

Michael R Stratton

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127
papers

67,304
citations

82
h-index

134
g-index

134
ext. papers

81,361
ext. citations

32.2
avg, IF

7.03
L-index

#	Paper	IF	Citations
127	Mutations of the BRAF gene in human cancer. <i>Nature</i> , 2002 , 417, 949-54	50.4	7962
126	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013 , 500, 415-21	50.4	5895
125	Identification of the breast cancer susceptibility gene BRCA2. <i>Nature</i> , 1995 , 378, 789-92	50.4	2780
124	A census of human cancer genes. <i>Nature Reviews Cancer</i> , 2004 , 4, 177-83	31.3	2424
123	Patterns of somatic mutation in human cancer genomes. <i>Nature</i> , 2007 , 446, 153-8	50.4	2400
122	The cancer genome. <i>Nature</i> , 2009 , 458, 719-24	50.4	2272
121	COSMIC: exploring the world's knowledge of somatic mutations in human cancer. <i>Nucleic Acids Research</i> , 2015 , 43, D805-11	20.1	1795
120	Systematic identification of genomic markers of drug sensitivity in cancer cells. <i>Nature</i> , 2012 , 483, 570-5	50.4	1699
119	Massive genomic rearrangement acquired in a single catastrophic event during cancer development. <i>Cell</i> , 2011 , 144, 27-40	56.2	1628
118	International network of cancer genome projects. <i>Nature</i> , 2010 , 464, 993-8	50.4	1613
117	Localization of a breast cancer susceptibility gene, BRCA2, to chromosome 13q12-13. <i>Science</i> , 1994 , 265, 2088-90	33.3	1480
116	A comprehensive catalogue of somatic mutations from a human cancer genome. <i>Nature</i> , 2010 , 463, 191-5	50.4	1303
115	Mutational processes molding the genomes of 21 breast cancers. <i>Cell</i> , 2012 , 149, 979-93	56.2	1279
114	The landscape of cancer genes and mutational processes in breast cancer. <i>Nature</i> , 2012 , 486, 400-4	50.4	1264
113	Prospective derivation of a living organoid biobank of colorectal cancer patients. <i>Cell</i> , 2015 , 161, 933-45	56.2	1215
112	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016 , 534, 47-54	50.4	1193
111	Clinical and biological implications of driver mutations in myelodysplastic syndromes. <i>Blood</i> , 2013 , 122, 3616-27; quiz 3699	2.2	1169

110	Genomics of Drug Sensitivity in Cancer (GDSC): a resource for therapeutic biomarker discovery in cancer cells. <i>Nucleic Acids Research</i> , 2013 , 41, D955-61	20.1	1163
109	The patterns and dynamics of genomic instability in metastatic pancreatic cancer. <i>Nature</i> , 2010 , 467, 1109-13	50.4	1013
108	JAK2 exon 12 mutations in polycythemia vera and idiopathic erythrocytosis. <i>New England Journal of Medicine</i> , 2007 , 356, 459-68	59.2	996
107	Tumor evolution. High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015 , 348, 880-6	33.3	983
106	The life history of 21 breast cancers. <i>Cell</i> , 2012 , 149, 994-1007	56.2	979
105	Exome sequencing of hepatocellular carcinomas identifies new mutational signatures and potential therapeutic targets. <i>Nature Genetics</i> , 2015 , 47, 505-511	36.3	956
104	Exome sequencing identifies frequent mutation of the SWI/SNF complex gene PBRM1 in renal carcinoma. <i>Nature</i> , 2011 , 469, 539-42	50.4	943
103	Systematic sequencing of renal carcinoma reveals inactivation of histone modifying genes. <i>Nature</i> , 2010 , 463, 360-3	50.4	927
102	A Landscape of Pharmacogenomic Interactions in Cancer. <i>Cell</i> , 2016 , 166, 740-754	56.2	892
101	A small-cell lung cancer genome with complex signatures of tobacco exposure. <i>Nature</i> , 2010 , 463, 184-90	50.4	852
100	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020 , 578, 94-101	50.4	849
99	Deciphering signatures of mutational processes operative in human cancer. <i>Cell Reports</i> , 2013 , 3, 246-59	10.6	725
98	Complex landscapes of somatic rearrangement in human breast cancer genomes. <i>Nature</i> , 2009 , 462, 1005-10	50.4	684
97	Identification of somatically acquired rearrangements in cancer using genome-wide massively parallel paired-end sequencing. <i>Nature Genetics</i> , 2008 , 40, 722-9	36.3	666
96	Lung cancer: intragenic ERBB2 kinase mutations in tumours. <i>Nature</i> , 2004 , 431, 525-6	50.4	655
95	Somatic mutations of the histone H3K27 demethylase gene UTX in human cancer. <i>Nature Genetics</i> , 2009 , 41, 521-3	36.3	627
94	Universal Patterns of Selection in Cancer and Somatic Tissues. <i>Cell</i> , 2017 , 171, 1029-1041.e21	56.2	576
93	Mutational signatures associated with tobacco smoking in human cancer. <i>Science</i> , 2016 , 354, 618-622	33.3	562

92	Signatures of mutation and selection in the cancer genome. <i>Nature</i> , 2010 , 463, 893-8	50.4	538
91	Clock-like mutational processes in human somatic cells. <i>Nature Genetics</i> , 2015 , 47, 1402-7	36.3	531
90	Tissue-specific mutation accumulation in human adult stem cells during life. <i>Nature</i> , 2016 , 538, 260-264	50.4	523
89	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. <i>Nature Medicine</i> , 2015 , 21, 751-9	50.5	521
88	Exploring the genomes of cancer cells: progress and promise. <i>Science</i> , 2011 , 331, 1553-8	33.3	488
87	Somatic mutant clones colonize the human esophagus with age. <i>Science</i> , 2018 , 362, 911-917	33.3	465
86	A census of amplified and overexpressed human cancer genes. <i>Nature Reviews Cancer</i> , 2010 , 10, 59-64	31.3	415
85	Somatic mutations of the protein kinase gene family in human lung cancer. <i>Cancer Research</i> , 2005 , 65, 7591-5	10.1	392
84	Genomic Evolution of Breast Cancer Metastasis and Relapse. <i>Cancer Cell</i> , 2017 , 32, 169-184.e7	24.3	346
83	Timing, rates and spectra of human germline mutation. <i>Nature Genetics</i> , 2016 , 48, 126-133	36.3	338
82	A hypermutation phenotype and somatic MSH6 mutations in recurrent human malignant gliomas after alkylator chemotherapy. <i>Cancer Research</i> , 2006 , 66, 3987-91	10.1	328
81	Mutation analysis of 24 known cancer genes in the NCI-60 cell line set. <i>Molecular Cancer Therapeutics</i> , 2006 , 5, 2606-12	6.1	322
80	Loss of the mismatch repair protein MSH6 in human glioblastomas is associated with tumor progression during temozolomide treatment. <i>Clinical Cancer Research</i> , 2007 , 13, 2038-45	12.9	318
79	Mutational signatures: the patterns of somatic mutations hidden in cancer genomes. <i>Current Opinion in Genetics and Development</i> , 2014 , 24, 52-60	4.9	299
78	Intra-tumour diversification in colorectal cancer at the single-cell level. <i>Nature</i> , 2018 , 556, 457-462	50.4	294
77	A screen of the complete protein kinase gene family identifies diverse patterns of somatic mutations in human breast cancer. <i>Nature Genetics</i> , 2005 , 37, 590-2	36.3	289
76	High-resolution analysis of DNA copy number using oligonucleotide microarrays. <i>Genome Research</i> , 2004 , 14, 287-95	9.7	288
75	Subclonal phylogenetic structures in cancer revealed by ultra-deep sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 13081-6	11.5	283

74	Mobile DNA in cancer. Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014 , 345, 1251343	33.3	250
73	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014 , 513, 422-425	50.4	249
72	Genomics and the continuum of cancer care. <i>New England Journal of Medicine</i> , 2011 , 364, 340-50	59.2	247
71	DNA deaminases induce break-associated mutation showers with implication of APOBEC3B and 3A in breast cancer kataegis. <i>ELife</i> , 2013 , 2, e00534	8.9	246
70	Population dynamics of normal human blood inferred from somatic mutations. <i>Nature</i> , 2018 , 561, 473-478	58.4	245
69	The International Human Epigenome Consortium: A Blueprint for Scientific Collaboration and Discovery. <i>Cell</i> , 2016 , 167, 1145-1149	56.2	232
68	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , 2014 , 3,	8.9	229
67	The landscape of somatic mutation in normal colorectal epithelial cells. <i>Nature</i> , 2019 , 574, 532-537	50.4	217
66	Association of a germline copy number polymorphism of APOBEC3A and APOBEC3B with burden of putative APOBEC-dependent mutations in breast cancer. <i>Nature Genetics</i> , 2014 , 46, 487-91	36.3	208
65	Genome-wide mutational signatures of aristolochic acid and its application as a screening tool. <i>Science Translational Medicine</i> , 2013 , 5, 197ra101	17.5	194
64	Constitutional and somatic rearrangement of chromosome 21 in acute lymphoblastic leukaemia. <i>Nature</i> , 2014 , 508, 98-102	50.4	192
63	Alcohol and endogenous aldehydes damage chromosomes and mutate stem cells. <i>Nature</i> , 2018 , 553, 171-177	50.4	183
62	The topography of mutational processes in breast cancer genomes. <i>Nature Communications</i> , 2016 , 7, 11383	17.4	172
61	Characterizing Mutational Signatures in Human Cancer Cell Lines Reveals Episodic APOBEC Mutagenesis. <i>Cell</i> , 2019 , 176, 1282-1294.e20	56.2	165
60	Use of cancer-specific genomic rearrangements to quantify disease burden in plasma from patients with solid tumors. <i>Genes Chromosomes and Cancer</i> , 2010 , 49, 1062-9	5	161
59	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017 , 543, 714-718	50.4	157
58	Architectures of somatic genomic rearrangement in human cancer amplicons at sequence-level resolution. <i>Genome Research</i> , 2007 , 17, 1296-303	9.7	152
57	Tobacco smoking and somatic mutations in human bronchial epithelium. <i>Nature</i> , 2020 , 578, 266-272	50.4	150

56	The mutational landscape of normal human endometrial epithelium. <i>Nature</i> , 2020 , 580, 640-646	50.4	148
55	Mutation allele burden remains unchanged in chronic myelomonocytic leukaemia responding to hypomethylating agents. <i>Nature Communications</i> , 2016 , 7, 10767	17.4	140
54	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017 , 8, 15936	17.4	125
53	Single-cell paired-end genome sequencing reveals structural variation per cell cycle. <i>Nucleic Acids Research</i> , 2013 , 41, 6119-38	20.1	125
52	<i>C. elegans</i> whole-genome sequencing reveals mutational signatures related to carcinogens and DNA repair deficiency. <i>Genome Research</i> , 2014 , 24, 1624-36	9.7	125
51	Statistical analysis of pathogenicity of somatic mutations in cancer. <i>Genetics</i> , 2006 , 173, 2187-98	4	125
50	The genomic landscape of cutaneous SCC reveals drivers and a novel azathioprine associated mutational signature. <i>Nature Communications</i> , 2018 , 9, 3667	17.4	121
49	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. <i>Nature</i> , 2019 , 574, 538-542	50.4	120
48	Transmissible [corrected] dog cancer genome reveals the origin and history of an ancient cell lineage. <i>Science</i> , 2014 , 343, 437-440	33.3	116
47	The genome as a record of environmental exposure. <i>Mutagenesis</i> , 2015 , 30, 763-70	2.8	115
46	A mutational signature in gastric cancer suggests therapeutic strategies. <i>Nature Communications</i> , 2015 , 6, 8683	17.4	103
45	Processed pseudogenes acquired somatically during cancer development. <i>Nature Communications</i> , 2014 , 5, 3644	17.4	68
44	Extensive heterogeneity in somatic mutation and selection in the human bladder. <i>Science</i> , 2020 , 370, 75-82	33.3	67
43	The Repertoire of Mutational Signatures in Human Cancer		67
42	Somatic mutation landscapes at single-molecule resolution. <i>Nature</i> , 2021 , 593, 405-410	50.4	57
41	SigProfilerMatrixGenerator: a tool for visualizing and exploring patterns of small mutational events. <i>BMC Genomics</i> , 2019 , 20, 685	4.5	56
40	Genome resequencing and genetic variation. <i>Nature Biotechnology</i> , 2008 , 26, 65-6	44.5	50
39	Somatic Evolution in Non-neoplastic IBD-Affected Colon. <i>Cell</i> , 2020 , 182, 672-684.e11	56.2	50

38	Pan-cancer analysis of homozygous deletions in primary tumours uncovers rare tumour suppressors. <i>Nature Communications</i> , 2017 , 8, 1221	17.4	40
37	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019 , 366, 1247-1251	33.3	40
36	Mapping the temporal and spatial dynamics of the human endometrium in vivo and in vitro. <i>Nature Genetics</i> , 2021 , 53, 1698-1711	36.3	32
35	The mutational landscape of human somatic and germline cells. <i>Nature</i> , 2021 , 597, 381-386	50.4	32
34	Somatic evolution and global expansion of an ancient transmissible cancer lineage. <i>Science</i> , 2019 , 365,	33.3	31
33	Direct Transcriptional Consequences of Somatic Mutation in Breast Cancer. <i>Cell Reports</i> , 2016 , 16, 2032-46.6	46.6	30
32	Journeys into the genome of cancer cells. <i>EMBO Molecular Medicine</i> , 2013 , 5, 169-72	12	21
31	Extensive phylogenies of human development inferred from somatic mutations. <i>Nature</i> , 2021 , 597, 387-392	39.2	21
30	Partially methylated domains are hypervariable in breast cancer and fuel widespread CpG island hypermethylation. <i>Nature Communications</i> , 2019 , 10, 1749	17.4	19
29	Uncovering novel mutational signatures by de novo extraction with SigProfilerExtractor		17
28	The landscape of somatic mutation in normal colorectal epithelial cells		14
27	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. <i>Nature Genetics</i> , 2021 , 53, 1434-1442	36.3	13
26	Mutational signatures in esophageal squamous cell carcinoma from eight countries with varying incidence. <i>Nature Genetics</i> , 2021 , 53, 1553-1563	36.3	12
25	Short inverted repeats contribute to localized mutability in human somatic cells. <i>Nucleic Acids Research</i> , 2017 , 45, 11213-11221	20.1	11
24	Tissue-Biased Expansion of DNMT3A-Mutant Clones in a Mosaic Individual Is Associated with Conserved Epigenetic Erosion. <i>Cell Stem Cell</i> , 2020 , 27, 326-335.e4	18	11
23	In vitro differential sensitivity of melanomas to phenothiazines is based on the presence of codon 600 BRAF mutation. <i>Molecular Cancer Therapeutics</i> , 2008 , 7, 1337-46	6.1	10
22	Evolution and lineage dynamics of a transmissible cancer in Tasmanian devils. <i>PLoS Biology</i> , 2020 , 18, e3000926	9.7	10
21	Convergent somatic mutations in metabolism genes in chronic liver disease. <i>Nature</i> , 2021 , 598, 473-478	50.4	10

20	Elevated somatic mutation burdens in normal human cells due to defective DNA polymerases		10
19	The mutational landscape of normal human endometrial epithelium		9
18	Mutagenicity of acrylamide and glycidamide in human TP53 knock-in (Hupki) mouse embryo fibroblasts. <i>Archives of Toxicology</i> , 2020 , 94, 4173-4196	5.8	9
17	Somatic mutation rates scale with lifespan across mammals.. <i>Nature</i> , 2022 ,	50.4	9
16	Universal patterns of selection in cancer and somatic tissues		7
15	Development, maturation, and maintenance of human prostate inferred from somatic mutations. <i>Cell Stem Cell</i> , 2021 , 28, 1262-1274.e5	18	7
14	Clonal dynamics of haematopoiesis across the human lifespan. <i>Nature</i> ,	50.4	7
13	Life without mismatch repair		6
12	The mutational landscape of human somatic and germline cells		5
11	Abstract 970: The mutational landscape of normal human endometrial epithelium 2019 ,		4
10	Mutational signatures associated with tobacco smoking in human cancer		4
9	Somatic mutation rates scale with lifespan across mammals		4
8	Mutagenicity of 2-hydroxyamino-1-methyl-6-phenylimidazo[4,5-b]pyridine (N-OH-PhIP) in human TP53 knock-in (Hupki) mouse embryo fibroblasts. <i>Food and Chemical Toxicology</i> , 2021 , 147, 111855	4.7	3
7	The APOBEC3A deaminase drives episodic mutagenesis in cancer cells		3
6	Mutational signatures in esophageal squamous cell carcinoma from eight countries of varying incidence		2
5	Clonal dynamics of haematopoiesis across the human lifespan		2
4	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells		1
3	Comprehensive Analysis of Indels in Whole-genome Microsatellite Regions and Microsatellite Instability across 21 Cancer Types		1

2 Extensive phylogenies of human development reveal variable embryonic patterns 1

1 Mutational landscape of normal epithelial cells in Lynch Syndrome patients.. *Nature Communications*, 2022, 13, 2710 17.4 1