

Rehan Akbani

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.

86
papers

35,966
citations

57
h-index

89
g-index

89
ext. papers

49,235
ext. citations

21.7
avg, IF

5.39
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 86 | Whole-genome characterization of lung adenocarcinomas lacking the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021 , 34, 108707 | 10.6 | 7 |
| 85 | Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. <i>Cancer Cell</i> , 2020 , 38, 829-843.e4 | 24.3 | 13 |
| 84 | Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. <i>JCO Clinical Cancer Informatics</i> , 2020 , 4, 399-411 | 5.2 | 6 |
| 83 | SAMMI: a semi-automated tool for the visualization of metabolic networks. <i>Bioinformatics</i> , 2020 , 36, 2616-2617 | 7.2 | 1 |
| 82 | NEXUS: Bayesian simultaneous network estimation across unequal sample sizes. <i>Bioinformatics</i> , 2020 , 36, 798-804 | 7.2 | |
| 81 | Identification and validation of a prognostic proteomic signature for cervical cancer. <i>Gynecologic Oncology</i> , 2019 , 155, 324-330 | 4.9 | 5 |
| 80 | TCPA v3.0: An Integrative Platform to Explore the Pan-Cancer Analysis of Functional Proteomic Data. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, S15-S25 | 7.6 | 25 |
| 79 | Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019 , 569, 503-508 | 50.4 | 962 |
| 78 | Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons Data. <i>Cell Systems</i> , 2019 , 9, 24-34.e10 | 10.6 | 64 |
| 77 | Integrated Analysis of TP53 Gene and Pathway Alterations in The Cancer Genome Atlas. <i>Cell Reports</i> , 2019 , 28, 1370-1384.e5 | 10.6 | 161 |
| 76 | Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019 , 8, | 3.6 | 11 |
| 75 | Interactive Clustered Heat Map Builder: An easy web-based tool for creating sophisticated clustered heat maps. <i>F1000Research</i> , 2019 , 8, 1750 | 3.6 | 13 |
| 74 | Analytical Platforms 3: Processing Samples via the RPPA Pipeline to Generate Large-Scale Data for Clinical Studies. <i>Advances in Experimental Medicine and Biology</i> , 2019 , 1188, 113-147 | 3.6 | 3 |
| 73 | Generation of Raw RPPA Data and Their Conversion to Analysis-Ready Data. <i>Advances in Experimental Medicine and Biology</i> , 2019 , 1188, 165-180 | 3.6 | 2 |
| 72 | Bayesian Hierarchical Varying-sparsity Regression Models with Application to Cancer Proteogenomics. <i>Journal of the American Statistical Association</i> , 2019 , 114, 48-60 | 2.8 | 7 |
| 71 | An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018 , 173, 400-416.e11 | 56.2 | 1072 |
| 70 | Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018 , 173, 371-385.e18 | 56.2 | 854 |

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| 69 | Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. <i>Cell</i> , 2018 , 173, 291-304.e6 | 56.2 | 888 |
| 68 | Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10 | 56.2 | 166 |
| 67 | Machine Learning Identifies Stemness Features Associated with Oncogenic Dedifferentiation. <i>Cell</i> , 2018 , 173, 338-354.e15 | 56.2 | 560 |
| 66 | Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018 , 173, 321-337.e10 | 56.2 | 1124 |
| 65 | Somatic Mutational Landscape of Splicing Factor Genes and Their Functional Consequences across 33 Cancer Types. <i>Cell Reports</i> , 2018 , 23, 282-296.e4 | 10.6 | 188 |
| 64 | Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018 , 23, 227-238.e3 | 10.6 | 235 |
| 63 | Genomic, Pathway Network, and Immunologic Features Distinguishing Squamous Carcinomas. <i>Cell Reports</i> , 2018 , 23, 194-212.e6 | 10.6 | 146 |
| 62 | The Cancer Genome Atlas Comprehensive Molecular Characterization of Renal Cell Carcinoma. <i>Cell Reports</i> , 2018 , 23, 313-326.e5 | 10.6 | 295 |
| 61 | Spatial Organization and Molecular Correlation of Tumor-Infiltrating Lymphocytes Using Deep Learning on Pathology Images. <i>Cell Reports</i> , 2018 , 23, 181-193.e7 | 10.6 | 366 |
| 60 | The Immune Landscape of Cancer. <i>Immunity</i> , 2018 , 48, 812-830.e14 | 32.3 | 1754 |
| 59 | Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018 , 23, 213-226.e3 | 26.6 | 56 |
| 58 | Genomic and Molecular Landscape of DNA Damage Repair Deficiency across The Cancer Genome Atlas. <i>Cell Reports</i> , 2018 , 23, 239-254.e6 | 10.6 | 405 |
| 57 | The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10 | 24.3 | 150 |
| 56 | Genomic Assessment of Muscle-Invasive Bladder Cancer: Insights from the Cancer Genome Atlas (TCGA) Project. <i>Molecular Pathology Library</i> , 2018 , 43-64 | | |
| 55 | Credentialing Individual Samples for Proteogenomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1515-1530 | 7.6 | 3 |
| 54 | Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018 , 6, 271-281.e7 | 10.6 | 320 |
| 53 | Pan-cancer Alterations of the MYC Oncogene and Its Proximal Network across the Cancer Genome Atlas. <i>Cell Systems</i> , 2018 , 6, 282-300.e2 | 10.6 | 159 |
| 52 | Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018 , 33, 676-689.e3 | 24.3 | 377 |

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| 51 | Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8 | 24.3 | 228 |
| 50 | A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9 | 24.3 | 277 |
| 49 | Analysis of Genomes and Transcriptomes of Hepatocellular Carcinomas Identifies Mutations and Gene Expression Changes in the Transforming Growth Factor- β Pathway. <i>Gastroenterology</i> , 2018 , 154, 195-210 | 13.3 | 68 |
| 48 | Comprehensive Analysis of Alternative Splicing Across Tumors from 8,705 Patients. <i>Cancer Cell</i> , 2018 , 34, 211-224.e6 | 24.3 | 327 |
| 47 | Integrated Molecular Characterization of Testicular Germ Cell Tumors. <i>Cell Reports</i> , 2018 , 23, 3392-3406.e10 | 10.6 | 200 |
| 46 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7 | 10.6 | 85 |
| 45 | Personalized Integrated Network Modeling of the Cancer Proteome Atlas. <i>Scientific Reports</i> , 2018 , 8, 14924 | 4.9 | 6 |
| 44 | Integrative Molecular Characterization of Malignant Pleural Mesothelioma. <i>Cancer Discovery</i> , 2018 , 8, 1548-1565 | 24.4 | 258 |
| 43 | Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193 | 24.3 | 350 |
| 42 | Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. <i>Cancer Cell</i> , 2017 , 31, 225-239.e3 | 24.3 | 139 |
| 41 | A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017 , 31, 820-832.e3 | 24.3 | 286 |
| 40 | Molecular heterogeneity at the network level: high-dimensional testing, clustering and a TCGA case study. <i>Bioinformatics</i> , 2017 , 33, 2890-2896 | 7.2 | 10 |
| 39 | Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423 | 24.3 | 210 |
| 38 | Integrative Genomic Analysis of Cholangiocarcinoma Identifies Distinct IDH-Mutant Molecular Profiles. <i>Cell Reports</i> , 2017 , 18, 2780-2794 | 10.6 | 247 |
| 37 | Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017 , 77, e51-e54 | 10.1 | 50 |
| 36 | Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e25 | 24.3 | 961 |
| 35 | Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15 | 24.3 | 391 |
| 34 | Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13 | 24.3 | 96 |

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| 33 | A Galaxy Implementation of Next-Generation Clustered Heatmaps for Interactive Exploration of Molecular Profiling Data. <i>Cancer Research</i> , 2017 , 77, e23-e26 | 10.1 | 22 |
| 32 | Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28 | 56.2 | 451 |
| 31 | Multilevel Genomics-Based Taxonomy of Renal Cell Carcinoma. <i>Cell Reports</i> , 2016 , 14, 2476-89 | 10.6 | 228 |
| 30 | Molecular Profiling Reveals Biologically Discrete Subsets and Pathways of Progression in Diffuse Glioma. <i>Cell</i> , 2016 , 164, 550-63 | 56.2 | 1140 |
| 29 | TCGASpliceSeq a compendium of alternative mRNA splicing in cancer. <i>Nucleic Acids Research</i> , 2016 , 44, D1018-22 | 20.1 | 181 |
| 28 | Comprehensive Molecular Characterization of Papillary Renal-Cell Carcinoma. <i>New England Journal of Medicine</i> , 2016 , 374, 135-45 | 59.2 | 753 |
| 27 | Mutational Profiles Reveal an Aberrant TGF- β Regulated Pathway in Colon Adenomas. <i>PLoS ONE</i> , 2016 , 11, e0153933 | 3.7 | 13 |
| 26 | Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736 | 24.3 | 324 |
| 25 | Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016 , 48, 607-16 | 36.3 | 613 |
| 24 | Using reverse-phase protein arrays as pharmacodynamic assays for functional proteomics, biomarker discovery, and drug development in cancer. <i>Seminars in Oncology</i> , 2016 , 43, 476-83 | 5.5 | 40 |
| 23 | Genomic Classification of Cutaneous Melanoma. <i>Cell</i> , 2015 , 161, 1681-96 | 56.2 | 1807 |
| 22 | Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. <i>New England Journal of Medicine</i> , 2015 , 372, 2481-98 | 59.2 | 1828 |
| 21 | The Molecular Taxonomy of Primary Prostate Cancer. <i>Cell</i> , 2015 , 163, 1011-25 | 56.2 | 1713 |
| 20 | Invasive Bladder Cancer: Genomic Insights and Therapeutic Promise. <i>Clinical Cancer Research</i> , 2015 , 21, 4514-24 | 12.9 | 85 |
| 19 | Comprehensive Molecular Portraits of Invasive Lobular Breast Cancer. <i>Cell</i> , 2015 , 163, 506-19 | 56.2 | 1055 |
| 18 | Development of a robust classifier for quality control of reverse-phase protein arrays. <i>Bioinformatics</i> , 2015 , 31, 912-8 | 7.2 | 33 |
| 17 | Update on The Cancer Genome Atlas Project on Muscle-invasive Bladder Cancer. <i>European Urology Focus</i> , 2015 , 1, 94-95 | 5.1 | 4 |
| 16 | The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330 | 24.3 | 521 |

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| 15 | Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. <i>Cell</i> , 2014 , 158, 929-944 | 56.2 | 935 |
| 14 | A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014 , 5, 3887-3900 | 17.4 | 324 |
| 13 | A comprehensive comparison of normalization methods for loading control and variance stabilization of reverse-phase protein array data. <i>Cancer Informatics</i> , 2014 , 13, 109-17 | 2.4 | 17 |
| 12 | Focal adhesion kinase: an alternative focus for anti-angiogenesis therapy in ovarian cancer. <i>Cancer Biology and Therapy</i> , 2014 , 15, 919-29 | 4.6 | 33 |
| 11 | Integrated genomic characterization of papillary thyroid carcinoma. <i>Cell</i> , 2014 , 159, 676-90 | 56.2 | 1660 |
| 10 | Realizing the promise of reverse phase protein arrays for clinical, translational, and basic research: a workshop report: the RPPA (Reverse Phase Protein Array) society. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1625-43 | 7.6 | 117 |
| 9 | Tumour angiogenesis regulation by the miR-200 family. <i>Nature Communications</i> , 2013 , 4, 2427 | 17.4 | 295 |
| 8 | Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013 , 497, 67-73 | 50.4 | 2800 |
| 7 | Genomic and epigenomic landscapes of adult de novo acute myeloid leukemia. <i>New England Journal of Medicine</i> , 2013 , 368, 2059-74 | 59.2 | 3137 |
| 6 | TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013 , 10, 1046-7 | 21.6 | 288 |
| 5 | Mobile Ad-Hoc Networks Security. <i>Lecture Notes in Electrical Engineering</i> , 2012 , 659-666 | 0.2 | 14 |
| 4 | EMLTrust: An enhanced Machine Learning based Reputation System for MANETs. <i>Ad Hoc Networks</i> , 2012 , 10, 435-457 | 4.8 | 22 |
| 3 | Enhancing role-based trust management with a reputation system for MANETs. <i>Eurasip Journal on Wireless Communications and Networking</i> , 2011 , 2011, | 3.2 | 4 |
| 2 | HEAP: A packet authentication scheme for mobile ad hoc networks. <i>Ad Hoc Networks</i> , 2008 , 6, 1134-1150 | 4.8 | 19 |
| 1 | Large-scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines | | 1 |