Rehan Akbani

List of Publications by Year
in descending order

86 papers	58,369 citations	22153 59 h-index	51608 86 g-index
89 all docs	89 docs citations	89 times ranked	69098 citing authors

#	ARTICLE	IF	CITATIONS
1	Consensus subtypes of hepatocellular carcinoma associated with clinical outcomes and genomic phenotypes. Hepatology, 2022, 76, 1634-1648.	7.3	10
2	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	6.4	16
3	NExUS: Bayesian simultaneous network estimation across unequal sample sizes. Bioinformatics, 2020, 36, 798-804.	4.1	2
4	SAMMI: a semi-automated tool for the visualization of metabolic networks. Bioinformatics, 2020, 36, 2616-2617.	4.1	3
5	Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. Cancer Cell, 2020, 38, 829-843.e4.	16.8	40
6	Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. JCO Clinical Cancer Informatics, 2020, 4, 399-411.	2.1	13
7	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. Cell Systems, 2019, 9, 24-34.e10.	6.2	103
8	Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. Cell Reports, 2019, 28, 1370-1384.e5.	6.4	382
9	Identification and validation of a prognostic proteomic signature for cervical cancer. Gynecologic Oncology, 2019, 155, 324-330.	1.4	8
10	TCPA v3.0: An Integrative Platform to Explore the Pan-Cancer Analysis of Functional Proteomic Data. Molecular and Cellular Proteomics, 2019, 18, S15-S25.	3.8	61
11	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	27.8	2,149
12	Bayesian Hierarchical Varying-Sparsity Regression Models with Application to Cancer Proteogenomics. Journal of the American Statistical Association, 2019, 114, 48-60.	3.1	15
13	Analytical Platforms 3: Processing Samples via the RPPA Pipeline to Generate Large-Scale Data for Clinical Studies. Advances in Experimental Medicine and Biology, 2019, 1188, 113-147.	1.6	9
14	Generation of Raw RPPA Data and Their Conversion to Analysis-Ready Data. Advances in Experimental Medicine and Biology, 2019, 1188, 165-180.	1.6	2
15	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. F1000Research, 2019, 8, 1750.	1.6	31
16	Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. F1000Research, 2019, 8, 1750.	1.6	31
17	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	28.9	2,277
18	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670

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19	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	28.9	1,718
20	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. Cell, 2018, 173, 305-320.e10.	28.9	272
21	Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. Cell, 2018, 173, 338-354.e15.	28.9	1,417
22	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	28.9	2,111
23	Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. Cell Reports, 2018, 23, 282-296.e4.	6.4	333
24	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
25	Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. Cell Reports, 2018, 23, 194-212.e6.	6.4	245
26	The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. Cell Reports, 2018, 23, 313-326.e5.	6.4	523
27	Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. Cell Reports, 2018, 23, 181-193.e7.	6.4	683
28	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
29	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	6.4	83
30	Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. Cell Reports, 2018, 23, 239-254.e6.	6.4	801
31	The Integrated Genomic Landscape of Thymic Epithelial Tumors. Cancer Cell, 2018, 33, 244-258.e10.	16.8	270
32	Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. Molecular Pathology Library, 2018, , 43-64.	0.1	0
33	Credentialing Individual Samples for Proteogenomic Analysis. Molecular and Cellular Proteomics, 2018, 17, 1515-1530.	3.8	5
34	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	6.2	605
35	Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. Cell Systems, 2018, 6, 282-300.e2.	6.2	284
36	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	16.8	750

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37	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. Cancer Cell, 2018, 33, 721-735.e8.	16.8	396
38	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. Cancer Cell, 2018, 33, 690-705.e9.	16.8	478
39	Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor-β Pathway. Gastroenterology, 2018, 154, 195-210.	1.3	105
40	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF-β Superfamily. Cell Systems, 2018, 7, 422-437.e7.	6.2	134
41	Personalized Integrated Network Modeling of the Cancer Proteome Atlas. Scientific Reports, 2018, 8, 14924.	3.3	14
42	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
43	Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. Cancer Cell, 2018, 34, 211-224.e6.	16.8	623
44	Integrated Molecular Characterization of Testicular Germ Cell Tumors. Cell Reports, 2018, 23, 3392-3406.	6.4	324
45	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. Cancer Cell, 2017, 31, 181-193.	16.8	532
46	Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. Cancer Cell, 2017, 31, 225-239.	16.8	190
47	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	16.8	433
48	Molecular heterogeneity at the network level: high-dimensional testing, clustering and a TCGA case study. Bioinformatics, 2017, 33, 2890-2896.	4.1	13
49	Integrated Molecular Characterization of Uterine Carcinosarcoma. Cancer Cell, 2017, 31, 411-423.	16.8	309
50	Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. Cell Reports, 2017, 18, 2780-2794.	6.4	416
51	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. Cancer Research, 2017, 77, e51-e54.	0.9	101
52	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
53	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
54	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428

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55	A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. Cancer Research, 2017, 77, e23-e26.	0.9	32
56	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
57	Mutational Profiles Reveal an Aberrant TGF-Î²-CEA Regulated Pathway in Colon Adenomas. PLoS ONE, 2016, 11, e0153933.	2.5	17
58	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. Cancer Cell, 2016, 29, 723-736.	16.8	482
59	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	21.4	933
60	Using reverse-phase protein arrays as pharmacodynamic assays for functional proteomics, biomarker discovery, and drug development in cancer. Seminars in Oncology, 2016, 43, 476-483.	2.2	55
61	Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. Cell Reports, 2016, 14, 2476-2489.	6.4	298
62	Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. Cell, 2016, 164, 550-563.	28.9	1,695
63	TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. Nucleic Acids Research, 2016, 44, D1018-D1022.	14.5	358
64	Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. New England Journal of Medicine, 2016, 374, 135-145.	27.0	1,040
65	The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. European Urology Focus, 2015, 1, 94-95.	3.1	7
66	Genomic Classification of Cutaneous Melanoma. Cell, 2015, 161, 1681-1696.	28.9	2,562
67	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
68	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
69	Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. Clinical Cancer Research, 2015, 21, 4514-4524.	7.0	110
70	Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. Cell, 2015, 163, 506-519.	28.9	1,485
71	Development of a robust classifier for quality control of reverse-phase protein arrays. Bioinformatics, 2015, 31, 912-918.	4.1	43
72	Focal adhesion kinase. Cancer Biology and Therapy, 2014, 15, 919-929.	3.4	42

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73	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
74	Realizing the Promise of Reverse Phase Protein Arrays for Clinical, Translational, and Basic Research: A Workshop Report. Molecular and Cellular Proteomics, 2014, 13, 1625-1643.	3.8	152
75	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
76	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
77	A pan-cancer proteomic perspective on The Cancer Genome Atlas. Nature Communications, 2014, 5, 3887.	12.8	456
78	A Comprehensive Comparison of Normalization Methods for Loading Control and Variance Stabilization of Reverse-Phase Protein Array Data. Cancer Informatics, 2014, 13, CIN.S13329.	1.9	19
79	Tumour angiogenesis regulation by the miR-200 family. Nature Communications, 2013, 4, 2427.	12.8	363
80	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
81	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
82	TCPA: a resource for cancer functional proteomics data. Nature Methods, 2013, 10, 1046-1047.	19.0	446
83	Mobile Ad-Hoc Networks Security. Lecture Notes in Electrical Engineering, 2012, , 659-666.	0.4	28
84	EMLTrust: An enhanced Machine Learning based Reputation System for MANETs. Ad Hoc Networks, 2012, 10, 435-457.	5.5	31
85	Enhancing role-based trust management with a reputation system for MANETs. Eurasip Journal on Wireless Communications and Networking, 2011, 2011, .	2.4	6
86	HEAP: A packet authentication scheme for mobile ad hoc networks. Ad Hoc Networks, 2008, 6, 1134-1150.	5.5	24