Barry S Taylor

List of Publications by Year
in descending order

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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	Tumor Suppressor Par-4 Regulates Complement Factor C3 and Obesity. Frontiers in Oncology, 2022, 12, 860446.	1.3	1
2	The evolution of RET inhibitor resistance in RET-driven lung and thyroid cancers. Nature Communications, 2022, 13, 1450.	5.8	47
3	Anatomic position determines oncogenic specificity in melanoma. Nature, 2022, 604, 354-361.	13.7	44
4	AKT mutant allele-specific activation dictates pharmacologic sensitivities. Nature Communications, 2022, 13, 2111.	5.8	10
5	Germline Pathogenic Variants Impact Clinicopathology of Advanced Lung Cancer. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1450-1459.	1.1	10
6	ARAF protein kinase activates RAS by antagonizing its binding to RASGAP NF1. Molecular Cell, 2022, 82, 2443-2457.e7.	4.5	9
7	TRK xDFG Mutations Trigger a Sensitivity Switch from Type I to II Kinase Inhibitors. Cancer Discovery, 2021, 11, 126-141.	7.7	34
8	Overcoming MET-Dependent Resistance to Selective RET Inhibition in Patients with RET Fusionâ€“Positive Lung Cancer by Combining Selpercatinib with Crizotinib. Clinical Cancer Research, 2021, 27, 34-42.	3.2	87
9	Combined Inhibition of GÎ±q and MEK Enhances Therapeutic Efficacy in Uveal Melanoma. Clinical Cancer Research, 2021, 27, 1476-1490.	3.2	29
10	Targeting Germline- and Tumor-Associated Nucleotide Excision Repair Defects in Cancer. Clinical Cancer Research, 2021, 27, 1997-2010.	3.2	15
11	Mutant Allele Imbalance in Cancer. Annual Review of Cancer Biology, 2021, 5, 221-234.	2.3	2
12	Prevalence and Characterization of Biallelic and Monoallelic NTHL1 and MSH3 Variant Carriers From a Pan-Cancer Patient Population. JCO Precision Oncology, 2021, 5, 455-465.	1.5	10
13	Respiratory complex and tissue lineage drive recurrent mutations in tumour mtDNA. Nature Metabolism, 2021, 3, 558-570.	5.1	58
14	Homing in on genomic instability as a therapeutic target in cancer. Nature Communications, 2021, 12, 3663.	5.8	16
15	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
16	A Comprehensive Comparison of Early-Onset and Average-Onset Colorectal Cancers. Journal of the National Cancer Institute, 2021, 113, 1683-1692.	3.0	66
17	Developmental chromatin programs determine oncogenic competence in melanoma. Science, 2021, 373, eabc1048.	6.0	80
18	The Genetic Evolution of Treatment-Resistant Cutaneous, Acral, and Uveal Melanomas. Clinical Cancer Research, 2021, 27, 1516-1525.	3.2	6

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19	AKT1 E17K Inhibits Cancer Cell Migration by Abrogating Î²-Catenin Signaling. Molecular Cancer Research, 2021, 19, 573-584.	1.5	10
20	The context-specific role of germline pathogenicity in tumorigenesis. Nature Genetics, 2021, 53, 1577-1585.	9.4	44
21	Development of Genome-Derived Tumor Type Prediction to Inform Clinical Cancer Care. JAMA Oncology, 2020, 6, 84.	3.4	66
22	TRK Fusions Are Enriched in Cancers with Uncommon Histologies and the Absence of Canonical Driver Mutations. Clinical Cancer Research, 2020, 26, 1624-1632.	3.2	103
23	Discovery through clinical sequencing in oncology. Nature Cancer, 2020, 1, 774-783.	5.7	29
24	The Genomic Landscape of SMARCA4 Alterations and Associations with Outcomes in Patients with Lung Cancer. Clinical Cancer Research, 2020, 26, 5701-5708.	3.2	133
25	Germ Cell Tumor Molecular Heterogeneity Revealed Through Analysis of Primary and Metastasis Pairs. JCO Precision Oncology, 2020, 4, 1307-1320.	1.5	9
26	Bridging the Gap: The Impact of Genetic Ancestry on Routes to Tumorigenesis. Cancer Cell, 2020, 37, 619-621.	7.7	1
27	First-line pembrolizumab and trastuzumab in HER2-positive oesophageal, gastric, or gastro-oesophageal junction cancer: an open-label, single-arm, phase 2 trial. Lancet Oncology, The, 2020, 21, 821-831.	5.1	243
28	Protein-altering germline mutations implicate novel genes related to lung cancer development. Nature Communications, 2020, 11, 2220.	5.8	31
29	Phase and context shape the function of composite oncogenic mutations. Nature, 2020, 582, 100-103.	13.7	31
30	Altered RNA Splicing by Mutant p53 Activates Oncogenic RAS Signaling in Pancreatic Cancer. Cancer Cell, 2020, 38, 198-211.e8.	7.7	99
31	The Evolutionary Origins of Recurrent Pancreatic Cancer. Cancer Discovery, 2020, 10, 792-805.	7.7	71
32	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. PLoS Genetics, 2020, 16, e1008422.	1.5	17
33	Leveraging Systematic Functional Analysis to Benchmark an In Silico Framework Distinguishes Driver from Passenger MEK Mutants in Cancer. Cancer Research, 2020, 80, 4233-4243.	0.4	18
34	Loss of glucocorticoid receptor expression mediates in vivo dexamethasone resistance in T-cell acute lymphoblastic leukemia. Leukemia, 2020, 34, 2025-2037.	3.3	27
35	Regorafenib in Combination with Firstâ€Line Chemotherapy for Metastatic Esophagogastric Cancer. Oncologist, 2020, 25, e68-e74.	1.9	10
36	Prognostic and radiographic correlates of a prospectively collected molecularly profiled cohort of IDH1/2 â€wildtype astrocytomas. Brain Pathology, 2020, 30, 653-660.	2.1	3

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37	Efficacy and Determinants of Response to HER Kinase Inhibition in HER2-Mutant Metastatic Breast Cancer. Cancer Discovery, 2020, 10, 198-213.	7.7	83
38	Coaltered Ras/B-raf and TP53 Is Associated with Extremes of Survivorship and Distinct Patterns of Metastasis in Patients with Metastatic Colorectal Cancer. Clinical Cancer Research, 2020, 26, 1077-1085.	3.2	62
39	Capivasertib, an AKT Kinase Inhibitor, as Monotherapy or in Combination with Fulvestrant in Patients withAKT1E17K-Mutant, ER-Positive Metastatic Breast Cancer. Clinical Cancer Research, 2020, 26, 3947-3957.	3.2	54
40	Toward a More Precise Future for Oncology. Cancer Cell, 2020, 37, 431-442.	7.7	21
41	Genomic Landscape of Uterine Sarcomas Defined Through Prospective Clinical Sequencing. Clinical Cancer Research, 2020, 26, 3881-3888.	3.2	59
42	Germ cell tumors and associated hematologic malignancies evolve from a common shared precursor. Journal of Clinical Investigation, 2020, 130, 6668-6676.	3.9	28
43	Co-Targeting BET Bromodomain Proteins and Aberrant Signaling in AML. Blood, 2020, 136, 5-6.	0.6	0
44	Germline Contributions to Clonal Hematopoiesis in Solid Cancer Patients. Blood, 2020, 136, 30-31.	0.6	1
45	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
46	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
47	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
48	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
49	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
50	Modeling cancer genomic data in yeast reveals selection against ATM function during tumorigenesis. , 2020, 16, e1008422.		0
51	Tumour lineage shapes BRCA-mediated phenotypes. Nature, 2019, 571, 576-579.	13.7	295
52	Nbnâ”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
53	Altered Nuclear Export Signal Recognition as a Driver of Oncogenesis. Cancer Discovery, 2019, 9, 1452-1467.	7.7	60
54	Genomic Correlates of Disease Progression and Treatment Response in Prospectively Characterized Gliomas. Clinical Cancer Research, 2019, 25, 5537-5547.	3.2	107

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55	Double PIK3CA mutations in cis increase oncogenicity and sensitivity to PI3KÎ± inhibitors. Science, 2019, 366, 714-723.	6.0	185
56	V211D Mutation in MEK1 Causes Resistance to MEK Inhibitors in Colon Cancer. Cancer Discovery, 2019, 9, 1182-1191.	7.7	27
57	Rare BRAF mutations in pancreatic neuroendocrine tumors may predict response to RAF and MEK inhibition. PLoS ONE, 2019, 14, e0217399.	1.1	12
58	Convergent genetic aberrations in murine and human T lineage acute lymphoblastic leukemias. PLoS Genetics, 2019, 15, e1008168.	1.5	5
59	Microsatellite Instability Is Associated With the Presence of Lynch Syndrome Pan-Cancer. Journal of Clinical Oncology, 2019, 37, 286-295.	0.8	397
60	Analysis of the Prevalence of Microsatellite Instability in Prostate Cancer and Response to Immune Checkpoint Blockade. JAMA Oncology, 2019, 5, 471.	3.4	426
61	EGFR and MET Amplifications Determine Response to HER2 Inhibition in ERBB2-Amplified Esophagogastric Cancer. Cancer Discovery, 2019, 9, 199-209.	7.7	115
62	Clonal Relatedness and Mutational Differences between Upper Tract and Bladder Urothelial Carcinoma. Clinical Cancer Research, 2019, 25, 967-976.	3.2	164
63	Allele-Specific Mechanisms of Activation of MEK1 Mutants Determine Their Properties. Cancer Discovery, 2018, 8, 648-661.	7.7	97
64	Unifying cancer and normal RNA sequencing data from different sources. Scientific Data, 2018, 5, 180061.	2.4	152
65	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
66	Tumor Evolution and Drug Response in Patient-Derived Organoid Models of Bladder Cancer. Cell, 2018, 173, 515-528.e17.	13.5	540
67	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
68	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	13.5	620
69	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	2.9	801
70	HER kinase inhibition in patients with HER2- and HER3-mutant cancers. Nature, 2018, 554, 189-194.	13.7	572
71	Transforming Biomarker Development with Exceptional Responders. Trends in Cancer, 2018, 4, 3-6.	3.8	2
72	Accelerating Discovery of Functional Mutant Alleles in Cancer. Cancer Discovery, 2018, 8, 174-183.	7.7	275

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73	Clinical Sequencing Defines the Genomic Landscape of Metastatic Colorectal Cancer. Cancer Cell, 2018, 33, 125-136.e3.	7.7	589
74	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
75	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	7.7	478
76	The long tail of oncogenic drivers in prostate cancer. Nature Genetics, 2018, 50, 645-651.	9.4	601
77	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. Clinical Cancer Research, 2018, 24, 1965-1973.	3.2	85
78	Genetic Predictors of Response to Systemic Therapy in Esophagogastric Cancer. Cancer Discovery, 2018, 8, 49-58.	7.7	275
79	Marked Response of a Hypermutated ACTH-Secreting Pituitary Carcinoma to Ipilimumab and Nivolumab. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 3925-3930.	1.8	106
80	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
81	Widespread Selection for Oncogenic Mutant Allele Imbalance in Cancer. Cancer Cell, 2018, 34, 852-862.e4.	7.7	73
82	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	7.7	633
83	Genetic and epigenetic evolution as a contributor to WT1-mutant leukemogenesis. Blood, 2018, 132, 1265-1278.	0.6	39
84	Clinical Utility of Prospective Molecular Characterization in Advanced Endometrial Cancer. Clinical Cancer Research, 2018, 24, 5939-5947.	3.2	100
85	Genome doubling shapes the evolution and prognosis of advanced cancers. Nature Genetics, 2018, 50, 1189-1195.	9.4	411
86	A Secondary Mutation in BRAF Confers Resistance to RAF Inhibition in a BRAFV600E-Mutant Brain Tumor. Cancer Discovery, 2018, 8, 1130-1141.	7.7	56
87	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
88	Tumor copy number alteration burden is a pan-cancer prognostic factor associated with recurrence and death. ELife, 2018, 7, .	2.8	217
89	3D clusters of somatic mutations in cancer reveal numerous rare mutations as functional targets. Genome Medicine, 2017, 9, 4.	3.6	170
90	Transcriptional Mechanisms of Resistance to Antiâ€“PD-1 Therapy. Clinical Cancer Research, 2017, 23, 3168-3180.	3.2	67

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91	KRAS Allelic Imbalance Enhances Fitness and Modulates MAP Kinase Dependence in Cancer. Cell, 2017, 168, 817-829.e15.	13.5	148
92	Implementing Genome-Driven Oncology. Cell, 2017, 168, 584-599.	13.5	405
93	Mutational landscape of metastatic cancer revealed from prospective clinical sequencing of 10,000 patients. Nature Medicine, 2017, 23, 703-713.	15.2	2,473
94	A Next-Generation TRK Kinase Inhibitor Overcomes Acquired Resistance to Prior TRK Kinase Inhibition in Patients with TRK Fusionâ€“Positive Solid Tumors. Cancer Discovery, 2017, 7, 963-972.	7.7	331
95	Prospective Comprehensive Molecular Characterization of Lung Adenocarcinomas for Efficient Patient Matching to Approved and Emerging Therapies. Cancer Discovery, 2017, 7, 596-609.	7.7	490
96	Novel computational method for predicting polytherapy switching strategies to overcome tumor heterogeneity and evolution. Scientific Reports, 2017, 7, 44206.	1.6	28
97	Treatment-Induced Mutagenesis and Selective Pressures Sculpt Cancer Evolution. Cold Spring Harbor Perspectives in Medicine, 2017, 7, a026617.	2.9	59
98	A pooled mutational analysis identifies ionizing radiation-associated mutational signatures conserved between mouse and human malignancies. Scientific Reports, 2017, 7, 7645.	1.6	22
99	Tumours with class 3 BRAF mutants are sensitive to the inhibition of activated RAS. Nature, 2017, 548, 234-238.	13.7	394
100	EGFR feedback-inhibition by Ran-binding protein 6 is disrupted in cancer. Nature Communications, 2017, 8, 2035.	5.8	23
101	Prospective Genomic Profiling of Prostate Cancer Across Disease States Reveals Germline and Somatic Alterations That May Affect Clinical Decision Making. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	286
102	AKT Inhibition in Solid Tumors With AKT1 Mutations. Journal of Clinical Oncology, 2017, 35, 2251-2259.	0.8	240
103	OncoKB: A Precision Oncology Knowledge Base. JCO Precision Oncology, 2017, 2017, 1-16.	1.5	1,266
104	Oncogenic Mutations in XPO1 Promote Lymphoid Transformation By Altering Nuclear/Cytoplasmic Localization of NFÎºB Signaling Intermediates. Blood, 2017, 130, 879-879.	0.6	0
105	Recurrent activating mutations of G-protein-coupled receptor CYSLTR2 in uveal melanoma. Nature Genetics, 2016, 48, 675-680.	9.4	236
106	Proteasome Addiction Defined in Ewing Sarcoma Is Effectively Targeted by a Novel Class of 19S Proteasome Inhibitors. Cancer Research, 2016, 76, 4525-4534.	0.4	33
107	deconstructSigs: delineating mutational processes in single tumors distinguishes DNA repair deficiencies and patterns of carcinoma evolution. Genome Biology, 2016, 17, 31.	3.8	917
108	Diverse and Targetable Kinase Alterations Drive Histiocytic Neoplasms. Cancer Discovery, 2016, 6, 154-165.	7.7	372

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109	Frequent somatic CDH1 loss-of-function mutations in plasmacytoid variant bladder cancer. Nature Genetics, 2016, 48, 356-358.	9.4	143
110	Identifying recurrent mutations in cancer reveals widespread lineage diversity and mutational specificity. Nature Biotechnology, 2016, 34, 155-163.	9.4	634
111	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
112	DNA Methylation and Somatic Mutations Converge on the Cell Cycle and Define Similar Evolutionary Histories in Brain Tumors. Cancer Cell, 2015, 28, 307-317.	7.7	221
113	NF2 Loss Promotes Oncogenic RAS-Induced Thyroid Cancers via YAP-Dependent Transactivation of RAS Proteins and Sensitizes Them to MEK Inhibition. Cancer Discovery, 2015, 5, 1178-1193.	7.7	107
114	Copy number alteration burden predicts prostate cancer relapse. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 11139-11144.	3.3	299
115	Synthetic Lethality in ATM-Deficient RAD50-Mutant Tumors Underlies Outlier Response to Cancer Therapy. Cancer Discovery, 2014, 4, 1014-1021.	7.7	114
116	Mutational Analysis Reveals the Origin and Therapy-Driven Evolution of Recurrent Glioma. Science, 2014, 343, 189-193.	6.0	1,147
117	Genome Sequencing Identifies a Basis for Everolimus Sensitivity. Science, 2012, 338, 221-221.	6.0	681
118	Integrative Genomic Profiling of Human Prostate Cancer. Cancer Cell, 2010, 18, 11-22.	7.7	3,151