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	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
2	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
3	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
4	Cancer-Causative Mutations Occurring in Early Embryogenesis. Cancer Discovery, 2022, 12, 949-957.	9.4	21
5	FACETS: Fraction and Allele-Specific Copy Number Estimates from Tumor Sequencing. Methods in Molecular Biology, 2022, , 89-105.	0.9	5
6	Using the "Hidden" genome to improve classification of cancer types. Biometrics, 2021, 77, 1445-1455.	1.4	5
7	*MET* Exon 14–altered Lung Cancers and MET Inhibitor Resistance. Clinical Cancer Research, 2021, 27, 799-806.	7.0	35
8	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	4.3	52
9	Bayesian network-driven clustering analysis with feature selection for high-dimensional multi-modal molecular data. Scientific Reports, 2021, 11, 5146.	3.3	3
10	Mining mutation contexts across the cancer genome to map tumor site of origin. Nature Communications, 2021, 12, 3051.	12.8	8
11	Genome-Derived Classification Signature for Ampullary Adenocarcinoma to Improve Clinical Cancer Care. Clinical Cancer Research, 2021, 27, 5891-5899.	7.0	9
12	LAG-3 expression on peripheral blood cells identifies patients with poorer outcomes after immune checkpoint blockade. Science Translational Medicine, 2021, 13, .	12.4	54
13	Clinical utility of next-generation sequencing-based ctDNA testing for common and novel ALK fusions. Lung Cancer, 2021, 159, 66-73.	2.0	17
14	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
15	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
16	Concurrent Mutations in STK11 and KEAP1 Promote Ferroptosis Protection and SCD1 Dependence in Lung Cancer. Cell Reports, 2020, 33, 108444.	6.4	118
17	Pan-cancer identification of clinically relevant genomic subtypes using outcome-weighted integrative clustering. Genome Medicine, 2020, 12, 110.	8.2	22
18	Unraveling tumor–immune heterogeneity in advanced ovarian cancer uncovers immunogenic effect of chemotherapy. Nature Genetics, 2020, 52, 582-593.	21.4	136

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19	Human genes differ by their UV sensitivity estimated through analysis of UV‐induced silent mutations in melanoma. Human Mutation, 2020, 41, 1751-1760.	2.5	0
20	Alterations in PTEN and ESR1 promote clinical resistance to alpelisib plus aromatase inhibitors. Nature Cancer, 2020, 1, 382-393.	13.2	96
21	HER2-Mediated Internalization of Cytotoxic Agents in *ERBB2* Amplified or Mutant Lung Cancers. Cancer Discovery, 2020, 10, 674-687.	9.4	149
22	Concurrent RB1 and TP53 Alterations Define a Subset of EGFR-Mutant Lung Cancers at risk for Histologic Transformation and Inferior Clinical Outcomes. Journal of Thoracic Oncology, 2019, 14, 1784-1793.	1.1	232
23	Lessons learned from routine, targeted assessment of liquid biopsies for *EGFR* T790M resistance mutation in patients with *EGFR* mutant lung cancers. Acta Oncológica, 2019, 58, 1634-1639.	1.8	10
24	Variance prior specification for a basket trial design using Bayesian hierarchical modeling. Clinical Trials, 2019, 16, 142-153.	1.6	25
25	Using association signal annotations to boost similarity network fusion. Bioinformatics, 2019, 35, 3718-3726.	4.1	20
26	Using somatic variant richness to mine signals from rare variants in the cancer genome. Nature Communications, 2019, 10, 5506.	12.8	10
27	High-intensity sequencing reveals the sources of plasma circulating cell-free DNA variants. Nature Medicine, 2019, 25, 1928-1937.	30.7	485
28	Harnessing Clinical Sequencing Data for Survival Stratification of Patients With Metastatic Lung Adenocarcinomas. JCO Precision Oncology, 2019, 3, 1-9.	3.0	26
29	Tumor mutational load predicts survival after immunotherapy across multiple cancer types. Nature Genetics, 2019, 51, 202-206.	21.4	2,702
30	A fully Bayesian latent variable model for integrative clustering analysis of multi-type omics data. Biostatistics, 2018, 19, 71-86.	1.5	158
31	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
32	Dissecting Pathway Disturbances Using Network Topology and Multi-platform Genomics Data. Statistics in Biosciences, 2018, 10, 86-106.	1.2	9
33	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
34	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
35	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
36	Integrative Molecular Characterization of Malignant Pleural Mesothelioma. Cancer Discovery, 2018, 8, 1548-1565.	9.4	422

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37	The Genomic Landscape of Endocrine-Resistant Advanced Breast Cancers. Cancer Cell, 2018, 34, 427-438.e6.	16.8	633
38	An efficient basket trial design. Statistics in Medicine, 2017, 36, 1568-1579.	1.6	82
39	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. Cell, 2017, 169, 1327-1341.e23.	28.9	1,794
40	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
41	Genetic Heterogeneity in Therapy-Naïve Synchronous Primary Breast Cancers and Their Metastases. Clinical Cancer Research, 2017, 23, 4402-4415.	7.0	91
42	Pan-cancer analysis of bi-allelic alterations in homologous recombination DNA repair genes. Nature Communications, 2017, 8, 857.	12.8	182
43	Integrating Clinical and Multiple Omics Data for Prognostic Assessment across Human Cancers. Scientific Reports, 2017, 7, 16954.	3.3	79
44	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. Cell, 2017, 171, 950-965.e28.	28.9	738
45	Basket Trials in Oncology: A Trade-Off Between Complexity and Efficiency. Journal of Clinical Oncology, 2017, 35, 271-273.	1.6	110
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	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
48	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
49	Translating neoadjuvant therapy into survival benefits: one size does not fit all. Nature Reviews Clinical Oncology, 2016, 13, 566-579.	27.6	38
50	Next-Generation Sequencing of Pulmonary Large Cell Neuroendocrine Carcinoma Reveals Small Cell Carcinoma–like and Non–Small Cell Carcinoma–like Subsets. Clinical Cancer Research, 2016, 22, 3618-3629.	7.0	342
51	Comprehensive, Integrative Genomic Analysis of Diffuse Lower-Grade Gliomas. New England Journal of Medicine, 2015, 372, 2481-2498.	27.0	2,582
52	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
53	Cooperative loss of RAS feedback regulation drives myeloid leukemogenesis. Nature Genetics, 2015, 47, 539-543.	21.4	39
54	The Molecular Taxonomy of Primary Prostate Cancer. Cell, 2015, 163, 1011-1025.	28.9	2,435

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55	Genomic landscape of adenoid cystic carcinoma of the breast. Journal of Pathology, 2015, 237, 179-189.	4.5	133
56	Metastatic breast carcinomas display genomic and transcriptomic heterogeneity. Modern Pathology, 2015, 28, 340-351.	5.5	80
57	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
58	Rationale for co-targeting IGF-1R and ALK in ALK fusion–positive lung cancer. Nature Medicine, 2014, 20, 1027-1034.	30.7	243
59	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
60	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
61	Sparse integrative clustering of multiple omics data sets. Annals of Applied Statistics, 2013, 7, 269-294.	1.1	84
62	Integrative Subtype Discovery in Glioblastoma Using iCluster. PLoS ONE, 2012, 7, e35236.	2.5	196
63	Time to Recurrence and Survival in Serous Ovarian Tumors Predicted from Integrated Genomic Profiles. PLoS ONE, 2011, 6, e24709.	2.5	88
64	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
65	Pathway analysis reveals functional convergence of gene expression profiles in breast cancer. BMC Medical Genomics, 2008, 1, 28.	1.5	30
66	Modeling intra–tumor protein expression heterogeneity in tissue microarray experiments. Statistics in Medicine, 2008, 27, 1944-1959.	1.6	5
67	Reconstructing tumor-wise protein expression in tissue microarray studies using a Bayesian cell mixture model. Bioinformatics, 2008, 24, 2880-2886.	4.1	5
68	Decreased α-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
69	Prognostic meta-signature of breast cancer developed by two-stage mixture modeling of microarray data. BMC Genomics, 2004, 5, 94.	2.8	104
70	A Latent Variable Approach for Integrative Clustering of Multiple Genomic Data Types. , 0, , 155-173.		0
71	Genomic determinants of early recurrences in low-stage low-grade endometrioid endometrial carcinoma. Journal of the National Cancer Institute, 0, , .	6.3	1