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List of Publications by Year in descending order

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Version: 2024-02-01

62
papers

11,189
citations

172207

29
h-index

128067

60
g-index

73
all docs

73
docs citations

73
times ranked

20620
citing authors

#	ARTICLE	IF	CITATIONS
1	The consensus molecular subtypes of colorectal cancer. <i>Nature Medicine</i> , 2015, 21, 1350-1356.	15.2	3,596
2	Genome-wide Methylation Profiles Reveal Quantitative Views of Human Aging Rates. <i>Molecular Cell</i> , 2013, 49, 359-367.	4.5	2,734
3	Consensus molecular subtypes and the evolution of precision medicine in colorectal cancer. <i>Nature Reviews Cancer</i> , 2017, 17, 79-92.	12.8	686
4	The National COVID Cohort Collaborative (N3C): Rationale, design, infrastructure, and deployment. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 427-443.	2.2	342
5	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	13.5	334
6	Key Parameters of Tumor Epitope Immunogenicity Revealed Through a Consortium Approach Improve Neoantigen Prediction. <i>Cell</i> , 2020, 183, 818-834.e13.	13.5	287
7	American Joint Committee on Cancer acceptance criteria for inclusion of risk models for individualized prognosis in the practice of precision medicine. <i>Ca-A Cancer Journal for Clinicians</i> , 2016, 66, 370-374.	157.7	280
8	Evidence for type II cells as cells of origin of K-Ras ^{WT} -induced distal lung adenocarcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 4910-4915.	3.3	242
9	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. <i>Nature Communications</i> , 2019, 10, 2674.	5.8	240
10	Evaluation of Combined Artificial Intelligence and Radiologist Assessment to Interpret Screening Mammograms. <i>JAMA Network Open</i> , 2020, 3, e200265.	2.8	236
11	Clinical Characterization and Prediction of Clinical Severity of SARS-CoV-2 Infection Among US Adults Using Data From the US National COVID Cohort Collaborative. <i>JAMA Network Open</i> , 2021, 4, e2116901.	2.8	179
12	Colorectal Cancer Consensus Molecular Subtypes Translated to Preclinical Models Uncover Potentially Targetable Cancer Cell Dependencies. <i>Clinical Cancer Research</i> , 2018, 24, 794-806.	3.2	177
13	<i>BRAF</i> ^{V600E} Mutant Colorectal Cancer Subtypes Based on Gene Expression. <i>Clinical Cancer Research</i> , 2017, 23, 104-115.	3.2	167
14	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. <i>Lancet Oncology</i> , 2017, 18, 132-142.	5.1	124
15	Database of Genomic Biomarkers for Cancer Drugs and Clinical Targetability in Solid Tumors. <i>Cancer Discovery</i> , 2015, 5, 118-123.	7.7	109
16	Systematic Analysis of Challenge-Driven Improvements in Molecular Prognostic Models for Breast Cancer. <i>Science Translational Medicine</i> , 2013, 5, 181re1.	5.8	108
17	KRAS Mutation and Consensus Molecular Subtypes 2 and 3 Are Independently Associated with Reduced Immune Infiltration and Reactivity in Colorectal Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 224-233.	3.2	101
18	Outcomes of COVID-19 in Patients With Cancer: Report From the National COVID Cohort Collaborative (N3C). <i>Journal of Clinical Oncology</i> , 2021, 39, 2232-2246.	0.8	97

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19	Genomic Determinants of Protein Abundance Variation in Colorectal Cancer Cells. <i>Cell Reports</i> , 2017, 20, 2201-2214.	2.9	95
20	Improving Breast Cancer Survival Analysis through Competition-Based Multidimensional Modeling. <i>PLoS Computational Biology</i> , 2013, 9, e1003047.	1.5	76
21	Predictive Genes in Adjacent Normal Tissue Are Preferentially Altered by sCNV during Tumorigenesis in Liver Cancer and May Rate Limiting. <i>PLoS ONE</i> , 2011, 6, e20090.	1.1	68
22	Spatiotemporal Loss of <i>NF1</i> in Schwann Cell Lineage Leads to Different Types of Cutaneous Neurofibroma Susceptible to Modification by the Hippo Pathway. <i>Cancer Discovery</i> , 2019, 9, 114-129.	7.7	65
23	Modeling Cancer Progression via Pathway Dependencies. <i>PLoS Computational Biology</i> , 2008, 4, e28.	1.5	60
24	Alternative models for sharing confidential biomedical data. <i>Nature Biotechnology</i> , 2018, 36, 391-392.	9.4	56
25	Crowdsourced mapping of unexplored target space of kinase inhibitors. <i>Nature Communications</i> , 2021, 12, 3307.	5.8	41
26	Modeling RAS Phenotype in Colorectal Cancer Uncovers Novel Molecular Traits of RAS Dependency and Improves Prediction of Response to Targeted Agents in Patients. <i>Clinical Cancer Research</i> , 2014, 20, 265-272.	3.2	36
27	Multiple Myeloma DREAM Challenge reveals epigenetic regulator PHF19 as marker of aggressive disease. <i>Leukemia</i> , 2020, 34, 1866-1874.	3.3	36
28	Integrated molecular and clinical analysis of low-grade gliomas in children with neurofibromatosis type 1 (NF1). <i>Acta Neuropathologica</i> , 2021, 141, 605-617.	3.9	36
29	A community challenge for a pancancer drug mechanism of action inference from perturbational profile data. <i>Cell Reports Medicine</i> , 2022, 3, 100492.	3.3	33
30	Impact of Bioinformatic Procedures in the Development and Translation of High-Throughput Molecular Classifiers in Oncology. <i>Clinical Cancer Research</i> , 2013, 19, 4315-4325.	3.2	32
31	Integrating Genetic Association, Genetics of Gene Expression, and Single Nucleotide Polymorphism Set Analysis to Identify Susceptibility Loci for Type 2 Diabetes Mellitus. <i>American Journal of Epidemiology</i> , 2012, 176, 423-430.	1.6	31
32	Association of Early Aspirin Use With In-Hospital Mortality in Patients With Moderate COVID-19. <i>JAMA Network Open</i> , 2022, 5, e223890.	2.8	31
33	The NIH BD2K center for big data in translational genomics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015, 22, 1143-1147.	2.2	30
34	Cutaneous neurofibromas in the genomics era: current understanding and open questions. <i>British Journal of Cancer</i> , 2018, 118, 1539-1548.	2.9	29
35	A high-throughput molecular data resource for cutaneous neurofibromas. <i>Scientific Data</i> , 2017, 4, 170045.	2.4	22
36	Functional Precision Medicine Identifies Novel Druggable Targets and Therapeutic Options in Head and Neck Cancer. <i>Clinical Cancer Research</i> , 2018, 24, 2828-2843.	3.2	20

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37	Pharmacological and genomic profiling of neurofibromatosis type 1 plexiform neurofibroma-derived schwann cells. <i>Scientific Data</i> , 2018, 5, 180106.	2.4	20
38	Correlation Between Surrogate End Points and Overall Survival in a Multi-institutional Clinicogenomic Cohort of Patients With Nonâ€“Small Cell Lung or Colorectal Cancer. <i>JAMA Network Open</i> , 2021, 4, e2117547.	2.8	20
39	Gene selection for optimal prediction of cell position in tissues from single-cell transcriptomics data. <i>Life Science Alliance</i> , 2020, 3, e202000867.	1.3	20
40	Reproducible biomedical benchmarking in the cloud: lessons from crowd-sourced data challenges. <i>Genome Biology</i> , 2019, 20, 195.	3.8	19
41	A clinically and genomically annotated nerve sheath tumor biospecimen repository. <i>Scientific Data</i> , 2020, 7, 184.	2.4	19
42	Brigatinib causes tumor shrinkage in both NF2-deficient meningioma and schwannoma through inhibition of multiple tyrosine kinases but not ALK. <i>PLoS ONE</i> , 2021, 16, e0252048.	1.1	19
43	Traditional and systems biology based drug discovery for the rare tumor syndrome neurofibromatosis type 2. <i>PLoS ONE</i> , 2018, 13, e0197350.	1.1	17
44	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. <i>PLoS ONE</i> , 2019, 14, e0216527.	1.1	15
45	A community challenge to evaluate RNA-seq, fusion detection, and isoform quantification methods for cancer discovery. <i>Cell Systems</i> , 2021, 12, 827-838.e5.	2.9	15
46	Impact of centralization on aCGH-based genomic profiles for precision medicine in oncology. <i>Annals of Oncology</i> , 2015, 26, 582-588.	0.6	13
47	Multi-targeting Drug Community Challenge. <i>Cell Chemical Biology</i> , 2017, 24, 1434-1435.	2.5	13
48	Bayesian multi-source regression and monocyte-associated gene expression predict BCL-2 inhibitor resistance in acute myeloid leukemia. <i>Npj Precision Oncology</i> , 2021, 5, 71.	2.3	12
49	Integrative Analysis Identifies Candidate Tumor Microenvironment and Intracellular Signaling Pathways that Define Tumor Heterogeneity in NF1. <i>Genes</i> , 2020, 11, 226.	1.0	11
50	Probing the chemicalâ€“biological relationship space with the Drug Target Explorer. <i>Journal of Cheminformatics</i> , 2018, 10, 41.	2.8	10
51	Engaging a community to enable disease-centric data sharing with the NF Data Portal. <i>Scientific Data</i> , 2019, 6, 319.	2.4	8
52	A Continuously Benchmarked and Crowdsourced Challenge for Rapid Development and Evaluation of Models to Predict COVID-19 Diagnosis and Hospitalization. <i>JAMA Network Open</i> , 2021, 4, e2124946.	2.8	8
53	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). <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2022, 29, 1350-1365.	2.2	8
54	Pursuing Better Biomarkers for Immunotherapy Response in Cancer Through a Crowdsourced Data Challenge. <i>JCO Precision Oncology</i> , 2021, 5, 51-54.	1.5	7

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55	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.	1.5	7
56	A 10-Gene Progenitor Cell Signature Predicts Poor Prognosis in Lung Adenocarcinoma. Annals of Thoracic Surgery, 2011, 91, 1046-1050.	0.7	6
57	Estimating variable structure and dependence in multitask learning via gradients. Machine Learning, 2011, 83, 265-287.	3.4	6
58	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.	2.2	6
59	Society for Immunotherapy of Cancer clinical and biomarkers data sharing resource document: Volume II "practical challenges. ", 2020, 8, e001472.		4
60	Comparative Analysis of Independent Ex Vivo functional Drug Screens Identifies Predictive Biomarkers of BCL-2 Inhibitor Response in AML. Blood, 2018, 132, 2763-2763.	0.6	1
61	Community mining of open clinical trial data. Oncotarget, 2017, 8, 81721-81722.	0.8	1
62	Crowdsourced High-Risk Classifiers for Multiple Myeloma Patients Commonly Identify PHF19 As a Robust Progression Biomarker. Blood, 2019, 134, 4370-4370.	0.6	0