.	5.8	179
80	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. Nature Communications, 2016, 7, 10767.	5.8	177
81	The genome as a record of environmental exposure. Mutagenesis, 2015, 30, gev073.	1.0	174
82	Use of cancerâ€specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. Genes Chromosomes and Cancer, 2010, 49, 1062-1069.	1.5	172
83	C. elegans whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. Genome Research, 2014, 24, 1624-1636.	2.4	164
84	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. BMC Genomics, 2019, 20, 685.	1.2	162
85	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	13.7	160
86	Statistical Analysis of Pathogenicity of Somatic Mutations in Cancer. Genetics, 2006, 173, 2187-2198.	1.2	146
87	A mutational signature in gastric cancer suggests therapeutic strategies. Nature Communications, 2015, 6, 8683.	5.8	146
88	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	6.0	144
89	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. Nucleic Acids Research, 2013, 41, 6119-6138.	6.5	142
90	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	13.5	122

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91	Embryonal precursors of Wilms tumor. Science, 2019, 366, 1247-1251.	6.0	101
92	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	13.7	87
93	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	13.7	87
94	Processed pseudogenes acquired somatically during cancer development. Nature Communications, 2014, 5, 3644.	5.8	86
95	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	9.4	85
96	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. Nature Communications, 2017, 8, 1221.	5.8	75
97	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. Nature Genetics, 2021, 53, 1553-1563.	9.4	71
98	Genome resequencing and genetic variation. Nature Biotechnology, 2008, 26, 65-66.	9.4	63
99	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	6.0	58
100	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. Nature Communications, 2019, 10, 1749.	5.8	46
101	Functional patient-derived organoid screenings identify MCLA-158 as a therapeutic EGFR Ã— LGR5 bispecific antibody with efficacy in epithelial tumors. Nature Cancer, 2022, 3, 418-436.	5.7	46
102	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. Cell Reports, 2016, 16, 2032-2046.	2.9	36
103	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	5.8	30
104	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
105	Journeys into the genome of cancer cells. EMBO Molecular Medicine, 2013, 5, 169-172.	3.3	27
106	Short inverted repeats contribute to localized mutability in human somatic cells. Nucleic Acids Research, 2017, 45, 11213-11221.	6.5	26
107	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. Cell Stem Cell, 2020, 27, 326-335.e4.	5.2	25
108	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. PLoS Biology, 2020, 18, e3000926.	2.6	23

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109	Mutagenicity of acrylamide and glycidamide in human TP53 knock-in (Hupki) mouse embryo fibroblasts. Archives of Toxicology, 2020, 94, 4173-4196.	1.9	21
110	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	5.8	19
111	In vitro differential sensitivity of melanomas to phenothiazines is based on the presence of codon 600 BRAF mutation. Molecular Cancer Therapeutics, 2008, 7, 1337-1346.	1.9	14
112	Mutagenicity of 2-hydroxyamino-1-methyl-6-phenylimidazo[4,5-b]pyridine (Nâ€“OH-PhIP) in human TP53 knock-in (Hupki) mouse embryo fibroblasts. Food and Chemical Toxicology, 2021, 147, 111855.	1.8	4
113	Abstract 970: The mutational landscape of normal human endometrial epithelium. , 2019, , .		4