

# Todd R Golub

## List of Publications by Year in Descending Order

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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	Liquid biopsy detection of genomic alterations in pediatric brain tumors from cell-free DNA in peripheral blood, CSF, and urine.. <i>Neuro-Oncology</i> , <b>2022</b> ,	1	4
112	Massively parallel enrichment of low-frequency alleles enables duplex sequencing at low depth.. <i>Nature Biomedical Engineering</i> , <b>2022</b> ,	19	1
111	Copper induces cell death by targeting lipoylated TCA cycle proteins.. <i>Science</i> , <b>2022</b> , 375, 1254-1261	33.3	89
110	DNA-based copy number analysis confirms genomic evolution of PDX models.. <i>Npj Precision Oncology</i> , <b>2022</b> , 6, 30	9.8	1
109	A first-generation pediatric cancer dependency map. <i>Nature Genetics</i> , <b>2021</b> , 53, 529-538	36.3	21
108	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. <i>Cancer Discovery</i> , <b>2021</b> , 11, 2282-2299	24.4	4
107	FATTY ACID SYNTHESIS IS REQUIRED FOR BREAST CANCER BRAIN METASTASIS. <i>Nature Cancer</i> , <b>2021</b> , 2, 414-428	15.4	31
106	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. <i>Nature Genetics</i> , <b>2021</b> , 53, 1196-1206	36.3	9
105	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. <i>Nature Biotechnology</i> , <b>2021</b> , 39, 697-704	44.5	17
104	Cancer research needs a better map. <i>Nature</i> , <b>2021</b> , 589, 514-516	50.4	19
103	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. <i>Nature</i> , <b>2021</b> , 590, 486-491	50.4	34
102	A metastasis map of human cancer cell lines. <i>Nature</i> , <b>2020</b> , 588, 331-336	50.4	76
101	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. <i>Nature Genetics</i> , <b>2020</b> , 52, 662-668	36.3	69
100	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. <i>Nature</i> , <b>2020</b> , 585, 293-297	50.4	93
99	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. <i>Clinical Cancer Research</i> , <b>2020</b> , 26, 2556-2564	12.9	32
98	The Angiosarcoma Project: enabling genomic and clinical discoveries in a rare cancer through patient-partnered research. <i>Nature Medicine</i> , <b>2020</b> , 26, 181-187	50.5	69
97	Discovering the anti-cancer potential of non-oncology drugs by systematic viability profiling. <i>Nature Cancer</i> , <b>2020</b> , 1, 235-248	15.4	137

96	EXTH-37. TARGETING EPIGENETIC VULNERABILITIES IDENTIFIED FROM A CRISPR SCREEN IN H3.3K27M DIPG. <i>Neuro-Oncology</i> , <b>2020</b> , 22, ii95-ii95	1	
95	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. <i>Neuro-Oncology</i> , <b>2020</b> , 22, iii471-iii471	1	78
94	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. <i>Nature Communications</i> , <b>2020</b> , 11, 4296	17.4	37
93	Synthetic Lethal Interaction between the ESCRT Paralog Enzymes VPS4A and VPS4B in Cancers Harboring Loss of Chromosome 18q or 16q. <i>Cell Reports</i> , <b>2020</b> , 33, 108493	10.6	7
92	Small-Molecule and CRISPR Screening Converge to Reveal Receptor Tyrosine Kinase Dependencies in Pediatric Rhabdoid Tumors. <i>Cell Reports</i> , <b>2019</b> , 28, 2331-2344.e8	10.6	20
91	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. <i>Nature Medicine</i> , <b>2019</b> , 25, 1415-1421	50.5	161
90	Mitochondrial metabolism promotes adaptation to proteotoxic stress. <i>Nature Chemical Biology</i> , <b>2019</b> , 15, 681-689	11.7	62
89	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , <b>2019</b> , 569, 503-508	50.4	962
88	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. <i>Nature</i> , <b>2019</b> , 568, 551-556	50.4	137
87	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. <i>Nature Communications</i> , <b>2019</b> , 10, 3166	17.4	9
86	A Multi-center Study on the Reproducibility of Drug-Response Assays in Mammalian Cell Lines. <i>Cell Systems</i> , <b>2019</b> , 9, 35-48.e5	10.6	46
85	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. <i>Cancer Cell</i> , <b>2019</b> , 36, 528-544.e10	24.3	66
84	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. <i>Nature Communications</i> , <b>2019</b> , 10, 5817	17.4	70
83	Genomic evolution of cancer models: perils and opportunities. <i>Nature Reviews Cancer</i> , <b>2019</b> , 19, 97-109	31.3	104
82	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. <i>Science</i> , <b>2018</b> , 360, 331-335	33.3	255
81	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. <i>Cell Systems</i> , <b>2018</b> , 6, 424-443.e7	10.6	47
80	The Library of Integrated Network-Based Cellular Signatures NIH Program: System-Level Cataloging of Human Cells Response to Perturbations. <i>Cell Systems</i> , <b>2018</b> , 6, 13-24	10.6	199
79	Molecular subtypes of diffuse large B cell lymphoma are associated with distinct pathogenic mechanisms and outcomes. <i>Nature Medicine</i> , <b>2018</b> , 24, 679-690	50.5	659

78	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. <i>Nature Genetics</i> , <b>2018</b> , 50, 1240-1246	36.3	94
77	Genetic and transcriptional evolution alters cancer cell line drug response. <i>Nature</i> , <b>2018</b> , 560, 325-330	50.4	379
76	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. <i>Journal of Clinical Investigation</i> , <b>2018</b> , 128, 446-462	15.9	72
75	Protection of tissue physicochemical properties using polyfunctional crosslinkers. <i>Nature Biotechnology</i> , <b>2018</b> ,	44.5	123
74	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> , <b>2018</b> , 36, 543-553	2.2	113
73	Improved estimation of cancer dependencies from large-scale RNAi screens using model-based normalization and data integration. <i>Nature Communications</i> , <b>2018</b> , 9, 4610	17.4	155
72	Drug and disease signature integration identifies synergistic combinations in glioblastoma. <i>Nature Communications</i> , <b>2018</b> , 9, 5315	17.4	44
71	The Drug Repurposing Hub: a next-generation drug library and information resource. <i>Nature Medicine</i> , <b>2017</b> , 23, 405-408	50.5	381
70	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. <i>Science</i> , <b>2017</b> , 355,	33.3	455
69	Computational correction of copy number effect improves specificity of CRISPR-Cas9 essentiality screens in cancer cells. <i>Nature Genetics</i> , <b>2017</b> , 49, 1779-1784	36.3	740
68	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. <i>Nature Communications</i> , <b>2017</b> , 8, 1186	17.4	38
67	Patient-derived xenografts undergo mouse-specific tumor evolution. <i>Nature Genetics</i> , <b>2017</b> , 49, 1567-1576	36.3	384
66	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. <i>Science</i> , <b>2017</b> , 357, 1156-1160	33.3	577
65	Defining a Cancer Dependency Map. <i>Cell</i> , <b>2017</b> , 170, 564-576.e16	56.2	844
64	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. <i>Cell</i> , <b>2017</b> , 171, 1437-1452.e17	56.2	1132
63	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. <i>Nature Communications</i> , <b>2017</b> , 8, 1324	17.4	314
62	Direct evidence for a polygenic etiology in familial multiple myeloma. <i>Blood Advances</i> , <b>2017</b> , 1, 619-623	7.8	13
61	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. <i>PLoS Biology</i> , <b>2017</b> , 15, e2003213	9.7	99

60	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. <i>Nature Communications</i> , <b>2016</b> , 7, 12160	17.4	36
59	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. <i>Nature</i> , <b>2016</b> , 539, 309-313	50.4	561
58	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. <i>Science Translational Medicine</i> , <b>2016</b> , 8, 363ra147	17.5	93
57	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. <i>Cancer Discovery</i> , <b>2016</b> , 6, 914-29	24.4	343
56	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. <i>Cancer Cell</i> , <b>2016</b> , 29, 214-28	24.3	118
55	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 419-23	44.5	127
54	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. <i>Cancer Discovery</i> , <b>2016</b> , 6, 714-26	24.4	100
53	Targetable genetic features of primary testicular and primary central nervous system lymphomas. <i>Blood</i> , <b>2016</b> , 127, 869-81	2.2	317
52	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , <b>2016</b> , 30, 214-228	24.3	119
51	An ecosystem of cancer cell line factories to support a cancer dependency map. <i>Nature Reviews Genetics</i> , <b>2015</b> , 16, 373-4	30.1	42
50	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> , <b>2015</b> , 112, E5486-95	11.5	142
49	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. <i>JAMA Oncology</i> , <b>2015</b> , 1, 238-44	13.4	41
48	A Maltose-Binding Protein Fusion Construct Yields a Robust Crystallography Platform for MCL1. <i>PLoS ONE</i> , <b>2015</b> , 10, e0125010	3.7	23
47	Expression profiles of 151 pediatric low-grade gliomas reveal molecular differences associated with location and histological subtype. <i>Neuro-Oncology</i> , <b>2015</b> , 17, 1486-96	1	33
46	Niche-Based Screening in Multiple Myeloma Identifies a Kinesin-5 Inhibitor with Improved Selectivity over Hematopoietic Progenitors. <i>Cell Reports</i> , <b>2015</b> , 10, 755-770	10.6	18
45	Widespread genetic heterogeneity in multiple myeloma: implications for targeted therapy. <i>Cancer Cell</i> , <b>2014</b> , 25, 91-101	24.3	657
44	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. <i>Blood</i> , <b>2014</b> , 123, e123-33	2.2	264
43	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 479-84	44.5	434

42	Discovery and saturation analysis of cancer genes across 21 tumour types. <i>Nature</i> , <b>2014</b> , 505, 495-501	50.4	1990
41	A functional screen identifies miRs that induce radioresistance in glioblastomas. <i>Molecular Cancer Research</i> , <b>2014</b> , 12, 1767-78	6.6	19
40	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> , <b>2014</b> , 111, 10911-6	11.5	141
39	A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity. <i>Nature Chemical Biology</i> , <b>2014</b> , 10, 656-63	11.7	54
38	A phase II study of the EGFR inhibitor gefitinib in patients with acute myeloid leukemia. <i>Leukemia Research</i> , <b>2014</b> , 38, 430-4	2.7	18
37	Parallel genome-scale loss of function screens in 216 cancer cell lines for the identification of context-specific genetic dependencies. <i>Scientific Data</i> , <b>2014</b> , 1, 140035	8.2	251
36	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> , <b>2014</b> , 111, E5564-73	11.5	275
35	LINCS Canvas Browser: interactive web app to query, browse and interrogate LINCS L1000 gene expression signatures. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W449-60	20.1	204
34	Single Diastereomer of a Macrolactam Core Binds Specifically to Myeloid Cell Leukemia 1 (MCL1). <i>ACS Medicinal Chemistry Letters</i> , <b>2014</b> , 5, 1308-12	4.3	22
33	The genomic landscape of pediatric Ewing sarcoma. <i>Cancer Discovery</i> , <b>2014</b> , 4, 1326-41	24.4	302
32	SYK inhibition modulates distinct PI3K/AKT- dependent survival pathways and cholesterol biosynthesis in diffuse large B cell lymphomas. <i>Cancer Cell</i> , <b>2013</b> , 23, 826-38	24.3	120
31	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , <b>2013</b> , 499, 214-218	50.4	3616
30	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> , <b>2012</b> , 22, 359-72	24.3	148
29	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. <i>Nature</i> , <b>2012</b> , 483, 603-7	50.4	4648
28	Tumour micro-environment elicits innate resistance to RAF inhibitors through HGF secretion. <i>Nature</i> , <b>2012</b> , 487, 500-4	50.4	1308
27	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> , <b>2012</b> , 109, 3879-84	11.5	735
26	The genomic complexity of primary human prostate cancer. <i>Nature</i> , <b>2011</b> , 470, 214-20	50.4	984
25	Initial genome sequencing and analysis of multiple myeloma. <i>Nature</i> , <b>2011</b> , 471, 467-72	50.4	1117

24	The landscape of somatic copy-number alteration across human cancers. <i>Nature</i> , <b>2010</b> , 463, 899-905	50.4	2590
23	Counterpoint: Data first. <i>Nature</i> , <b>2010</b> , 464, 679	50.4	37
22	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> , <b>2010</b> , 116, 3268-77	2.2	903
21	Integrated genomic analysis identifies clinically relevant subtypes of glioblastoma characterized by abnormalities in PDGFRA, IDH1, EGFR, and NF1. <i>Cancer Cell</i> , <b>2010</b> , 17, 98-110	24.3	4782
20	Highly parallel identification of essential genes in cancer cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 20380-5	11.5	424
19	Identification of RPS14 as the 5q-Syndrome Gene by RNA Interference Screen.. <i>Blood</i> , <b>2007</b> , 110, 1-1	2.2	9
18	A method for high-throughput gene expression signature analysis. <i>Genome Biology</i> , <b>2006</b> , 7, R61	18.3	175
17	The Connectivity Map: using gene-expression signatures to connect small molecules, genes, and disease. <i>Science</i> , <b>2006</b> , 313, 1929-35	33.3	3392
16	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> , <b>2006</b> , 108, 469-469	2.2	1
15	All Memory Lymphocytes Share a Common Differentiation Program.. <i>Blood</i> , <b>2006</b> , 108, 865-865	2.2	
14	Molecular profiling of diffuse large B-cell lymphoma identifies robust subtypes including one characterized by host inflammatory response. <i>Blood</i> , <b>2005</b> , 105, 1851-61	2.2	654
13	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> , <b>2005</b> , 102, 15545-50	11.5	24578
12	Activating mutation in the tyrosine kinase JAK2 in polycythemia vera, essential thrombocythemia, and myeloid metaplasia with myelofibrosis. <i>Cancer Cell</i> , <b>2005</b> , 7, 387-97	24.3	2353
11	Characterization of Distinct Molecular Signatures in Myeloproliferative Diseases with the JAK2V617F Mutation and Wild Type JAK2.. <i>Blood</i> , <b>2005</b> , 106, 119-119	2.2	
10	Metagenes and molecular pattern discovery using matrix factorization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 4164-9	11.5	1178
9	A molecular signature of metastasis in primary solid tumors. <i>Nature Genetics</i> , <b>2003</b> , 33, 49-54	36.3	1973
8	A mechanism of cyclin D1 action encoded in the patterns of gene expression in human cancer. <i>Cell</i> , <b>2003</b> , 114, 323-34	56.2	353
7	Phosphate dysregulation via the XPR1:KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer		1

6	Multiplexed single-cell profiling of post-perturbation transcriptional responses to define cancer vulnerabilities and therapeutic mechanism of action	3
5	Gene expression has more power for predicting in vitro cancer cell vulnerabilities than genomics	12
4	Non-canonical open reading frames encode functional proteins essential for cancer cell survival	2
3	Selective vulnerability of aneuploid human cancer cells to inhibition of the spindle assembly checkpoint	4
2	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency datasets	2
1	Non-oncology drugs are a source of previously unappreciated anti-cancer activity	6