

# Todd R Golub

## List of Publications by Year in descending order

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Version: 2024-02-01

108  
papers

108,612  
citations

10351

72  
h-index

23472

111  
g-index

126  
all docs

126  
docs citations

126  
times ranked

129246  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 15545-15550.	3.3	38,922
2	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , 2012, 483, 603-607.	13.7	6,473
3	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.	7.7	6,138
4	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
5	The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. <i>Science</i> , 2006, 313, 1929-1935.	6.0	4,472
6	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , 2010, 463, 899-905.	13.7	3,331
7	Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis. <i>Cancer Cell</i> , 2005, 7, 387-397.	7.7	2,695
8	Discovery and saturation analysis of cancer genes across 21 tumour types. <i>Nature</i> , 2014, 505, 495-501.	13.7	2,586
9	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , 2017, 171, 1437-1452.e17.	13.5	2,281
10	A molecular signature of metastasis in primary solid tumors. <i>Nature Genetics</i> , 2003, 33, 49-54.	9.4	2,261
11	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	13.7	2,149
12	Defining a Cancer Dependency Map. <i>Cell</i> , 2017, 170, 564-576.e16.	13.5	1,794
13	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, 4164-4169.	3.3	1,649
14	Tumour micro-environment elicits innate resistance to RAF inhibitors through HGF secretion. <i>Nature</i> , 2012, 487, 500-504.	13.7	1,561
15	Copper induces cell death by targeting lipoylated TCA cycle proteins. <i>Science</i> , 2022, 375, 1254-1261.	6.0	1,539
16	Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , 2017, 49, 1779-1784.	9.4	1,436
17	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , 2011, 471, 467-472.	13.7	1,288
18	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , 2018, 24, 679-690.	15.2	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. <i>Blood</i> , 2010, 116, 3268-3277.	0.6	1,122
20	The genomic complexity of primary human prostate cancer. <i>Nature</i> , 2011, 470, 214-220.	13.7	1,107
21	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <i>Science</i> , 2017, 357, 1156-1160.	6.0	1,059
22	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , 2016, 539, 309-313.	13.7	875
23	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, 3879-3884.	3.3	853
24	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. <i>Cancer Cell</i> , 2014, 25, 91-101.	7.7	847
25	Molecular profiling of diffuse large B-cell lymphoma identifies robust subtypes including one characterized by host inflammatory response. <i>Blood</i> , 2005, 105, 1851-1861.	0.6	778
26	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , 2017, 355, .	6.0	743
27	The Drug Repurposing Hub: a next-generation drug library and information resource. <i>Nature Medicine</i> , 2017, 23, 405-408.	15.2	689
28	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , 2018, 560, 325-330.	13.7	662
29	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , 2017, 8, 1324.	5.8	584
30	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , 2017, 49, 1567-1575.	9.4	546
31	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, 20380-20385.	3.3	499
32	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , 2014, 32, 479-484.	9.4	495
33	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , 2016, 6, 914-929.	7.7	485
34	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , 2018, 360, 331-335.	6.0	461
35	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , 2020, 1, 235-248.	5.7	430
36	Targetable genetic features of primary testicular and primary central nervous system lymphomas. <i>Blood</i> , 2016, 127, 869-881.	0.6	429

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37	The Genomic Landscape of Pediatric Ewing Sarcoma. <i>Cancer Discovery</i> , 2014, 4, 1326-1341.	7.7	415
38	A Mechanism of Cyclin D1 Action Encoded in the Patterns of Gene Expression in Human Cancer. <i>Cell</i> , 2003, 114, 323-334.	13.5	395
39	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , 2019, 25, 1415-1421.	15.2	359
40	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.	3.3	355
41	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. <i>Blood</i> , 2014, 123, e123-e133.	0.6	337
42	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.	2.4	328
43	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.	2.9	327
44	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. <i>Nature Communications</i> , 2018, 9, 4610.	5.8	290
45	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , 2014, 42, W449-W460.	6.5	280
46	Mitochondrial metabolism promotes adaptation to proteotoxic stress. <i>Nature Chemical Biology</i> , 2019, 15, 681-689.	3.9	275
47	Protection of tissue physicochemical properties using polyfunctional crosslinkers. <i>Nature Biotechnology</i> , 2019, 37, 73-83.	9.4	262
48	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , 2019, 568, 551-556.	13.7	253
49	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. <i>Nature Biotechnology</i> , 2016, 34, 419-423.	9.4	245
50	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. <i>Nature</i> , 2020, 585, 293-297.	13.7	219
51	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , 2016, 29, 214-228.	7.7	216
52	A metastasis map of human cancer cell lines. <i>Nature</i> , 2020, 588, 331-336.	13.7	214
53	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , 2018, 50, 1240-1246.	9.4	199
54	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.	3.3	195

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55	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, 10911-10916.	3.3	191
56	A method for high-throughput gene expression signature analysis. <i>Genome Biology</i> , 2006, 7, R61.	13.9	190
57	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, 359-372.	7.7	179
58	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	7.7	171
59	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , 2020, 52, 662-668.	9.4	168
60	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.	0.8	162
61	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , 2019, 10, 5817.	5.8	160
62	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , 2019, 19, 97-109.	12.8	158
63	The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. <i>Nature Medicine</i> , 2020, 26, 181-187.	15.2	158
64	SYK Inhibition Modulates Distinct PI3K/AKT- Dependent Survival Pathways and Cholesterol Biosynthesis in Diffuse Large B Cell Lymphomas. <i>Cancer Cell</i> , 2013, 23, 826-838.	7.7	152
65	Fatty acid synthesis is required for breast cancer brain metastasis. <i>Nature Cancer</i> , 2021, 2, 414-428.	5.7	147
66	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , 2016, 6, 714-726.	7.7	139
67	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. <i>PLoS Biology</i> , 2017, 15, e2003213.	2.6	136
68	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , 2021, 590, 486-491.	13.7	135
69	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , 2019, 36, 528-544.e10.	7.7	128
70	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , 2016, 8, 363ra147.	5.8	126
71	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , 2017, 128, 446-462.	3.9	117
72	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , 2020, 26, 2556-2564.	3.2	109

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73	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , 2020, 11, 4296.	5.8	98
74	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , 2019, 9, 35-48.e5.	2.9	95
75	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , 2021, 39, 697-704.	9.4	85
76	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , 2017, 8, 1186.	5.8	78
77	Drug and disease signature integration identifies synergistic combinations in glioblastoma. <i>Nature Communications</i> , 2018, 9, 5315.	5.8	78
78	A first-generation pediatric cancer dependency map. <i>Nature Genetics</i> , 2021, 53, 529-538.	9.4	76
79	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , 2018, 6, 424-443.e7.	2.9	68
80	A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity. <i>Nature Chemical Biology</i> , 2014, 10, 656-663.	3.9	66
81	An ecosystem of cancer cell line factories to support a cancer dependency map. <i>Nature Reviews Genetics</i> , 2015, 16, 373-374.	7.7	65
82	Cancer research needs a better map. <i>Nature</i> , 2021, 589, 514-516.	13.7	57
83	Counterpoint: Data first. <i>Nature</i> , 2010, 464, 679-679.	13.7	49
84	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. <i>Nature Genetics</i> , 2021, 53, 1196-1206.	9.4	47
85	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. <i>JAMA Oncology</i> , 2015, 1, 238.	3.4	44
86	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. <i>Nature Communications</i> , 2016, 7, 12160.	5.8	43
87	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. <i>Neuro-Oncology</i> , 2015, 17, 1486-1496.	0.6	39
88	Massively parallel enrichment of low-frequency alleles enables duplex sequencing at low depth. <i>Nature Biomedical Engineering</i> , 2022, 6, 257-266.	11.6	32
89	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, 24, 1352-1363.	0.6	29
90	A Functional Screen Identifies miRs That Induce Radioresistance in Glioblastomas. <i>Molecular Cancer Research</i> , 2014, 12, 1767-1778.	1.5	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. <i>Cell Reports</i> , 2020, 33, 108493.	2.9	28
92	A Maltose-Binding Protein Fusion Construct Yields a Robust Crystallography Platform for MCL1. <i>PLoS ONE</i> , 2015, 10, e0125010.	1.1	26
93	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.	2.9	24
94	Single Diastereomer of a Macrolactam Core Binds Specifically to Myeloid Cell Leukemia 1 (MCL1). <i>ACS Medicinal Chemistry Letters</i> , 2014, 5, 1308-1312.	1.3	23
95	A phase II study of the EGFR inhibitor gefitinib in patients with acute myeloid leukemia. <i>Leukemia Research</i> , 2014, 38, 430-434.	0.4	23
96	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.	2.9	21
97	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. <i>Nature Communications</i> , 2019, 10, 3166.	5.8	21
98	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , 2021, 11, 2282-2299.	7.7	21
99	Phosphate dysregulation via the XPR1-KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. <i>Nature Cancer</i> , 2022, 3, 681-695.	5.7	21
100	Identification of RPS14 as the 5q-Syndrome Gene by RNA Interference Screen. <i>Blood</i> , 2007, 110, 1-1.	0.6	16
101	Direct evidence for a polygenic etiology in familial multiple myeloma. <i>Blood Advances</i> , 2017, 1, 619-623.	2.5	15
102	Duplex-Repair enables highly accurate sequencing, despite DNA damage. <i>Nucleic Acids Research</i> , 2022, 50, e1-e1.	6.5	10
103	DNA-based copy number analysis confirms genomic evolution of PDX models. <i>Npj Precision Oncology</i> , 2022, 6, 30.	2.3	10
104	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.	0.6	1
105	Characterization of Distinct Molecular Signatures in Myeloproliferative Diseases with the JAK2V617F Mutation and Wild Type JAK2. <i>Blood</i> , 2005, 106, 119-119.	0.6	0
106	All Memory Lymphocytes Share a Common Differentiation Program. <i>Blood</i> , 2006, 108, 865-865.	0.6	0
107	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. <i>Neuro-Oncology</i> , 2020, 22, iii471-iii471.	0.6	0
108	EXTH-37. TARGETING EPIGENETIC VULNERABILITIES IDENTIFIED FROM A CRISPR SCREEN IN H3.3K27M DIPG. <i>Neuro-Oncology</i> , 2020, 22, ii95-ii95.	0.6	0