

Todd R Golub

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

113
papers

72,487
citations

68
h-index

126
g-index

126
ext. papers

94,471
ext. citations

23.9
avg, IF

6.96
L-index

#	Paper	IF	Citations
113	Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15545-50	11.5	24578
112	Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , 2010 , 17, 98-110	24.3	4782
111	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012 , 483, 603-7	50.4	4648
110	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013 , 499, 214-218	50.4	3616
109	The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease. <i>Science</i> , 2006 , 313, 1929-35	33.3	3392
108	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010 , 463, 899-905	50.4	2590
107	Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis. <i>Cancer Cell</i> , 2005 , 7, 387-97	24.3	2353
106	Discovery and saturation analysis of cancer genes across 21 tumour types. <i>Nature</i> , 2014 , 505, 495-501	50.4	1990
105	A molecular signature of metastasis in primary solid tumors. <i>Nature Genetics</i> , 2003 , 33, 49-54	36.3	1973
104	Tumour micro-environment elicits innate resistance to RAF inhibitors through HGF secretion. <i>Nature</i> , 2012 , 487, 500-4	50.4	1308
103	Metagenes and molecular pattern discovery using matrix factorization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 4164-9	11.5	1178
102	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017 , 171, 1437-1452.e17	56.2	1132
101	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011 , 471, 467-72	50.4	1117
100	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011 , 470, 214-20	50.4	984
99	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019 , 569, 503-508	50.4	962
98	Integrative analysis reveals selective 9p24.1 amplification, increased PD-1 ligand expression, and further induction via JAK2 in nodular sclerosing Hodgkin lymphoma and primary mediastinal large B-cell lymphoma. <i>Blood</i> , 2010 , 116, 3268-77	2.2	903
97	Defining a Cancer Dependency Map. <i>Cell</i> , 2017 , 170, 564-576.e16	56.2	844

96	Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , 2017 , 49, 1779-1784	36.3	740
95	Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 3879-84	11.5	735
94	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018 , 24, 679-690	50.5	659
93	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. <i>Cancer Cell</i> , 2014 , 25, 91-101	24.3	657
92	Molecular profiling of diffuse large B-cell lymphoma identifies robust subtypes including one characterized by host inflammatory response. <i>Blood</i> , 2005 , 105, 1851-61	2.2	654
91	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <i>Science</i> , 2017 , 357, 1156-1160	33.3	577
90	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016 , 539, 309-313	50.4	561
89	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017 , 355,	33.3	455
88	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014 , 32, 479-84	44.5	434
87	Highly parallel identification of essential genes in cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 20380-5	11.5	424
86	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , 2017 , 49, 1567-1575	35.3	384
85	The Drug Repurposing Hub: a next-generation drug library and information resource. <i>Nature Medicine</i> , 2017 , 23, 405-408	50.5	381
84	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018 , 560, 325-330	50.4	379
83	A mechanism of cyclin D1 action encoded in the patterns of gene expression in human cancer. <i>Cell</i> , 2003 , 114, 323-34	56.2	353
82	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016 , 6, 914-29	24.4	343
81	Targetable genetic features of primary testicular and primary central nervous system lymphomas. <i>Blood</i> , 2016 , 127, 869-81	2.2	317
80	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017 , 8, 1324	17.4	314
79	The genomic landscape of pediatric Ewing sarcoma. <i>Cancer Discovery</i> , 2014 , 4, 1326-41	24.4	302

78	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E5564-73	11.5	275
77	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. <i>Blood</i> , 2014 , 123, e123-33	2.2	264
76	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018 , 360, 331-335	33.3	255
75	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , 2014 , 1, 140035	8.2	251
74	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014 , 42, W449-60	20.1	204
73	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , 2018 , 6, 13-24	10.6	199
72	A method for high-throughput gene expression signature analysis. <i>Genome Biology</i> , 2006 , 7, R61	18.3	175
71	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019 , 25, 1415-1421	50.5	161
70	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. <i>Nature Communications</i> , 2018 , 9, 4610	17.4	155
69	Integrative analysis reveals an outcome-associated and targetable pattern of p53 and cell cycle deregulation in diffuse large B cell lymphoma. <i>Cancer Cell</i> , 2012 , 22, 359-72	24.3	148
68	Comprehensive assessment of cancer missense mutation clustering in protein structures. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E5486-95	11.5	142
67	Toward performance-diverse small-molecule libraries for cell-based phenotypic screening using multiplexed high-dimensional profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 10911-6	11.5	141
66	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , 2019 , 568, 551-556	50.4	137
65	Discovering the anti-cancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020 , 1, 235-248	15.4	137
64	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. <i>Nature Biotechnology</i> , 2016 , 34, 419-23	44.5	127
63	Protection of tissue physicochemical properties using polyfunctional crosslinkers. <i>Nature Biotechnology</i> , 2018 ,	44.5	123
62	SYK inhibition modulates distinct PI3K/AKT- dependent survival pathways and cholesterol biosynthesis in diffuse large B cell lymphomas. <i>Cancer Cell</i> , 2013 , 23, 826-38	24.3	120
61	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016 , 30, 214-228	24.3	119

60	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , 2016 , 29, 214-28	24.3	118
59	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. <i>Journal of Clinical Oncology</i> , 2018 , 36, 543-553	2.2	113
58	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , 2019 , 19, 97-109	31.3	104
57	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016 , 6, 714-26	24.4	100
56	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. <i>PLoS Biology</i> , 2017 , 15, e2003213	9.7	99
55	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018 , 50, 1240-1246	36.3	94
54	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. <i>Nature</i> , 2020 , 585, 293-297	37.4	93
53	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , 2016 , 8, 363ra147	17.5	93
52	Copper induces cell death by targeting lipoylated TCA cycle proteins.. <i>Science</i> , 2022 , 375, 1254-1261	33.3	89
51	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. <i>Neuro-Oncology</i> , 2020 , 22, iii471-iii471	1	78
50	A metastasis map of human cancer cell lines. <i>Nature</i> , 2020 , 588, 331-336	50.4	76
49	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2018 , 128, 446-462	15.9	72
48	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019 , 10, 5817	17.4	70
47	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , 2020 , 52, 662-668	36.3	69
46	The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. <i>Nature Medicine</i> , 2020 , 26, 181-187	50.5	69
45	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , 2019 , 36, 528-544.e10	24.3	66
44	Mitochondrial metabolism promotes adaptation to proteotoxic stress. <i>Nature Chemical Biology</i> , 2019 , 15, 681-689	11.7	62
43	A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity. <i>Nature Chemical Biology</i> , 2014 , 10, 656-63	11.7	54

42	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018 , 6, 424-443.e7	10.6	47
41	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019 , 9, 35-48.e5	10.6	46
40	Drug and disease signature integration identifies synergistic combinations in glioblastoma. <i>Nature Communications</i> , 2018 , 9, 5315	17.4	44
39	An ecosystem of cancer cell line factories to support a cancer dependency map. <i>Nature Reviews Genetics</i> , 2015 , 16, 373-4	30.1	42
38	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. <i>JAMA Oncology</i> , 2015 , 1, 238-44	13.4	41
37	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017 , 8, 1186	17.4	38
36	Counterpoint: Data first. <i>Nature</i> , 2010 , 464, 679	50.4	37
35	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020 , 11, 4296	17.4	37
34	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. <i>Nature Communications</i> , 2016 , 7, 12160	17.4	36
33	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , 2021 , 590, 486-491	50.4	34
32	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. <i>Neuro-Oncology</i> , 2015 , 17, 1486-96	1	33
31	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2020 , 26, 2556-2564	12.9	32
30	FATTY ACID SYNTHESIS IS REQUIRED FOR BREAST CANCER BRAIN METASTASIS. <i>Nature Cancer</i> , 2021 , 2, 414-428	15.4	31
29	A Maltose-Binding Protein Fusion Construct Yields a Robust Crystallography Platform for MCL1. <i>PLoS ONE</i> , 2015 , 10, e0125010	3.7	23
28	Single Diastereomer of a Macrolactam Core Binds Specifically to Myeloid Cell Leukemia 1 (MCL1). <i>ACS Medicinal Chemistry Letters</i> , 2014 , 5, 1308-12	4.3	22
27	A first-generation pediatric cancer dependency map. <i>Nature Genetics</i> , 2021 , 53, 529-538	36.3	21
26	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. <i>Cell Reports</i> , 2019 , 28, 2331-2344.e8	10.6	20
25	A functional screen identifies miRs that induce radioresistance in glioblastomas. <i>Molecular Cancer Research</i> , 2014 , 12, 1767-78	6.6	19

24	Cancer research needs a better map. <i>Nature</i> , 2021 , 589, 514-516	50.4	19
23	A phase II study of the EGFR inhibitor gefitinib in patients with acute myeloid leukemia. <i>Leukemia Research</i> , 2014 , 38, 430-4	2.7	18
22	Niche-Based Screening in Multiple Myeloma Identifies a Kinesin-5 Inhibitor with Improved Selectivity over Hematopoietic Progenitors. <i>Cell Reports</i> , 2015 , 10, 755-770	10.6	18
21	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021 , 39, 697-704	44.5	17
20	Direct evidence for a polygenic etiology in familial multiple myeloma. <i>Blood Advances</i> , 2017 , 1, 619-623	7.8	13
19	Gene expression has more power for predicting in vitro cancer cell vulnerabilities than genomics		12
18	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. <i>Nature Communications</i> , 2019 , 10, 3166	17.4	9
17	Identification of RPS14 as the 5q-Syndrome Gene by RNA Interference Screen.. <i>Blood</i> , 2007 , 110, 1-1	2.2	9
16	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. <i>Nature Genetics</i> , 2021 , 53, 1196-1206	36.3	9
15	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. <i>Cell Reports</i> , 2020 , 33, 108493	10.6	7
14	Non-oncology drugs are a source of previously unappreciated anti-cancer activity		6
13	Liquid biopsy detection of genomic alterations in pediatric brain tumors from cell-free DNA in peripheral blood, CSF, and urine.. <i>Neuro-Oncology</i> , 2022 ,	1	4
12	Selective vulnerability of aneuploid human cancer cells to inhibition of the spindle assembly checkpoint		4
11	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , 2021 , 11, 2282-2299	24.4	4
10	Multiplexed single-cell profiling of post-perturbation transcriptional responses to define cancer vulnerabilities and therapeutic mechanism of action		3
9	Non-canonical open reading frames encode functional proteins essential for cancer cell survival		2
8	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency datasets		2
7	Hodgkin's Lymphoma Reed Sternberg Cells over Express the T-Cell Inhibitory Carbohydrate-Binding Lectin, Galectin 1: Role of AP-1 and Likely Mechanism of Tumor Immune Escape.. <i>Blood</i> , 2006 , 108, 469-469	2.2	1

6	Phosphate dysregulation via the XPR1:KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer		1
5	Massively parallel enrichment of low-frequency alleles enables duplex sequencing at low depth.. <i>Nature Biomedical Engineering</i> , 2022 ,	19	1
4	DNA-based copy number analysis confirms genomic evolution of PDX models.. <i>Npj Precision Oncology</i> , 2022 , 6, 30	9.8	1
3	EXTH-37. TARGETING EPIGENETIC VULNERABILITIES IDENTIFIED FROM A CRISPR SCREEN IN H3.3K27M DIPG. <i>Neuro-Oncology</i> , 2020 , 22, ii95-ii95		1
2	Characterization of Distinct Molecular Signatures in Myeloproliferative Diseases with the JAK2V617F Mutation and Wild Type JAK2.. <i>Blood</i> , 2005 , 106, 119-119	2.2	
1	All Memory Lymphocytes Share a Common Differentiation Program.. <i>Blood</i> , 2006 , 108, 865-865	2.2	