

Han Liang

List of Publications by Year in descending order

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Version: 2024-02-01

144
papers

33,886
citations

11608

70
h-index

8138

148
g-index

161
all docs

161
docs citations

161
times ranked

46557
citing authors

#	ARTICLE	IF	CITATIONS
1	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	4,075
2	The Immune Landscape of Cancer. <i>Immunity</i> , 2018, 48, 812-830.e14.	6.6	3,706
3	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. <i>Cell</i> , 2018, 173, 400-416.e11.	13.5	2,277
4	Oncogenic Signaling Pathways in The Cancer Genome Atlas. <i>Cell</i> , 2018, 173, 321-337.e10.	13.5	2,111
5	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.	13.5	1,718
6	Comprehensive Characterization of Cancer Driver Genes and Mutations. <i>Cell</i> , 2018, 173, 371-385.e18.	13.5	1,670
7	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. <i>Nature</i> , 2014, 512, 155-160.	13.7	911
8	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. <i>Cancer Cell</i> , 2018, 33, 676-689.e3.	7.7	750
9	Human polymorphism at microRNAs and microRNA target sites. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3300-3305.	3.3	616
10	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. <i>Cell Systems</i> , 2018, 6, 271-281.e7.	2.9	605
11	Long noncoding RNA MALAT1 suppresses breast cancer metastasis. <i>Nature Genetics</i> , 2018, 50, 1705-1715.	9.4	561
12	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. <i>Cancer Research</i> , 2015, 75, 3728-3737.	0.4	518
13	A pan-cancer proteomic perspective on The Cancer Genome Atlas. <i>Nature Communications</i> , 2014, 5, 3887.	5.8	456
14	TCPA: a resource for cancer functional proteomics data. <i>Nature Methods</i> , 2013, 10, 1046-1047.	9.0	446
15	The LINK-A lncRNA activates normoxic HIF1 α signalling in triple-negative breast cancer. <i>Nature Cell Biology</i> , 2016, 18, 213-224.	4.6	444
16	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. <i>Cancer Cell</i> , 2017, 31, 820-832.e3.	7.7	433
17	The Genomic Landscape and Clinical Relevance of A-to-I RNA Editing in Human Cancers. <i>Cancer Cell</i> , 2015, 28, 515-528.	7.7	426
18	High Frequency of PIK3R1 and PIK3R2 Mutations in Endometrial Cancer Elucidates a Novel Mechanism for Regulation of PTEN Protein Stability. <i>Cancer Discovery</i> , 2011, 1, 170-185.	7.7	419

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19	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	2.9	407
20	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. <i>Cancer Cell</i> , 2018, 33, 706-720.e9.	7.7	400
21	Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. <i>Nature Communications</i> , 2014, 5, 3231.	5.8	385
22	ARID1A deficiency promotes mutability and potentiates therapeutic antitumor immunity unleashed by immune checkpoint blockade. <i>Nature Medicine</i> , 2018, 24, 556-562.	15.2	372
23	ATM-mediated stabilization of ZEB1 promotes DNA damage response and radioresistance through CHK1. <i>Nature Cell Biology</i> , 2014, 16, 864-875.	4.6	367
24	LIFR is a breast cancer metastasis suppressor upstream of the Hippo-YAP pathway and a prognostic marker. <i>Nature Medicine</i> , 2012, 18, 1511-1517.	15.2	361
25	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. <i>Cell Reports</i> , 2018, 25, 1304-1317.e5.	2.9	329
26	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. <i>Nature Biotechnology</i> , 2014, 32, 644-652.	9.4	257
27	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.	9.4	256
28	A ROR1-HER3-lncRNA signalling axis modulates the Hippo-YAP pathway to regulate bone metastasis. <i>Nature Cell Biology</i> , 2017, 19, 106-119.	4.6	253
29	Comprehensive Characterization of Molecular Differences in Cancer between Male and Female Patients. <i>Cancer Cell</i> , 2016, 29, 711-722.	7.7	242
30	lncRNA NBR2 engages a metabolic checkpoint by regulating AMPK under energy stress. <i>Nature Cell Biology</i> , 2016, 18, 431-442.	4.6	239
31	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. <i>Cell</i> , 2018, 173, 386-399.e12.	13.5	228
32	Systematic Functional Annotation of Somatic Mutations in Cancer. <i>Cancer Cell</i> , 2018, 33, 450-462.e10.	7.7	213
33	Whole-exome sequencing combined with functional genomics reveals novel candidate driver cancer genes in endometrial cancer. <i>Genome Research</i> , 2012, 22, 2120-2129.	2.4	206
34	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. <i>Cell Reports</i> , 2018, 23, 297-312.e12.	2.9	205
35	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. <i>Cell Reports</i> , 2018, 23, 255-269.e4.	2.9	204
36	The LINK-A lncRNA interacts with PtdIns(3,4,5)P3 to hyperactivate AKT and confer resistance to AKT inhibitors. <i>Nature Cell Biology</i> , 2017, 19, 238-251.	4.6	201

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37	Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. <i>Cancer Cell</i> , 2017, 31, 225-239.	7.7	190
38	Landscape of dietary factors associated with risk of gastric cancer: A systematic review and dose-response meta-analysis of prospective cohort studies. <i>European Journal of Cancer</i> , 2015, 51, 2820-2832.	1.3	187
39	Signalling pathway for RKIP and Let-7 regulates and predicts metastatic breast cancer. <i>EMBO Journal</i> , 2011, 30, 4500-4514.	3.5	175
40	A-to-I RNA Editing Contributes to Proteomic Diversity in Cancer. <i>Cancer Cell</i> , 2018, 33, 817-828.e7.	7.7	172
41	Characterization of hypoxia-associated molecular features to aid hypoxia-targeted therapy. <i>Nature Metabolism</i> , 2019, 1, 431-444.	5.1	158
42	Energy stress-induced lncRNA FILNC1 represses c-Myc-mediated energy metabolism and inhibits renal tumor development. <i>Nature Communications</i> , 2017, 8, 783.	5.8	157
43	MicroRNA regulation of human protein-protein interaction network. <i>Rna</i> , 2007, 13, 1402-1408.	1.6	153
44	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. <i>Nature Communications</i> , 2017, 8, 347.	5.8	151
45	miR-205 acts as a tumour radiosensitizer by targeting ZEB1 and Ubc13. <i>Nature Communications</i> , 2014, 5, 5671.	5.8	148
46	Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. <i>Genome Research</i> , 2017, 27, 1112-1125.	2.4	144
47	The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumour subtypes. <i>Nature Communications</i> , 2014, 5, 3963.	5.8	143
48	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. <i>Molecular Cell</i> , 2016, 61, 520-534.	4.5	142
49	RNA editing derived epitopes function as cancer antigens to elicit immune responses. <i>Nature Communications</i> , 2018, 9, 3919.	5.8	120
50	SKP2- and OTUD1-regulated non-proteolytic ubiquitination of YAP promotes YAP nuclear localization and activity. <i>Nature Communications</i> , 2018, 9, 2269.	5.8	117
51	A targetable LIFR-NF- κ B-LCN2 axis controls liver tumorigenesis and vulnerability to ferroptosis. <i>Nature Communications</i> , 2021, 12, 7333.	5.8	117
52	ILF2 Is a Regulator of RNA Splicing and DNA Damage Response in 1q21-Amplified Multiple Myeloma. <i>Cancer Cell</i> , 2017, 32, 88-100.e6.	7.7	114
53	miR-100 Induces Epithelial-Mesenchymal Transition but Suppresses Tumorigenesis, Migration and Invasion. <i>PLoS Genetics</i> , 2014, 10, e1004177.	1.5	110
54	Gene essentiality, gene duplicability and protein connectivity in human and mouse. <i>Trends in Genetics</i> , 2007, 23, 375-378.	2.9	107

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55	Next generation sequencing of pancreatic cyst fluid microRNAs from low grade-benign and high grade-invasive lesions. <i>Cancer Letters</i> , 2015, 356, 404-409.	3.2	105
56	CanDrA: Cancer-Specific Driver Missense Mutation Annotation with Optimized Features. <i>PLoS ONE</i> , 2013, 8, e77945.	1.1	104
57	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	2.9	103
58	Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. <i>Nature Genetics</i> , 2013, 45, 1121-1126.	9.4	102
59	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. <i>Cancer Research</i> , 2017, 77, e51-e54.	0.4	101
60	Immune Microenvironment in Microsatellite-Unstable Endometrial Cancers: Hereditary or Sporadic Origin Matters. <i>Clinical Cancer Research</i> , 2017, 23, 4473-4481.	3.2	96
61	Comparative genomic analysis of esophageal squamous cell carcinoma between Asian and Caucasian patient populations. <i>Nature Communications</i> , 2017, 8, 1533.	5.8	92
62	AMPK $\hat{\pm}$ Modulation in Cancer Progression: Multilayer Integrative Analysis of the Whole Transcriptome in Asian Gastric Cancer. <i>Cancer Research</i> , 2012, 72, 2512-2521.	0.4	91
63	HNF4 $\hat{\pm}$ is a therapeutic target that links AMPK to WNT signalling in early-stage gastric cancer. <i>Gut</i> , 2016, 65, 19-32.	6.1	91
64	NUAK2 is a critical YAP target in liver cancer. <i>Nature Communications</i> , 2018, 9, 4834.	5.8	88
65	Lowly Expressed Human MicroRNA Genes Evolve Rapidly. <i>Molecular Biology and Evolution</i> , 2009, 26, 1195-1198.	3.5	86
66	Telomere Dysfunction Drives Aberrant Hematopoietic Differentiation and Myelodysplastic Syndrome. <i>Cancer Cell</i> , 2015, 27, 644-657.	7.7	85
67	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. <i>Cell Reports</i> , 2018, 23, 213-226.e3.	2.9	83
68	Hypothesis: RNA editing of microRNA target sites in humans?. <i>Rna</i> , 2007, 13, 463-467.	1.6	80
69	Ablation of miR-10b Suppresses Oncogene-Induced Mammary Tumorigenesis and Metastasis and Reactivates Tumor-Suppressive Pathways. <i>Cancer Research</i> , 2016, 76, 6424-6435.	0.4	77
70	$\hat{\pm}$ -catenin acts as a tumour suppressor in E-cadherin-negative basal-like breast cancer by inhibiting NF- $\hat{\pm}$ B signalling. <i>Nature Cell Biology</i> , 2014, 16, 245-254.	4.6	74
71	Naturally Occurring Neomorphic PIK3R1 Mutations Activate the MAPK Pathway, Dictating Therapeutic Response to MAPK Pathway Inhibitors. <i>Cancer Cell</i> , 2014, 26, 479-494.	7.7	73
72	PATHOME: an algorithm for accurately detecting differentially expressed subpathways. <i>Oncogene</i> , 2014, 33, 4941-4951.	2.6	70

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73	Bacteria-to-Human Protein Networks Reveal Origins of Endogenous DNA Damage. <i>Cell</i> , 2019, 176, 127-143.e24.	13.5	69
74	A High-Resolution Map of Human Enhancer RNA Loci Characterizes Super-enhancer Activities in Cancer. <i>Cancer Cell</i> , 2020, 38, 701-715.e5.	7.7	69
75	The role of A-to-I RNA editing in cancer development. <i>Current Opinion in Genetics and Development</i> , 2018, 48, 51-56.	1.5	67
76	Verteporfin Inhibits PD-L1 through Autophagy and the STAT1-IRF1-TRIM28 Signaling Axis, Exerting Antitumor Efficacy. <i>Cancer Immunology Research</i> , 2020, 8, 952-965.	1.6	63
77	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.	2.5	61
78	Multi-omics characterization of molecular features of gastric cancer correlated with response to neoadjuvant chemotherapy. <i>Science Advances</i> , 2020, 6, eaay4211.	4.7	60
79	Protein Under-Wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. <i>PLoS Genetics</i> , 2008, 4, e11.	1.5	53
80	Identification of cancer sex-disparity in the functional integrity of p53 and its X chromosome network. <i>Nature Communications</i> , 2019, 10, 5385.	5.8	53
81	The somatic mutation landscape of premalignant colorectal adenoma. <i>Gut</i> , 2018, 67, 1299-1305.	6.1	52
82	Sex disparities in cancer. <i>Cancer Letters</i> , 2019, 466, 35-38.	3.2	50
83	Clinical and Biologic Significance of MYC Genetic Mutations in De Novo Diffuse Large B-cell Lymphoma. <i>Clinical Cancer Research</i> , 2016, 22, 3593-3605.	3.2	48
84	The evolutionary origin of a complex scrambled gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 15149-15154.	3.3	47
85	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. <i>Pharmacological Reviews</i> , 2019, 71, 1-19.	7.1	47
86	Comprehensive assessment of computational algorithms in predicting cancer driver mutations. <i>Genome Biology</i> , 2020, 21, 43.	3.8	47
87	A-to-I edited miRNA-379-5p inhibits cancer cell proliferation through CD97-induced apoptosis. <i>Journal of Clinical Investigation</i> , 2019, 129, 5343-5356.	3.9	46
88	Epstein-Barr Virus MicroRNAs are Expressed in Patients with Chronic Lymphocytic Leukemia and Correlate with Overall Survival. <i>EBioMedicine</i> , 2015, 2, 572-582.	2.7	43
89	ZRANB1 Is an EZH2 Deubiquitinase and a Potential Therapeutic Target in Breast Cancer. <i>Cell Reports</i> , 2018, 23, 823-837.	2.9	42
90	SWAKK: a web server for detecting positive selection in proteins using a sliding window substitution rate analysis. <i>Nucleic Acids Research</i> , 2006, 34, W382-W384.	6.5	41

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91	p53 deficiency linked to B cell translocation gene 2 (BTG2) loss enhances metastatic potential by promoting tumor growth in primary and metastatic sites in patient-derived xenograft (PDX) models of triple-negative breast cancer. <i>Breast Cancer Research</i> , 2016, 18, 13.	2.2	41
92	APAAtlas: decoding alternative polyadenylation across human tissues. <i>Nucleic Acids Research</i> , 2020, 48, D34-D39.	6.5	41
93	SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. <i>Cell Reports</i> , 2017, 18, 3117-3128.	2.9	40
94	Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. <i>Cancer Cell</i> , 2020, 38, 829-843.e4.	7.7	40
95	Ultraconserved long non-coding RNA uc.63 in breast cancer. <i>Oncotarget</i> , 2017, 8, 35669-35680.	0.8	38
96	Prevalent Homozygous Deletions of Type I Interferon and Defensin Genes in Human Cancers Associate with Immunotherapy Resistance. <i>Clinical Cancer Research</i> , 2018, 24, 3299-3308.	3.2	37
97	A genome-wide study of dual coding regions in human alternatively spliced genes. <i>Genome Research</i> , 2005, 16, 190-196.	2.4	36
98	Conservation of tandem stop codons in yeasts. <i>Genome Biology</i> , 2005, 6, R31.	13.9	36
99	Identifying molecular drivers of gastric cancer through next-generation sequencing. <i>Cancer Letters</i> , 2013, 340, 241-246.	3.2	36
100	Transcribed ultraconserved region 339 promotes carcinogenesis by modulating tumor suppressor microRNAs. <i>Nature Communications</i> , 2017, 8, 1801.	5.8	36
101	When MicroRNAs Meet RNA Editing in Cancer: A Nucleotide Change Can Make a Difference. <i>BioEssays</i> , 2018, 40, 1700188.	1.2	35
102	Predicting the lethal phenotype of the knockout mouse by integrating comprehensive genomic data. <i>Bioinformatics</i> , 2012, 28, 1246-1252.	1.8	34
103	Integrated genomic analysis of recurrence-associated small non-coding RNAs in oesophageal cancer. <i>Gut</i> , 2017, 66, 215-225.	6.1	34
104	A functional genomic screen in vivo identifies CEACAM5 as a clinically relevant driver of breast cancer metastasis. <i>Npj Breast Cancer</i> , 2018, 4, 9.	2.3	32
105	A pathway-based approach for identifying biomarkers of tumor progression to trastuzumab-resistant breast cancer. <i>Cancer Letters</i> , 2015, 356, 880-890.	3.2	31
106	Biosynthetic energy cost for amino acids decreases in cancer evolution. <i>Nature Communications</i> , 2018, 9, 4124.	5.8	27
107	Decoding the Decoding Region: Analysis of Eukaryotic Release Factor (eRF1) Stop Codon-Binding Residues. <i>Journal of Molecular Evolution</i> , 2005, 60, 337-344.	0.8	26
108	Functional compensation by duplicated genes in mouse. <i>Trends in Genetics</i> , 2009, 25, 441-442.	2.9	25

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109	Integrative Protein-Based Prognostic Model for Early-Stage Endometrioid Endometrial Cancer. <i>Clinical Cancer Research</i> , 2016, 22, 513-523.	3.2	25
110	Next-Generation Analytics for Omics Data. <i>Cancer Cell</i> , 2021, 39, 3-6.	7.7	24
111	Protein structure protection commits gene expression patterns. <i>Genome Biology</i> , 2008, 9, R107.	13.9	23
112	BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. <i>Biometrics</i> , 2011, 67, 1215-1224.	0.8	23
113	SurvNet: a web server for identifying network-based biomarkers that most correlate with patient survival data. <i>Nucleic Acids Research</i> , 2012, 40, W123-W126.	6.5	23
114	Distinct telomere length and molecular signatures in seminoma and non-seminoma of testicular germ cell tumor. <i>Briefings in Bioinformatics</i> , 2019, 20, 1502-1512.	3.2	22
115	Fast-Evolving Human-Specific Neural Enhancers Are Associated with Aging-Related Diseases. <i>Cell Systems</i> , 2018, 6, 604-611.e4.	2.9	20
116	A four-gene signature predicts survival and anti-CTLA4 immunotherapeutic responses based on immune classification of melanoma. <i>Communications Biology</i> , 2021, 4, 383.	2.0	20
117	Detecting positive selection in the budding yeast genome. <i>Journal of Evolutionary Biology</i> , 2009, 22, 2430-2437.	0.8	19
118	Protein profiling identifies mTOR pathway modulation and cytostatic effects of Pim kinase inhibitor, AZD1208, in acute myeloid leukemia. <i>Leukemia and Lymphoma</i> , 2016, 57, 2863-2873.	0.6	19
119	SRC-3 inhibition blocks tumor growth of pancreatic ductal adenocarcinoma. <i>Cancer Letters</i> , 2019, 442, 310-319.	3.2	17
120	Using Reverse Phase Protein Array (RPPA) to Identify and Target Adaptive Resistance. <i>Advances in Experimental Medicine and Biology</i> , 2019, 1188, 251-266.	0.8	17
121	Differential expression of MAGEA6 toggles autophagy to promote pancreatic cancer progression. <i>ELife</i> , 2020, 9, .	2.8	16
122	Fast Evolution of Core Promoters in Primate Genomes. <i>Molecular Biology and Evolution</i> , 2008, 25, 1239-1244.	3.5	15
123	Comparative analysis of somatic copy-number alterations across different human cancer types reveals two distinct classes of breakpoint hotspots. <i>Human Molecular Genetics</i> , 2012, 21, 4957-4965.	1.4	15
124	Personalized Integrated Network Modeling of the Cancer Proteome Atlas. <i>Scientific Reports</i> , 2018, 8, 14924.	1.6	14
125	Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 399-411.	1.0	13
126	Systematic functional interrogation of human pseudogenes using CRISPRi. <i>Genome Biology</i> , 2021, 22, 240.	3.8	13

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127	Genomic characterization of co-existing neoplasia and carcinoma lesions reveals distinct evolutionary paths of gallbladder cancer. <i>Nature Communications</i> , 2021, 12, 4753.	5.8	12
128	Ventilator-induced diaphragmatic dysfunction in <i>MDX</i> mice. <i>Muscle and Nerve</i> , 2018, 57, 442-448.	1.0	11
129	Predicting Cancer Cell Line Dependencies From the Protein Expression Data of Reverse-Phase Protein Arrays. <i>JCO Clinical Cancer Informatics</i> , 2020, 4, 357-366.	1.0	11
130	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. <i>Scientific Reports</i> , 2021, 11, 15713.	1.6	10
131	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.	0.8	9
132	A functional genomic approach to actionable gene fusions for precision oncology. <i>Science Advances</i> , 2022, 8, eabm2382.	4.7	9
133	Molecular mimicry: Quantitative methods to study structural similarity between protein and RNA. <i>Rna</i> , 2005, 11, 1167-1172.	1.6	8
134	RNA editing increases the nucleotide diversity of SARS-CoV-2 in human host cells. <i>PLoS Genetics</i> , 2022, 18, e1010130.	1.5	8
135	RNA editing in cancer: Mechanistic, prognostic, and therapeutic implications. <i>Molecular and Cellular Oncology</i> , 2016, 3, e1117702.	0.3	7
136	Analysis of the genomic landscape of yolk sac tumors reveals mechanisms of evolution and chemoresistance. <i>Nature Communications</i> , 2021, 12, 3579.	5.8	7
137	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. <i>BMC Genomics</i> , 2012, 13, S9.	1.2	6
138	Evolutionary constraints imposed by gene dosage balance. <i>Frontiers in Bioscience - Landmark</i> , 2008, Volume, 4373.	3.0	5
139	Credentialing Individual Samples for Proteogenomic Analysis. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1515-1530.	2.5	5
140	Decoding the dual-coding region: key factors influencing the translational potential of a two-ORF-containing transcript. <i>Cell Research</i> , 2010, 20, 508-509.	5.7	3
141	More reliable breast cancer risk assessment for every woman. <i>Cancer Cell</i> , 2021, 39, 457-459.	7.7	2
142	Are stop codons recognized by base triplets in the large ribosomal RNA subunit?. <i>Rna</i> , 2005, 11, 1478-1484.	1.6	1
143	Finding cancer drivers in the UPS system. <i>Nature Cancer</i> , 2020, 1, 20-21.	5.7	1
144	Convergent Usage of Amino Acids in Human Cancers as A Reversed Process of Tissue Development. <i>Genomics, Proteomics and Bioinformatics</i> , 2022, 20, 147-162.	3.0	1