Ronglai Shen

List of Publications by Year
in descending order

71 papers	23,937 citations	71102 41 h-index	98798 67 g-index
73 all docs	73 docs citations	73 times ranked	37148 citing authors

#	Article	IF	Citations
1	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
2	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. Nature Genetics, 2019, 51, 202-206.	21.4	2,702
3	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
4	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435
5	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
6	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
7	FACETS: allele-specific copy number and clonal heterogeneity analysis tool for high-throughput DNA sequencing. Nucleic Acids Research, 2016, 44, e131-e131.	14.5	809
8	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
9	Integrative clustering of multiple genomic data types using a joint latent variable model with application to breast and lung cancer subtype analysis. Bioinformatics, 2009, 25, 2906-2912.	4.1	671
10	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	16.8	633
11	High-intensity sequencing reveals the sources of plasma circulating cell-free DNA variants. Nature Medicine, 2019, 25, 1928-1937.	30.7	485
12	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422
13	Ado-Trastuzumab Emtansine for Patients With HER2-Mutant Lung Cancers: Results From a Phase II Basket Trial. Journal of Clinical Oncology, 2018, 36, 2532-2537.	1.6	381
14	Pattern discovery and cancer gene identification in integrated cancer genomic data. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 4245-4250.	7.1	361
15	Next-Generation Sequencing of Pulmonary Large Cell Neuroendocrine Carcinoma Reveals Small Cell Carcinomaâ€“like and Nonâ€“Small Cell Carcinomaâ€“like Subsets. Clinical Cancer Research, 2016, 22, 3618-3629.	7.0	342
16	Loss of the FAT1 Tumor Suppressor Promotes Resistance to CDK4/6 Inhibitors via the Hippo Pathway. Cancer Cell, 2018, 34, 893-905.e8.	16.8	307
17	Rationale for co-targeting IGF-1R and ALK in ALK fusionâ€“positive lung cancer. Nature Medicine, 2014, 20, 1027-1034.	30.7	243
18	Concurrent RB1 and TP53 Alterations Define aÂSubset of EGFR-Mutant Lung Cancers at risk forÂHistologic Transformation and Inferior Clinical Outcomes. Journal of Thoracic Oncology, 2019, 14, 1784-1793.	1.1	232

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19	Integrative Subtype Discovery in Glioblastoma Using iCluster. PLoS ONE, 2012, 7, e35236.	2.5	196
20	Pan-cancer analysis of bi-allelic alterations in homologous recombination DNA repair genes. Nature Communications, 2017, 8, 857.	12.8	182
21	A fully Bayesian latent variable model for integrative clustering analysis of multi-type omics data. Biostatistics, 2018, 19, 71-86.	1.5	158
22	Phase II Study of Hemithoracic Intensity-Modulated Pleural Radiation Therapy (IMPRINT) As Part of Lung-Sparing Multimodality Therapy in Patients With Malignant Pleural Mesothelioma. Journal of Clinical Oncology, 2016, 34, 2761-2768.	1.6	154
23	HER2-Mediated Internalization of Cytotoxic Agents inERBB2Amplified or Mutant Lung Cancers. Cancer Discovery, 2020, 10, 674-687.	9.4	149
24	Unraveling tumorâ€“immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	21.4	136
25	Genomic landscape of adenoid cystic carcinoma of the breast. Journal of Pathology, 2015, 237, 179-189.	4.5	133
26	Next-Generation Sequencing of Stage IV Squamous Cell Lung Cancers Reveals an Association of PI3K Aberrations and Evidence of Clonal Heterogeneity in Patients with Brain Metastases. Cancer Discovery, 2015, 5, 610-621.	9.4	129
27	Concurrent Mutations in STK11 and KEAP1 Promote Ferroptosis Protection and SCD1 Dependence in Lung Cancer. Cell Reports, 2020, 33, 108444.	6.4	118
28	Basket Trials in Oncology: A Trade-Off Between Complexity and Efficiency. Journal of Clinical Oncology, 2017, 35, 271-273.	1.6	110
29	A Phase Ib Open-Label Multicenter Study of AZD4547 in Patients with Advanced Squamous Cell Lung Cancers. Clinical Cancer Research, 2017, 23, 5366-5373.	7.0	109
30	Decreased Î±-Methylacyl CoA Racemase Expression in Localized Prostate Cancer is Associated with an Increased Rate of Biochemical Recurrence and Cancer-Specific Death. Cancer Epidemiology Biomarkers and Prevention, 2005, 14, 1424-1432.	2.5	105
31	Prognostic meta-signature of breast cancer developed by two-stage mixture modeling of microarray data. BMC Genomics, 2004, 5, 94.	2.8	104
32	Alterations in PTEN and ESR1 promote clinical resistance to alpelisib plus aromatase inhibitors. Nature Cancer, 2020, 1, 382-393.	13.2	96
33	Genetic Heterogeneity in Therapy-NaÃ¯ve Synchronous Primary Breast Cancers and Their Metastases. Clinical Cancer Research, 2017, 23, 4402-4415.	7.0	91
34	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. PLoS ONE, 2011, 6, e24709.	2.5	88
35	Small-Cell Carcinomas of the Bladder and Lung Are Characterized by a Convergent but Distinct Pathogenesis. Clinical Cancer Research, 2018, 24, 1965-1973.	7.0	85
36	Sparse integrative clustering of multiple omics data sets. Annals of Applied Statistics, 2013, 7, 269-294.	1.1	84

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37	An efficient basket trial design. Statistics in Medicine, 2017, 36, 1568-1579.	1.6	82
38	Metastatic breast carcinomas display genomic and transcriptomic heterogeneity. Modern Pathology, 2015, 28, 340-351.	5.5	80
39	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	3.3	79
40	LAG-3 expression on peripheral blood cells identifies patients with poorer outcomes after immune checkpoint blockade. Science Translational Medicine, 2021, 13, .	12.4	54
41	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	4.3	52
42	Cooperative loss of RAS feedback regulation drives myeloid leukemogenesis. Nature Genetics, 2015, 47, 539-543.	21.4	39
43	Translating neoadjuvant therapy into survival benefits: one size does not fit all. Nature Reviews Clinical Oncology, 2016, 13, 566-579.	27.6	38
44	MET Exon 14â€“altered Lung Cancers and MET Inhibitor Resistance. Clinical Cancer Research, 2021, 27, 799-806.	7.0	35
45	Pathway analysis reveals functional convergence of gene expression profiles in breast cancer. BMC Medical Genomics, 2008, 1, 28.	1.5	30
46	Utility of Routine PET Imaging to Predict Response and Survival After Induction Therapy for Non-Small Cell Lung Cancer. Annals of Thoracic Surgery, 2016, 101, 1052-1059.	1.3	28
47	Harnessing Clinical Sequencing Data for Survival Stratification of Patients With Metastatic Lung Adenocarcinomas. JCO Precision Oncology, 2019, 3, 1-9.	3.0	26
48	Variance prior specification for a basket trial design using Bayesian hierarchical modeling. Clinical Trials, 2019, 16, 142-153.	1.6	25
49	The use of a next-generation sequencing-derived machine-learning risk-prediction model (OncoCast-MPM) for malignant pleural mesothelioma: a retrospective study. The Lancet Digital Health, 2021, 3, e565-e576.	12.3	23
50	Pan-cancer identification of clinically relevant genomic subtypes using outcome-weighted integrative clustering. Genome Medicine, 2020, 12, 110.	8.2	22
51	Cancer-Causative Mutations Occurring in Early Embryogenesis. Cancer Discovery, 2022, 12, 949-957.	9.4	21
52	Predictive Performance of Microarray Gene Signatures: Impact of Tumor Heterogeneity and Multiple Mechanisms of Drug Resistance. Cancer Research, 2014, 74, 2946-2961.	0.9	20
53	Using association signal annotations to boost similarity network fusion. Bioinformatics, 2019, 35, 3718-3726.	4.1	20
54	Clinical utility of next-generation sequencing-based ctDNA testing for common and novel ALK fusions. Lung Cancer, 2021, 159, 66-73.	2.0	17

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55	Comparative genomics of primary prostate cancer and paired metastases: insights from 12 molecular case studies. Journal of Pathology, 2022, 257, 274-284.	4.5	13
56	Lessons learned from routine, targeted assessment of liquid biopsies for EGFR T790M resistance mutation in patients with EGFR mutant lung cancers. Acta OncolÃ³gica, 2019, 58, 1634-1639.	1.8	10
57	Using somatic variant richness to mine signals from rare variants in the cancer genome. Nature Communications, 2019, 10, 5506.	12.8	10
58	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. Statistics in Biosciences, 2018, 10, 86-106.	1.2	9
59	Genome-Derived Classification Signature for Ampullary Adenocarcinoma to Improve Clinical Cancer Care. Clinical Cancer Research, 2021, 27, 5891-5899.	7.0	9
60	Mining mutation contexts across the cancer genome to map tumor site of origin. Nature Communications, 2021, 12, 3051.	12.8	8
61	Modeling intraâ€tumor protein expression heterogeneity in tissue microarray experiments. Statistics in Medicine, 2008, 27, 1944-1959.	1.6	5
62	Reconstructing tumor-wise protein expression in tissue microarray studies using a Bayesian cell mixture model. Bioinformatics, 2008, 24, 2880-2886.	4.1	5
63	Using the â€œHiddenâ€•genome to improve classification of cancer types. Biometrics, 2021, 77, 1445-1455.	1.4	5
64	FACETS: Fraction and Allele-Specific Copy Number Estimates from Tumor Sequencing. Methods in Molecular Biology, 2022, , 89-105.	0.9	5
65	Accounting for Delayed Entry in Analyses of Overall Survival in Clinico-Genomic Databases. Cancer Epidemiology Biomarkers and Prevention, 2022, 31, 1195-1201.	2.5	4
66	Bayesian network-driven clustering analysis with feature selection for high-dimensional multi-modal molecular data. Scientific Reports, 2021, 11, 5146.	3.3	3
67	Exome-Wide Pan-Cancer Analysis of Germline Variants in 8,719 Individuals Finds Little Evidence of Rare Variant Associations. Human Heredity, 2021, 86, 34-44.	0.8	1
68	Same-Cell Co-Occurrence of RAS Hotspot and BRAF V600E Mutations in Treatment-Naive Colorectal Cancer. JCO Precision Oncology, 2022, 6, e2100365.	3.0	1
69	Genomic determinants of early recurrences in low-stage low-grade endometrioid endometrial carcinoma. Journal of the National Cancer Institute, 0, , .	6.3	1
70	A Latent Variable Approach for Integrative Clustering of Multiple Genomic Data Types. , 0, , 155-173.		0
71	Human genes differ by their UV sensitivity estimated through analysis of UVâ€induced silent mutations in melanoma. Human Mutation, 2020, 41, 1751-1760.	2.5	0