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	Duplex-Repair enables highly accurate sequencing, despite DNA damage. Nucleic Acids Research, 2022, 50, e1-e1.	14.5	10
2	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
3	Massively parallel enrichment of low-frequency alleles enables duplex sequencing at low depth. Nature Biomedical Engineering, 2022, 6, 257-266.	22.5	32
4	Copper induces cell death by targeting lipoylated TCA cycle proteins. Science, 2022, 375, 1254-1261.	12.6	1,539
5	Phosphate dysregulation via the XPR1â€“KIDINS220 protein complex is a therapeutic vulnerability in ovarian cancer. Nature Cancer, 2022, 3, 681-695.	13.2	21
6	DNA-based copy number analysis confirms genomic evolution of PDX models. Npj Precision Oncology, 2022, 6, 30.	5.4	10
7	Noncanonical open reading frames encode functional proteins essential for cancer cell survival. Nature Biotechnology, 2021, 39, 697-704.	17.5	85
8	Cancer research needs a better map. Nature, 2021, 589, 514-516.	27.8	57
9	Aneuploidy renders cancer cells vulnerable to mitotic checkpoint inhibition. Nature, 2021, 590, 486-491.	27.8	135
10	A first-generation pediatric cancer dependency map. Nature Genetics, 2021, 53, 529-538.	21.4	76
11	Selective Modulation of a Pan-Essential Protein as a Therapeutic Strategy in Cancer. Cancer Discovery, 2021, 11, 2282-2299.	9.4	21
12	Fatty acid synthesis is required for breast cancer brain metastasis. Nature Cancer, 2021, 2, 414-428.	13.2	147
13	Genome-scale screens identify factors regulating tumor cell responses to natural killer cells. Nature Genetics, 2021, 53, 1196-1206.	21.4	47
14	Multiplexed single-cell transcriptional response profiling to define cancer vulnerabilities and therapeutic mechanism of action. Nature Communications, 2020, 11, 4296.	12.8	98
15	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
16	A metastasis map of human cancer cell lines. Nature, 2020, 588, 331-336.	27.8	214
17	Cas9 activates the p53 pathway and selects for p53-inactivating mutations. Nature Genetics, 2020, 52, 662-668.	21.4	168
18	The CDK inhibitor CR8 acts as a molecular glue degrader that depletes cyclin K. Nature, 2020, 585, 293-297.	27.8	219

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19	Sensitive Detection of Minimal Residual Disease in Patients Treated for Early-Stage Breast Cancer. Clinical Cancer Research, 2020, 26, 2556-2564.	7.0	109
20	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
21	Discovering the anticancer potential of non-oncology drugs by systematic viability profiling. Nature Cancer, 2020, 1, 235-248.	13.2	430
22	TBIO-26. NON-CANONICAL OPEN READING FRAMES ENCODE FUNCTIONAL PROTEINS ESSENTIAL FOR CANCER CELL SURVIVAL. Neuro-Oncology, 2020, 22, iii471-iii471.	1.2	0
23	EXTH-37. TARGETING EPIGENETIC VULNERABILITIES IDENTIFIED FROM A CRISPR SCREEN IN H3.3K27M DIPG. Neuro-Oncology, 2020, 22, ii95-ii95.	1.2	0
24	Structural mechanism of synergistic activation of Aurora kinase B/C by phosphorylated INCENP. Nature Communications, 2019, 10, 3166.	12.8	21
25	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
26	Re-programing Chromatin with a Bifunctional LSD1/HDAC Inhibitor Induces Therapeutic Differentiation in DIPG. Cancer Cell, 2019, 36, 528-544.e10.	16.8	128
27	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
28	Liquid versus tissue biopsy for detecting acquired resistance and tumor heterogeneity in gastrointestinal cancers. Nature Medicine, 2019, 25, 1415-1421.	30.7	359
29	Mitochondrial metabolism promotes adaptation to proteotoxic stress. Nature Chemical Biology, 2019, 15, 681-689.	8.0	275
30	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	27.8	2,149
31	WRN helicase is a synthetic lethal target in microsatellite unstable cancers. Nature, 2019, 568, 551-556.	27.8	253
32	Agreement between two large pan-cancer CRISPR-Cas9 gene dependency data sets. Nature Communications, 2019, 10, 5817.	12.8	160
33	Protection of tissue physicochemical properties using polyfunctional crosslinkers. Nature Biotechnology, 2019, 37, 73-83.	17.5	262
34	Genomic evolution of cancer models: perils and opportunities. Nature Reviews Cancer, 2019, 19, 97-109.	28.4	158
35	Developmental and oncogenic programs in H3K27M gliomas dissected by single-cell RNA-seq. Science, 2018, 360, 331-335.	12.6	461
36	A Library of Phosphoproteomic and Chromatin Signatures for Characterizing Cellular Responses to Drug Perturbations. Cell Systems, 2018, 6, 424-443.e7.	6.2	68

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37	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
38	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
39	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
40	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
41	Drug and disease signature integration identifies synergistic combinations in glioblastoma. Nature Communications, 2018, 9, 5315.	12.8	78
42	Selective gene dependencies in MYCN-amplified neuroblastoma include the core transcriptional regulatory circuitry. Nature Genetics, 2018, 50, 1240-1246.	21.4	199
43	Genetic and transcriptional evolution alters cancer cell line drug response. Nature, 2018, 560, 325-330.	27.8	662
44	The Drug Repurposing Hub: a next-generation drug library and information resource. Nature Medicine, 2017, 23, 405-408.	30.7	689
45	Decoupling genetics, lineages, and microenvironment in IDH-mutant gliomas by single-cell RNA-seq. Science, 2017, 355, .	12.6	743
46	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
47	Common and cell-type specific responses to anti-cancer drugs revealed by high throughput transcript profiling. Nature Communications, 2017, 8, 1186.	12.8	78
48	Patient-derived xenografts undergo mouse-specific tumor evolution. Nature Genetics, 2017, 49, 1567-1575.	21.4	546
49	Potential role of intratumor bacteria in mediating tumor resistance to the chemotherapeutic drug gemcitabine. Science, 2017, 357, 1156-1160.	12.6	1,059
50	Defining a Cancer Dependency Map. Cell, 2017, 170, 564-576.e16.	28.9	1,794
51	A Next Generation Connectivity Map: L1000 Platform and the First 1,000,000 Profiles. Cell, 2017, 171, 1437-1452.e17.	28.9	2,281
52	Scalable whole-exome sequencing of cell-free DNA reveals high concordance with metastatic tumors. Nature Communications, 2017, 8, 1324.	12.8	584
53	Direct evidence for a polygenic etiology in familial multiple myeloma. Blood Advances, 2017, 1, 619-623.	5.2	15
54	CRISPR-Cas9 screen reveals a MYCN-amplified neuroblastoma dependency on EZH2. Journal of Clinical Investigation, 2017, 128, 446-462.	8.2	117

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55	Evaluation of RNAi and CRISPR technologies by large-scale gene expression profiling in the Connectivity Map. PLoS Biology, 2017, 15, e2003213.	5.6	136
56	Systematic Functional Interrogation of Rare Cancer Variants Identifies Oncogenic Alleles. Cancer Discovery, 2016, 6, 714-726.	9.4	139
57	Targetable genetic features of primary testicular and primary central nervous system lymphomas. Blood, 2016, 127, 869-881.	1.4	429
58	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	16.8	171
59	The landscape of chromosomal aberrations in breast cancer mouse models reveals driver-specific routes to tumorigenesis. Nature Communications, 2016, 7, 12160.	12.8	43
60	Single-cell RNA-seq supports a developmental hierarchy in human oligodendroglioma. Nature, 2016, 539, 309-313.	27.8	875
61	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. Science Translational Medicine, 2016, 8, 363ra147.	12.4	126
62	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	9.4	485
63	miR-126 Regulates Distinct Self-Renewal Outcomes in Normal and Malignant Hematopoietic Stem Cells. Cancer Cell, 2016, 29, 214-228.	16.8	216
64	High-throughput identification of genotype-specific cancer vulnerabilities in mixtures of barcoded tumor cell lines. Nature Biotechnology, 2016, 34, 419-423.	17.5	245
65	A Maltose-Binding Protein Fusion Construct Yields a Robust Crystallography Platform for MCL1. PLoS ONE, 2015, 10, e0125010.	2.5	26
66	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
67	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
68	An ecosystem of cancer cell line factories to support a cancer dependency map. Nature Reviews Genetics, 2015, 16, 373-374.	16.3	65
69	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
70	Genomic Correlate of Exceptional Erlotinib Response in Head and Neck Squamous Cell Carcinoma. JAMA Oncology, 2015, 1, 238.	7.1	44
71	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
72	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

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73	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
74	The Genomic Landscape of Pediatric Ewing Sarcoma. Cancer Discovery, 2014, 4, 1326-1341.	9.4	415
75	Widespread Genetic Heterogeneity in Multiple Myeloma: Implications for Targeted Therapy. Cancer Cell, 2014, 25, 91-101.	16.8	847
76	Integrated genomic analysis illustrates the central role of JAK-STAT pathway activation in myeloproliferative neoplasm pathogenesis. Blood, 2014, 123, e123-e133.	1.4	337
77	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
78	Discovery and saturation analysis of cancer genes across 21 tumour types. Nature, 2014, 505, 495-501.	27.8	2,586
79	A Functional Screen Identifies miRs That Induce Radioresistance in Glioblastomas. Molecular Cancer Research, 2014, 12, 1767-1778.	3.4	28
80	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
81	A high-throughput, multiplexed assay for superfamily-wide profiling of enzyme activity. Nature Chemical Biology, 2014, 10, 656-663.	8.0	66
82	A phase II study of the EGFR inhibitor gefitinib in patients with acute myeloid leukemia. Leukemia Research, 2014, 38, 430-434.	0.8	23
83	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
84	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
85	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	27.8	4,761
86	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
87	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
88	The Cancer Cell Line Encyclopedia enables predictive modelling of anticancer drug sensitivity. Nature, 2012, 483, 603-607.	27.8	6,473
89	Tumour micro-environment elicits innate resistance to RAF inhibitors through HGF secretion. Nature, 2012, 487, 500-504.	27.8	1,561
90	The genomic complexity of primary human prostate cancer. Nature, 2011, 470, 214-220.	27.8	1,107

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91	Initial genome sequencing and analysis of multiple myeloma. Nature, 2011, 471, 467-472.	27.8	1,288
92	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
93	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
94	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
95	Counterpoint: Data first. Nature, 2010, 464, 679-679.	27.8	49
96	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
97	Identification of RPS14 as the 5q-Syndrome Gene by RNA Interference Screen.. Blood, 2007, 110, 1-1.	1.4	16
98	A method for high-throughput gene expression signature analysis. Genome Biology, 2006, 7, R61.	9.6	190
99	The Connectivity Map: Using Gene-Expression Signatures to Connect Small Molecules, Genes, and Disease. Science, 2006, 313, 1929-1935.	12.6	4,472
100	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
101	All Memory Lymphocytes Share a Common Differentiation Program.. Blood, 2006, 108, 865-865.	1.4	0
102	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
103	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
104	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
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	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
107	A molecular signature of metastasis in primary solid tumors. Nature Genetics, 2003, 33, 49-54.	21.4	2,261
108	A Mechanism of Cyclin D1 Action Encoded in the Patterns of Gene Expression in Human Cancer. Cell, 2003, 114, 323-334.	28.9	395