Justin H Guinney

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. Cell Reports Medicine, 2022, 3, 100492.	6.5	33
2	Demonstrating an approach for evaluating synthetic geospatial and temporal epidemiologic data utility: results from analyzing >1.8 million SARS-CoV-2 tests in the United States National COVID Cohort Collaborative (N3C). Journal of the American Medical Informatics Association: JAMIA, 2022, 29, 1350-1365.	4.4	8
3	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. JAMA Network Open, 2022, 5, e223890.	5.9	31
4	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. Journal of the American Medical Informatics Association: JAMIA, 2021, 28, 427-443.	4.4	342
5	Pursuing Better Biomarkers for Immunotherapy Response in Cancer Through a Crowdsourced Data Challenge. JCO Precision Oncology, 2021, 5, 51-54.	3.0	7
6	Integrated molecular and clinical analysis of low-grade gliomas in children with neurofibromatosis type 1 (NF1). Acta Neuropathologica, 2021, 141, 605-617.	7.7	36
7	Crowdsourced mapping of unexplored target space of kinase inhibitors. Nature Communications, 2021, 12, 3307.	12.8	41
8	Bayesian multi-source regression and monocyte-associated gene expression predict BCL-2 inhibitor resistance in acute myeloid leukemia. Npj Precision Oncology, 2021, 5, 71.	5.4	12
9	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Non–Small Cell Lung or Colorectal Cancer. JAMA Network Open, 2021, 4, e2117547.	5.9	20
10	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. JAMA Network Open, 2021, 4, e2116901.	5.9	179
11	Outcomes of COVID-19 in Patients With Cancer: Report From the National COVID Cohort Collaborative (N3C). Journal of Clinical Oncology, 2021, 39, 2232-2246.	1.6	97
12	Brigatinib causes tumor shrinkage in both NF2-deficient meningioma and schwannoma through inhibition of multiple tyrosine kinases but not ALK. PLoS ONE, 2021, 16, e0252048.	2.5	19
13	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. Cell Systems, 2021, 12, 827-838.e5.	6.2	15
14	Crowdsourced identification of multi-target kinase inhibitors for RET- and TAU- based disease: The Multi-Targeting Drug DREAM Challenge. PLoS Computational Biology, 2021, 17, e1009302.	3.2	7
15	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. JAMA Network Open, 2021, 4, e2124946.	5.9	8
16	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. Cell, 2020, 183, 818-834.e13.	28.9	287
17	Piloting a model-to-data approach to enable predictive analytics in health care through patient mortality prediction. Journal of the American Medical Informatics Association: JAMIA, 2020, 27, 1393-1400.	4.4	6
18	Society for Immunotherapy of Cancer clinical and biomarkers data sharing resource document: Volume Il—practical challenges. , 2020, 8, e001472.		4

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19	A clinically and genomically annotated nerve sheath tumor biospecimen repository. Scientific Data, 2020, 7, 184.	5.3	19
20	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. Genes, 2020, 11, 226.	2.4	11
21	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. Leukemia, 2020, 34, 1866-1874.	7.2	36
22	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. JAMA Network Open, 2020, 3, e200265.	5.9	236
23	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. Cell, 2020, 181, 236-249.	28.9	334
24	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. Life Science Alliance, 2020, 3, e202000867.	2.8	20
25	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. Genome Biology, 2019, 20, 195.	8.8	19
26	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
27	The evolution and multi-molecular properties of NF1 cutaneous neurofibromas originating from C-fiber sensory endings and terminal Schwann cells at normal sites of sensory terminations in the skin. PLoS ONE, 2019, 14, e0216527.	2.5	15
28	Engaging a community to enable disease-centric data sharing with the NF Data Portal. Scientific Data, 2019, 6, 319.	5.3	8
29	Spatiotemporal Loss of <i>NF1</i> in Schwann Cell Lineage Leads to Different Types of Cutaneous Neurofibroma Susceptible to Modification by the Hippo Pathway. Cancer Discovery, 2019, 9, 114-129.	9.4	65
30	Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. Blood, 2019, 134, 4370-4370.	1.4	0
31	Cutaneous neurofibromas in the genomics era: current understanding and open questions. British Journal of Cancer, 2018, 118, 1539-1548.	6.4	29
32	Functional Precision Medicine Identifies Novel Druggable Targets and Therapeutic Options in Head and Neck Cancer. Clinical Cancer Research, 2018, 24, 2828-2843.	7.0	20
33	KRAS Mutation and Consensus Molecular Subtypes 2 and 3 Are Independently Associated with Reduced Immune Infiltration and Reactivity in Colorectal Cancer. Clinical Cancer Research, 2018, 24, 224-233.	7.0	101
34	Colorectal Cancer Consensus Molecular Subtypes Translated to Preclinical Models Uncover Potentially Targetable Cancer Cell Dependencies. Clinical Cancer Research, 2018, 24, 794-806.	7.0	177
35	Probing the chemicalâ \in "biological relationship space with the Drug Target Explorer. Journal of Cheminformatics, 2018, 10, 41.	6.1	10
36	Traditional and systems biology based drug discovery for the rare tumor syndrome neurofibromatosis type 2. PLoS ONE, 2018, 13, e0197350.	2.5	17

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37	Alternative models for sharing confidential biomedical data. Nature Biotechnology, 2018, 36, 391-392.	17.5	56
38	Pharmacological and genomic profiling of neurofibromatosis type 1 plexiform neurofibroma-derived schwann cells. Scientific Data, 2018, 5, 180106.	5.3	20
39	Comparative Analysis of Independent Ex Vivo functional Drug Screens Identifies Predictive Biomarkers of BCL-2 Inhibitor Response in AML. Blood, 2018, 132, 2763-2763.	1.4	1
40	<i>BRAF</i> â€^ <i>V600E</i> Mutant Colorectal Cancer Subtypes Based on Gene Expression. Clinical Cancer Research, 2017, 23, 104-115.	7.0	167
41	A high-throughput molecular data resource for cutaneous neurofibromas. Scientific Data, 2017, 4, 170045.	5.3	22
42	Consensus molecular subtypes and the evolution of precision medicine in colorectal cancer. Nature Reviews Cancer, 2017, 17, 79-92.	28.4	686
43	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. Cell Reports, 2017, 20, 2201-2214.	6.4	95
44	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. Lancet Oncology, The, 2017, 18, 132-142.	10.7	124
45	Multi-targeting Drug Community Challenge. Cell Chemical Biology, 2017, 24, 1434-1435.	5.2	13
46	Community mining of open clinical trial data. Oncotarget, 2017, 8, 81721-81722.	1.8	1
47	American Joint Committee on Cancer acceptance criteria for inclusion of risk models for individualized prognosis in the practice of precision medicine. Ca-A Cancer Journal for Clinicians, 2016, 66, 370-374.	329.8	280
48	Database of Genomic Biomarkers for Cancer Drugs and Clinical Targetability in Solid Tumors. Cancer Discovery, 2015, 5, 118-123.	9.4	109
49	The NIH BD2K center for big data in translational genomics. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1143-1147.	4.4	30
50	Impact of centralization on aCGH-based genomic profiles for precision medicine in oncology. Annals of Oncology, 2015, 26, 582-588.	1.2	13
51	The consensus molecular subtypes of colorectal cancer. Nature Medicine, 2015, 21, 1350-1356.	30.7	3,596
52	Modeling RAS Phenotype in Colorectal Cancer Uncovers Novel Molecular Traits of RAS Dependency and Improves Prediction of Response to Targeted Agents in Patients. Clinical Cancer Research, 2014, 20, 265-272.	7.0	36
53	Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates. Molecular Cell, 2013, 49, 359-367.	9.7	2,734
54	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. PLoS Computational Biology, 2013, 9, e1003047.	3.2	76

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55	Impact of Bioinformatic Procedures in the Development and Translation of High-Throughput Molecular Classifiers in Oncology. Clinical Cancer Research, 2013, 19, 4315-4325.	7.0	32
56	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. Science Translational Medicine, 2013, 5, 181re1.	12.4	108
57	Evidence for type II cells as cells of origin of K-Ras–induced distal lung adenocarcinoma. Proceedings of the United States of America, 2012, 109, 4910-4915.	7.1	242
58	Integrating Genetic Association, Genetics of Gene Expression, and Single Nucleotide Polymorphism Set Analysis to Identify Susceptibility Loci for Type 2 Diabetes Mellitus. American Journal of Epidemiology, 2012, 176, 423-430.	3.4	31
59	Predictive Genes in Adjacent Normal Tissue Are Preferentially Altered by sCNV during Tumorigenesis in Liver Cancer and May Rate Limiting. PLoS ONE, 2011, 6, e20090.	2.5	68
60	A 10-Gene Progenitor Cell Signature Predicts Poor Prognosis in Lung Adenocarcinoma. Annals of Thoracic Surgery, 2011, 91, 1046-1050.	1.3	6
61	Estimating variable structure and dependence inÂmultitask learning via gradients. Machine Learning, 2011, 83, 265-287.	5.4	6
62	Modeling Cancer Progression via Pathway Dependencies. PLoS Computational Biology, 2008, 4, e28.	3.2	60