Todd R Golub

List of Publications by Year
in descending order

108	108,612	10389 72	23533 111
papers	citations	h-index	g-index

126	126	126	129246
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15545-15550.	7.1	38,922
2	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 2012, 483, 603-607.	27.8	6,473
3	Integrated Genomic Analysis Identifies Clinically Relevant Subtypes of Glioblastoma Characterized by Abnormalities in PDGFRA, IDH1, EGFR, and NF1. Cancer Cell, 2010, 17, 98-110.	16.8	6,138
4	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	27.8	4,761
5	The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 2006, 313, 1929-1935.	12.6	4,472
6	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
7	Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis. Cancer Cell, 2005, 7, 387-397.	16.8	2,695
8	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	27.8	2,586
9	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. Cell, 2017, 171, 1437-1452.e17.	28.9	2,281
10	A molecular signature of metastasis in primary solid tumors. Nature Genetics, 2003, 33, 49-54.	21.4	2,261
11	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	27.8	2,149
12	Defining a Cancer Dependency Map. Cell, 2017, 170, 564-576.e16.	28.9	1,794
13	Metagenes and molecular pattern discovery using matrix factorization. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 4164-4169.	7.1	1,649
14	Tumour micro-environment elicits innate resistance to RAF inhibitors through HGF secretion. Nature, 2012, 487, 500-504.	27.8	1,561
15	Copper induces cell death by targeting lipoylated TCA cycle proteins. Science, 2022, 375, 1254-1261.	12.6	1,539
16	Computational correction of copy number effect improves specificity of CRISPRâ€“Cas9 essentiality screens in cancer cells. Nature Genetics, 2017, 49, 1779-1784.	21.4	1,436
17	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	27.8	1,288
18	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. Nature Medicine, 2018, 24, 679-690.	30.7	1,224

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19	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. Blood, 2010, 116, 3268-3277.	1.4	1,122
20	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	27.8	1,107
21	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. Science, 2017, 357, 1156-1160.	12.6	1,059
22	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
23	Discovery and prioritization of somatic mutations in diffuse large B-cell lymphoma (DLBCL) by whole-exome sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 3879-3884.	7.1	853
24	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	16.8	847
25	Molecular profiling of diffuse large B-cell lymphoma identifies robust subtypes including one characterized by host inflammatory response. Blood, 2005, 105, 1851-1861.	1.4	778
26	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
27	The Drug Repurposing Hub: a next-generation drug library and information resource. Nature Medicine, 2017, 23, 405-408.	30.7	689
28	Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330.	27.8	662
29	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	12.8	584
30	Patient-derived xenografts undergo mouse-specific tumor evolution. Nature Genetics, 2017, 49, 1567-1575.	21.4	546
31	Highly parallel identification of essential genes in cancer cells. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 20380-20385.	7.1	499
32	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
33	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	9.4	485
34	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461
35	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. Nature Cancer, 2020, 1, 235-248.	13.2	430
36	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429

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37	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	9.4	415
38	A Mechanism of Cyclin D1 Action Encoded in the Patterns of Gene Expression in Human Cancer. Cell, 2003, 114, 323-334.	28.9	395
39	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. Nature Medicine, 2019, 25, 1415-1421.	30.7	359
40	Complementary genomic approaches highlight the PI3K/mTOR pathway as a common vulnerability in osteosarcoma. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E5564-73.	7.1	355
41	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. Blood, 2014, 123, e123-e133.	1.4	337
42	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. Scientific Data, 2014, 1, 140035.	5.3	328
43	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. Cell Systems, 2018, 6, 13-24.	6.2	327
44	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. Nature Communications, 2018, 9, 4610.	12.8	290
45	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. Nucleic Acids Research, 2014, 42, W449-W460.	14.5	280
46	Mitochondrial metabolism promotes adaptation to proteotoxic stress. Nature Chemical Biology, 2019, 15, 681-689.	8.0	275
47	Protection of tissue physicochemical properties using polyfunctional crosslinkers. Nature Biotechnology, 2019, 37, 73-83.	17.5	262
48	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. Nature, 2019, 568, 551-556.	27.8	253
49	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. Nature Biotechnology, 2016, 34, 419-423.	17.5	245
50	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. Nature, 2020, 585, 293-297.	27.8	219
51	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. Cancer Cell, 2016, 29, 214-228.	16.8	216
52	A metastasis map of human cancer cell lines. Nature, 2020, 588, 331-336.	27.8	214
53	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. Nature Genetics, 2018, 50, 1240-1246.	21.4	199
54	Comprehensive assessment of cancer missense mutation clustering in protein structures. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5486-95.	7.1	195

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55	Toward performance-diverse small-molecule libraries for cell-based phenotypic screening using multiplexed high-dimensional profiling. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10911-10916.	7.1	191
56	A method for high-throughput gene expression signature analysis. Genome Biology, 2006, 7, R61.	9.6	190
57	Integrative Analysis Reveals an Outcome-Associated and Targetable Pattern of p53 and Cell Cycle Deregulation in Diffuse Large B Cell Lymphoma. Cancer Cell, 2012, 22, 359-372.	16.8	179
58	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	16.8	171
59	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. Nature Genetics, 2020, 52, 662-668.	21.4	168
60	Association of Cell-Free DNA Tumor Fraction and Somatic Copy Number Alterations With Survival in Metastatic Triple-Negative Breast Cancer. Journal of Clinical Oncology, 2018, 36, 543-553.	1.6	162
61	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
62	Genomic evolution of cancer models: perils and opportunities. Nature Reviews Cancer, 2019, 19, 97-109.	28.4	158
63	The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. Nature Medicine, 2020, 26, 181-187.	30.7	158
64	SYK Inhibition Modulates Distinct PI3K/AKT- Dependent Survival Pathways and Cholesterol Biosynthesis in Diffuse Large B Cell Lymphomas. Cancer Cell, 2013, 23, 826-838.	16.8	152
65	Fatty acid synthesis is required for breast cancer brain metastasis. Nature Cancer, 2021, 2, 414-428.	13.2	147
66	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. Cancer Discovery, 2016, 6, 714-726.	9.4	139
67	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. PLoS Biology, 2017, 15, e2003213.	5.6	136
68	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. Nature, 2021, 590, 486-491.	27.8	135
69	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. Cancer Cell, 2019, 36, 528-544.e10.	16.8	128
70	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. Science Translational Medicine, 2016, 8, 363ra147.	12.4	126
71	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. Journal of Clinical Investigation, 2017, 128, 446-462.	8.2	117
72	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. Clinical Cancer Research, 2020, 26, 2556-2564.	7.0	109

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73	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. Nature Communications, 2020, 11, 4296.	12.8	98
74	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. Cell Systems, 2019, 9, 35-48.e5.	6.2	95
75	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. Nature Biotechnology, 2021, 39, 697-704.	17.5	85
76	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186.	12.8	78
77	Drug and disease signature integration identifies synergistic combinations in glioblastoma. Nature Communications, 2018, 9, 5315.	12.8	78
78	A first-generation pediatric cancer dependency map. Nature Genetics, 2021, 53, 529-538.	21.4	76
79	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. Cell Systems, 2018, 6, 424-443.e7.	6.2	68
80	A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity. Nature Chemical Biology, 2014, 10, 656-663.	8.0	66
81	An ecosystem of cancer cell line factories to support a cancer dependency map. Nature Reviews Genetics, 2015, 16, 373-374.	16.3	65
82	Cancer research needs a better map. Nature, 2021, 589, 514-516.	27.8	57
83	Counterpoint: Data first. Nature, 2010, 464, 679-679.	27.8	49
84	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. Nature Genetics, 2021, 53, 1196-1206.	21.4	47
85	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2015, 1, 238.	7.1	44
86	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. Nature Communications, 2016, 7, 12160.	12.8	43
87	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. Neuro-Oncology, 2015, 17, 1486-1496.	1.2	39
88	Massively parallel enrichment of low-frequency alleles enables duplex sequencing at low depth. Nature Biomedical Engineering, 2022, 6, 257-266.	22.5	32
89	Liquid biopsy detection of genomic alterations in pediatric brain tumors from cell-free DNA in peripheral blood, CSF, and urine. Neuro-Oncology, 2022, 24, 1352-1363.	1.2	29
90	A Functional Screen Identifies miRs That Induce Radioresistance in Glioblastomas. Molecular Cancer Research, 2014, 12, 1767-1778.	3.4	28

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91	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. Cell Reports, 2020, 33, 108493.	6.4	28
92	A Maltose-Binding Protein Fusion Construct Yields a Robust Crystallography Platform for MCL1. PLoS ONE, 2015, 10, e0125010.	2.5	26
93	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. Cell Reports, 2019, 28, 2331-2344.e8.	6.4	24
94	Single Diastereomer of a Macrolactam Core Binds Specifically to Myeloid Cell Leukemia 1 (MCL1). ACS Medicinal Chemistry Letters, 2014, 5, 1308-1312.	2.8	23
95	A phase II study of the EGFR inhibitor gefitinib in patients with acute myeloid leukemia. Leukemia Research, 2014, 38, 430-434.	0.8	23
96	Niche-Based Screening in Multiple Myeloma Identifies a Kinesin-5 Inhibitor with Improved Selectivity over Hematopoietic Progenitors. Cell Reports, 2015, 10, 755-770.	6.4	21
97	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. Nature Communications, 2019, 10, 3166.	12.8	21
98	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. Cancer Discovery, 2021, 11, 2282-2299.	9.4	21
99	Phosphate dysregulation via the XPR1â€“KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. Nature Cancer, 2022, 3, 681-695.	13.2	21
100	Identification of RPS14 as the 5q-Syndrome Gene by RNA Interference Screen.. Blood, 2007, 110, 1-1.	1.4	16
101	Direct evidence for a polygenic etiology in familial multiple myeloma. Blood Advances, 2017, 1, 619-623.	5.2	15
102	Duplex-Repair enables highly accurate sequencing, despite DNA damage. Nucleic Acids Research, 2022, 50, e1-e1.	14.5	10
103	DNA-based copy number analysis confirms genomic evolution of PDX models. Npj Precision Oncology, 2022, 6, 30.	5.4	10
104	Hodgkinâ€™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.. Blood, 2006, 108, 469-469.	1.4	1
105	Characterization of Distinct Molecular Signatures in Myeloproliferative Diseases with the JAK2V617F Mutation and Wild Type JAK2.. Blood, 2005, 106, 119-119.	1.4	0
106	All Memory Lymphocytes Share a Common Differentiation Program.. Blood, 2006, 108, 865-865.	1.4	0
107	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. Neuro-Oncology, 2020, 22, iii471-iii471.	1.2	0
108	EXTH-37. TARGETING EPIGENETIC VULNERABILITIES IDENTIFIED FROM A CRISPR SCREEN IN H3.3K27M DIPG. Neuro-Oncology, 2020, 22, ii95-ii95.	1.2	0