

Barry S Taylor

List of Publications by Year in descending order

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Version: 2024-02-01

118
papers

30,277
citations

20797

60
h-index

22147

113
g-index

127
all docs

127
docs citations

127
times ranked

42430
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrative Genomic Profiling of Human Prostate Cancer. <i>Cancer Cell</i> , 2010, 18, 11-22.	7.7	3,151
2	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. <i>Nature Medicine</i> , 2017, 23, 703-713.	15.2	2,473
3	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
4	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
5	OncoKB: A Precision Oncology Knowledge Base. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	1.5	1,266
6	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. <i>Science</i> , 2014, 343, 189-193.	6.0	1,147
7	deconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. <i>Genome Biology</i> , 2016, 17, 31.	3.8	917
8	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018, 23, 239-254.e6.	2.9	801
9	Genome Sequencing Identifies a Basis for Everolimus Sensitivity. <i>Science</i> , 2012, 338, 221-221.	6.0	681
10	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. <i>Nature Biotechnology</i> , 2016, 34, 155-163.	9.4	634
11	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. <i>Cancer Cell</i> , 2018, 34, 427-438.e6.	7.7	633
12	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	13.5	620
13	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
14	The long tail of oncogenic drivers in prostate cancer. <i>Nature Genetics</i> , 2018, 50, 645-651.	9.4	601
15	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. <i>Cancer Cell</i> , 2018, 33, 125-136.e3.	7.7	589
16	HER kinase inhibition in patients with HER2- and HER3-mutant cancers. <i>Nature</i> , 2018, 554, 189-194.	13.7	572
17	Tumor Evolution and Drug Response in Patient-Derived Organoid Models of Bladder Cancer. <i>Cell</i> , 2018, 173, 515-528.e17.	13.5	540
18	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. <i>Cancer Discovery</i> , 2017, 7, 596-609.	7.7	490

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19	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
20	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. <i>JAMA Oncology</i> , 2019, 5, 471.	3.4	426
21	Genome doubling shapes the evolution and prognosis of advanced cancers. <i>Nature Genetics</i> , 2018, 50, 1189-1195.	9.4	411
22	Implementing Genome-Driven Oncology. <i>Cell</i> , 2017, 168, 584-599.	13.5	405
23	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. <i>Journal of Clinical Oncology</i> , 2019, 37, 286-295.	0.8	397
24	Tumours with class 3 BRAF mutants are sensitive to the inhibition of activated RAS. <i>Nature</i> , 2017, 548, 234-238.	13.7	394
25	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. <i>Cancer Discovery</i> , 2016, 6, 154-165.	7.7	372
26	A Next-Generation TRK Kinase Inhibitor Overcomes Acquired Resistance to Prior TRK Kinase Inhibition in Patients with TRK Fusion-Positive Solid Tumors. <i>Cancer Discovery</i> , 2017, 7, 963-972.	7.7	331
27	Copy number alteration burden predicts prostate cancer relapse. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 11139-11144.	3.3	299
28	Tumour lineage shapes BRCA-mediated phenotypes. <i>Nature</i> , 2019, 571, 576-579.	13.7	295
29	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. <i>JCO Precision Oncology</i> , 2017, 2017, 1-16.	1.5	286
30	Accelerating Discovery of Functional Mutant Alleles in Cancer. <i>Cancer Discovery</i> , 2018, 8, 174-183.	7.7	275
31	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. <i>Cancer Discovery</i> , 2018, 8, 49-58.	7.7	275
32	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. <i>Lancet Oncology</i> , The, 2020, 21, 821-831.	5.1	243
33	AKT Inhibition in Solid Tumors With <i>AKT1</i> Mutations. <i>Journal of Clinical Oncology</i> , 2017, 35, 2251-2259.	0.8	240
34	Recurrent activating mutations of G-protein-coupled receptor <i>CYSLTR2</i> in uveal melanoma. <i>Nature Genetics</i> , 2016, 48, 675-680.	9.4	236
35	DNA Methylation and Somatic Mutations Converge on the Cell Cycle and Define Similar Evolutionary Histories in Brain Tumors. <i>Cancer Cell</i> , 2015, 28, 307-317.	7.7	221
36	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. <i>ELife</i> , 2018, 7, .	2.8	217

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37	Double <i>PIK3CA</i> mutations in cis increase oncogenicity and sensitivity to PI3K inhibitors. <i>Science</i> , 2019, 366, 714-723.	6.0	185
38	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. <i>Genome Medicine</i> , 2017, 9, 4.	3.6	170
39	Clonal Relatedness and Mutational Differences between Upper Tract and Bladder Urothelial Carcinoma. <i>Clinical Cancer Research</i> , 2019, 25, 967-976.	3.2	164
40	Unifying cancer and normal RNA sequencing data from different sources. <i>Scientific Data</i> , 2018, 5, 180061.	2.4	152
41	<i>KRAS</i> Allelic Imbalance Enhances Fitness and Modulates MAP Kinase Dependence in Cancer. <i>Cell</i> , 2017, 168, 817-829.e15.	13.5	148
42	Frequent somatic <i>CDH1</i> loss-of-function mutations in plasmacytoid variant bladder cancer. <i>Nature Genetics</i> , 2016, 48, 356-358.	9.4	143
43	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018, 7, 422-437.e7.	2.9	134
44	The Genomic Landscape of <i>SMARCA4</i> Alterations and Associations with Outcomes in Patients with Lung Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 5701-5708.	3.2	133
45	<i>EGFR</i> and <i>MET</i> Amplifications Determine Response to HER2 Inhibition in <i>ERBB2</i> -Amplified Esophagogastric Cancer. <i>Cancer Discovery</i> , 2019, 9, 199-209.	7.7	115
46	Synthetic Lethality in ATM-Deficient <i>RAD50</i> -Mutant Tumors Underlies Outlier Response to Cancer Therapy. <i>Cancer Discovery</i> , 2014, 4, 1014-1021.	7.7	114
47	<i>NF2</i> Loss Promotes Oncogenic RAS-Induced Thyroid Cancers via YAP-Dependent Transactivation of RAS Proteins and Sensitizes Them to MEK Inhibition. <i>Cancer Discovery</i> , 2015, 5, 1178-1193.	7.7	107
48	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. <i>Clinical Cancer Research</i> , 2019, 25, 5537-5547.	3.2	107
49	Marked Response of a Hypermutated ACTH-Secreting Pituitary Carcinoma to Ipilimumab and Nivolumab. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2018, 103, 3925-3930.	1.8	106
50	TRK Fusions Are Enriched in Cancers with Uncommon Histologies and the Absence of Canonical Driver Mutations. <i>Clinical Cancer Research</i> , 2020, 26, 1624-1632.	3.2	103
51	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 5939-5947.	3.2	100
52	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. <i>Cancer Cell</i> , 2020, 38, 198-211.e8.	7.7	99
53	Allele-Specific Mechanisms of Activation of MEK1 Mutants Determine Their Properties. <i>Cancer Discovery</i> , 2018, 8, 648-661.	7.7	97
54	Overcoming MET-Dependent Resistance to Selective RET Inhibition in Patients with RET Fusion-Positive Lung Cancer by Combining Selpercatinib with Crizotinib. <i>Clinical Cancer Research</i> , 2021, 27, 34-42.	3.2	87

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55	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. <i>Clinical Cancer Research</i> , 2018, 24, 1965-1973.	3.2	85
56	Efficacy and Determinants of Response to HER Kinase Inhibition in <i>HER2</i> -Mutant Metastatic Breast Cancer. <i>Cancer Discovery</i> , 2020, 10, 198-213.	7.7	83
57	Developmental chromatin programs determine oncogenic competence in melanoma. <i>Science</i> , 2021, 373, eabc1048.	6.0	80
58	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. <i>Cancer Cell</i> , 2018, 34, 852-862.e4.	7.7	73
59	The Evolutionary Origins of Recurrent Pancreatic Cancer. <i>Cancer Discovery</i> , 2020, 10, 792-805.	7.7	71
60	Transcriptional Mechanisms of Resistance to Anti-PD-1 Therapy. <i>Clinical Cancer Research</i> , 2017, 23, 3168-3180.	3.2	67
61	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. <i>JAMA Oncology</i> , 2020, 6, 84.	3.4	66
62	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. <i>Journal of the National Cancer Institute</i> , 2021, 113, 1683-1692.	3.0	66
63	Coaltered <i>Ras/B-raf</i> and <i>TP53</i> Is Associated with Extremes of Survivorship and Distinct Patterns of Metastasis in Patients with Metastatic Colorectal Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 1077-1085.	3.2	62
64	Altered Nuclear Export Signal Recognition as a Driver of Oncogenesis. <i>Cancer Discovery</i> , 2019, 9, 1452-1467.	7.7	60
65	Treatment-Induced Mutagenesis and Selective Pressures Sculpt Cancer Evolution. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2017, 7, a026617.	2.9	59
66	Genomic Landscape of Uterine Sarcomas Defined Through Prospective Clinical Sequencing. <i>Clinical Cancer Research</i> , 2020, 26, 3881-3888.	3.2	59
67	Respiratory complex and tissue lineage drive recurrent mutations in tumour mtDNA. <i>Nature Metabolism</i> , 2021, 3, 558-570.	5.1	58
68	A Secondary Mutation in <i>BRAF</i> Confers Resistance to RAF Inhibition in a <i>BRAF</i> V600E-Mutant Brain Tumor. <i>Cancer Discovery</i> , 2018, 8, 1130-1141.	7.7	56
69	Capivasertib, an AKT Kinase Inhibitor, as Monotherapy or in Combination with Fulvestrant in Patients with <i>AKT1</i> E17K-Mutant, ER-Positive Metastatic Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 3947-3957.	3.2	54
70	The evolution of RET inhibitor resistance in RET-driven lung and thyroid cancers. <i>Nature Communications</i> , 2022, 13, 1450.	5.8	47
71	The context-specific role of germline pathogenicity in tumorigenesis. <i>Nature Genetics</i> , 2021, 53, 1577-1585.	9.4	44
72	Anatomic position determines oncogenic specificity in melanoma. <i>Nature</i> , 2022, 604, 354-361.	13.7	44

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73	Genetic and epigenetic evolution as a contributor to WT1-mutant leukemogenesis. <i>Blood</i> , 2018, 132, 1265-1278.	0.6	39
74	TRK xDFG Mutations Trigger a Sensitivity Switch from Type I to II Kinase Inhibitors. <i>Cancer Discovery</i> , 2021, 11, 126-141.	7.7	34
75	Proteasome Addiction Defined in Ewing Sarcoma Is Effectively Targeted by a Novel Class of 19S Proteasome Inhibitors. <i>Cancer Research</i> , 2016, 76, 4525-4534.	0.4	33
76	Protein-altering germline mutations implicate novel genes related to lung cancer development. <i>Nature Communications</i> , 2020, 11, 2220.	5.8	31
77	Phase and context shape the function of composite oncogenic mutations. <i>Nature</i> , 2020, 582, 100-103.	13.7	31
78	Discovery through clinical sequencing in oncology. <i>Nature Cancer</i> , 2020, 1, 774-783.	5.7	29
79	Combined Inhibition of G1±q and MEK Enhances Therapeutic Efficacy in Uveal Melanoma. <i>Clinical Cancer Research</i> , 2021, 27, 1476-1490.	3.2	29
80	Novel computational method for predicting polytherapy switching strategies to overcome tumor heterogeneity and evolution. <i>Scientific Reports</i> , 2017, 7, 44206.	1.6	28
81	Germ cell tumors and associated hematologic malignancies evolve from a common shared precursor. <i>Journal of Clinical Investigation</i> , 2020, 130, 6668-6676.	3.9	28
82	V211D Mutation in MEK1 Causes Resistance to MEK Inhibitors in Colon Cancer. <i>Cancer Discovery</i> , 2019, 9, 1182-1191.	7.7	27
83	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. <i>Leukemia</i> , 2020, 34, 2025-2037.	3.3	27
84	EGFR feedback-inhibition by Ran-binding protein 6 is disrupted in cancer. <i>Nature Communications</i> , 2017, 8, 2035.	5.8	23
85	A pooled mutational analysis identifies ionizing radiation-associated mutational signatures conserved between mouse and human malignancies. <i>Scientific Reports</i> , 2017, 7, 7645.	1.6	22
86	Toward a More Precise Future for Oncology. <i>Cancer Cell</i> , 2020, 37, 431-442.	7.7	21
87	Leveraging Systematic Functional Analysis to Benchmark an <i>In Silico</i> Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. <i>Cancer Research</i> , 2020, 80, 4233-4243.	0.4	18
88	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. <i>PLoS Genetics</i> , 2020, 16, e1008422.	1.5	17
89	Homing in on genomic instability as a therapeutic target in cancer. <i>Nature Communications</i> , 2021, 12, 3663.	5.8	16
90	Targeting Germline- and Tumor-Associated Nucleotide Excision Repair Defects in Cancer. <i>Clinical Cancer Research</i> , 2021, 27, 1997-2010.	3.2	15

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91	Rare BRAF mutations in pancreatic neuroendocrine tumors may predict response to RAF and MEK inhibition. PLoS ONE, 2019, 14, e0217399.	1.1	12
92	Regorafenib in Combination with First-Line Chemotherapy for Metastatic Esophagogastric Cancer. Oncologist, 2020, 25, e68-e74.	1.9	10
93	Prevalence and Characterization of Biallelic and Monoallelic <i>NTHL1</i> and <i>MSH3</i> Variant Carriers From a Pan-Cancer Patient Population. JCO Precision Oncology, 2021, 5, 455-465.	1.5	10
94	AKT1 E17K Inhibits Cancer Cell Migration by Abrogating β -Catenin Signaling. Molecular Cancer Research, 2021, 19, 573-584.	1.5	10
95	AKT mutant allele-specific activation dictates pharmacologic sensitivities. Nature Communications, 2022, 13, 2111.	5.8	10
96	Germline Pathogenic Variants Impact Clinicopathology of Advanced Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1450-1459.	1.1	10
97	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. JCO Precision Oncology, 2020, 4, 1307-1320.	1.5	9
98	ARAF protein kinase activates RAS by antagonizing its binding to RASGAP NF1. Molecular Cell, 2022, 82, 2443-2457.e7.	4.5	9
99	Nbn-Mre11 interaction is required for tumor suppression and genomic integrity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 15178-15183.	3.3	8
100	Recurrent Mutations in Cyclin D3 Confer Clinical Resistance to FLT3 Inhibitors in Acute Myeloid Leukemia. Clinical Cancer Research, 2021, 27, 4003-4011.	3.2	7
101	The Genetic Evolution of Treatment-Resistant Cutaneous, Acral, and Uveal Melanomas. Clinical Cancer Research, 2021, 27, 1516-1525.	3.2	6
102	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. PLoS Genetics, 2019, 15, e1008168.	1.5	5
103	Clinical Sequencing Contributes to aBRCA-Associated Cancer Rediagnosis That Guides an Effective Therapeutic Course. Journal of the National Comprehensive Cancer Network: JNCCN, 2015, 13, 835-845.	2.3	3
104	Prognostic and radiographic correlates of a prospectively collected molecularly profiled cohort of IDH1/2 wildtype astrocytomas. Brain Pathology, 2020, 30, 653-660.	2.1	3
105	Hematologic Malignancies Arising in Patients with Germ Cell Tumors: Secondary Somatic Differentiation of Hematopoietic Malignancies from Germ Cell Precursors. Blood, 2018, 132, 87-87.	0.6	3
106	Transforming Biomarker Development with Exceptional Responders. Trends in Cancer, 2018, 4, 3-6.	3.8	2
107	Mutant Allele Imbalance in Cancer. Annual Review of Cancer Biology, 2021, 5, 221-234.	2.3	2
108	Bridging the Gap: The Impact of Genetic Ancestry on Routes to Tumorigenesis. Cancer Cell, 2020, 37, 619-621.	7.7	1

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109	Germline Contributions to Clonal Hematopoiesis in Solid Cancer Patients. <i>Blood</i> , 2020, 136, 30-31.	0.6	1
110	Tumor Suppressor Par-4 Regulates Complement Factor C3 and Obesity. <i>Frontiers in Oncology</i> , 2022, 12, 860446.	1.3	1
111	Oncogenic Mutations in <i>XPO1</i> Promote Lymphoid Transformation By Altering Nuclear/Cytoplasmic Localization of NF κ B Signaling Intermediates. <i>Blood</i> , 2017, 130, 879-879.	0.6	0
112	Co-Targeting BET Bromodomain Proteins and Aberrant Signaling in AML. <i>Blood</i> , 2020, 136, 5-6.	0.6	0
113	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
114	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
115	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
116	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
117	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
118	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0