Matthew H Bailey

List of Publications by Year in Descending Order

54 papers	10,904 citations	36 h-index	59 g-index
59 ext. papers	16,566 ext. citations	19.8 avg, IF	3.81 L-index

#	Paper	IF	Citations
54	A human breast cancer-derived xenograft and organoid platform for drug discovery and precision oncology.. *Nature Cancer*, **2022**, 3, 232-250	15.4	13
53	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. *Nature Genetics*, **2021**, 53, 86-99	36.3	44
52	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidatesfor targeted treatment. *Nature Communications*, **2021**, 12, 5086	17.4	6
51	Moving pan-cancer studies from basic research toward the clinic.. *Nature Cancer*, **2021**, 2, 879-890	15.4	6
50	Discovery of driver non-coding splice-site-creating mutations in cancer. *Nature Communications*, **2020**, 11, 5573	17.4	8
49	Interpreting pathways to discover cancer driver genes with Moonlight. *Nature Communications*, **2020**, 11, 69	17.4	23
48	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. *Nature Communications*, **2020**, 11, 4748	17.4	10
47	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data CommonsaData. *Cell Systems*, **2019**, 9, 24-34.e10	10.6	64
46	Pan-cancer analysis of somatic mutations across 21 neuroendocrine tumor types. *Cell Research*, **2018**, 28, 601-604	24.7	3
45	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. *Cell*, **2018**, 173, 400-416.e11	56.2	1072
44	Comprehensive Characterization of Cancer Driver Genes and Mutations. *Cell*, **2018**, 173, 371-385.e18	56.2	854
43	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
42	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. *Cell*, **2018**, 173, 386-399.e12	56.2	133
41	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. *Cell*, **2018**, 173, 305-320.e10	56.2	166
40	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. *Cell*, **2018**, 173, 338-354.e15	56.2	560
39	Oncogenic Signaling Pathways in The Cancer Genome Atlas. *Cell*, **2018**, 173, 321-337.e10	56.2	1124
38	Pathogenic Germline Variants in 10,389 Adult Cancers. *Cell*, **2018**, 173, 355-370.e14	56.2	342

37	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
36	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. *Cell Reports*, **2018**, 23, 227-238.e3	10.6	235
35	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
34	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. *Cell Reports*, **2018**, 23, 313-326.e5	10.6	295
33	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
32	Machine Learning Detects Pan-cancer Ras Pathway Activation in The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 172-180.e3	10.6	66
31	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. *Cell Reports*, **2018**, 23, 213-226.e3	10.6	56
30	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. *Cell Reports*, **2018**, 23, 239-254.e6	10.6	405
29	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. *Cell Reports*, **2018**, 23, 255-269.e4	10.6	112
28	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. *Cell Reports*, **2018**, 23, 270-281.e3	10.6	121
27	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. *Cell Systems*, **2018**, 6, 271-281.e7	10.6	320
26	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
25	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
24	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. *Cancer Cell*, **2018**, 33, 676-689.e3	24.3	377
23	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. *Cancer Cell*, **2018**, 33, 721-735.e8	24.3	228
22	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. *Cancer Cell*, **2018**, 33, 690-705.e9	24.3	277
21	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. *Cancer Cell*, **2018**, 34, 211-224.e6	24.3	327
20	Integrative omics analyses broaden treatment targets in human cancer. *Genome Medicine*, **2018**, 10, 60	14.4	13

19	Characteristics of The Cancer Genome Atlas cases relative to U.S. general population cancer cases. *British Journal of Cancer*, **2018**, 119, 885-892	8.7	6
18	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
17	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. *Cell Reports*, **2018**, 25, 1304-1317.e5	10.6	152
16	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. *Cell*, **2017**, 171, 950-965.e28	56.2	451
15	Variants in ACPP are associated with cerebrospinal fluid Prostatic Acid Phosphatase levels. *BMC Genomics*, **2016**, 17 Suppl 3, 439	4.5	1
14	Variants in CCL16 are associated with blood plasma and cerebrospinal fluid CCL16 protein levels. *BMC Genomics*, **2016**, 17 Suppl 3, 437	4.5	1
13	Protein-structure-guided discovery of functional mutations across 19 cancer types. *Nature Genetics*, **2016**, 48, 827-37	36.3	88
12	Genetic studies of plasma analytes identify novel potential biomarkers for several complex traits. *Scientific Reports*, **2016**, 6,	4.9	20
11	Genome-wide association study of prolactin levels in blood plasma and cerebrospinal fluid. *BMC Genomics*, **2016**, 17 Suppl 3, 436	4.5	2
10	Mitochondrial genomic variation associated with higher mitochondrial copy number: the Cache County Study on Memory Health and Aging. *BMC Bioinformatics*, **2014**, 15 Suppl 7, S6	3.6	13
9	Population substructure in Cache County, Utah: the Cache County study. *BMC Bioinformatics*, **2014**, 15 Suppl 7, S8	3.6	7
8	Genome-wide association study of CSF levels of 59 alzheimeras disease candidate proteins: significant associations with proteins involved in amyloid processing and inflammation. *PLoS Genetics*, **2014**, 10, e1004758	6	84
7	Identification of specific Y chromosomes associated with increased prostate cancer risk. *Prostate*, **2014**, 74, 991-8	4.2	9
6	A versatile omnibus test for detecting mean and variance heterogeneity. *Genetic Epidemiology*, **2014**, 38, 51-59	2.6	33
5	Population-based analysis of Alzheimeras disease risk alleles implicates genetic interactions. *Biological Psychiatry*, **2014**, 75, 732-7	7.9	43
4	GWAS of cerebrospinal fluid tau levels identifies risk variants for Alzheimeras disease. *Neuron*, **2013**, 78, 256-68	13.9	255
3	Mitochondrial haplotypes associated with biomarkers for Alzheimeras disease. *PLoS ONE*, **2013**, 8, e74158	3.7	26
2	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts	2	

List of Publications