Han Liang

List of Publications by Year
in descending order

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	Convergent Usage of Amino Acids in Human Cancers as A Reversed Process of Tissue Development. Genomics, Proteomics and Bioinformatics, 2022, 20, 147-162.	3.0	1
2	RNA editing increases the nucleotide diversity of SARS-CoV-2 in human host cells. PLoS Genetics, 2022, 18, e1010130.	1.5	8
3	A functional genomic approach to actionable gene fusions for precision oncology. Science Advances, 2022, 8, eabm2382.	4.7	9
4	Next-Generation Analytics for Omics Data. Cancer Cell, 2021, 39, 3-6.	7.7	24
5	A four-gene signature predicts survival and anti-CTLA4 immunotherapeutic responses based on immune classification of melanoma. Communications Biology, 2021, 4, 383.	2.0	20
6	More reliable breast cancer risk assessment for every woman. Cancer Cell, 2021, 39, 457-459.	7.7	2
7	Analysis of the genomic landscape of yolk sac tumors reveals mechanisms of evolution and chemoresistance. Nature Communications, 2021, 12, 3579.	5.8	7
8	Immunogenomic pan-cancer landscape reveals immune escape mechanisms and immunoediting histories. Scientific Reports, 2021, 11, 15713.	1.6	10
9	Genomic characterization of co-existing neoplasia and carcinoma lesions reveals distinct evolutionary paths of gallbladder cancer. Nature Communications, 2021, 12, 4753.	5.8	12
10	Systematic functional interrogation of human pseudogenes using CRISPRi. Genome Biology, 2021, 22, 240.	3.8	13
11	A targetable LIFRâˆ'NF-ÎºBâˆ'LCN2 axis controls liver tumorigenesis and vulnerability to ferroptosis. Nature Communications, 2021, 12, 7333.	5.8	117
12	APAatlas: decoding alternative polyadenylation across human tissues. Nucleic Acids Research, 2020, 48, D34-D39.	6.5	41
13	Large-Scale Characterization of Drug Responses of Clinically Relevant Proteins in Cancer Cell Lines. Cancer Cell, 2020, 38, 829-843.e4.	7.7	40
14	Personalized Network Modeling of the Pan-Cancer Patient and Cell Line Interactome. JCO Clinical Cancer Informatics, 2020, 4, 399-411.	1.0	13
15	Multi-omics characterization of molecular features of gastric cancer correlated with response to neoadjuvant chemotherapy. Science Advances, 2020, 6, eaay4211.	4.7	60
16	Comprehensive assessment of computational algorithms in predicting cancer driver mutations. Genome Biology, 2020, 21, 43.	3.8	47
17	Finding cancer drivers in the UPS system. Nature Cancer, 2020, 1, 20-21.	5.7	1
18	Predicting Cancer Cell Line Dependencies From the Protein Expression Data of Reverse-Phase Protein Arrays. JCO Clinical Cancer Informatics, 2020, 4, 357-366.	1.0	11

#	Article	IF	Citations
19	Verteporfin Inhibits PD-L1 through Autophagy and the STAT1–IRF1–TRIM28 Signaling Axis, Exerting Antitumor Efficacy. Cancer Immunology Research, 2020, 8, 952-965.	1.6	63
20	A High-Resolution Map of Human Enhancer RNA Loci Characterizes Super-enhancer Activities in Cancer. Cancer Cell, 2020, 38, 701-715.e5.	7.7	69
21	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	9.4	256
22	Differential expression of MAGEA6 toggles autophagy to promote pancreatic cancer progression. ELife, 2020, 9, .	2.8	16
23	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons' Data. Cell Systems, 2019, 9, 24-34.e10.	2.9	103
24	Sex disparities in cancer. Cancer Letters, 2019, 466, 35-38.	3.2	50
25	TCPA v3.0: An Integrative Platform to Explore the Pan-Cancer Analysis of Functional Proteomic Data. Molecular and Cellular Proteomics, 2019, 18, S15-S25.	2.5	61
26	Characterization of hypoxia-associated molecular features to aid hypoxia-targeted therapy. Nature Metabolism, 2019, 1, 431-444.	5.1	158
27	Identification of cancer sex-disparity in the functional integrity of p53 and its X chromosome network. Nature Communications, 2019, 10, 5385.	5.8	53
28	SRC-3 inhibition blocks tumor growth of pancreatic ductal adenocarcinoma. Cancer Letters, 2019, 442, 310-319.	3.2	17
29	Bacteria-to-Human Protein Networks Reveal Origins of Endogenous DNA Damage. Cell, 2019, 176, 127-143.e24.	13.5	69
30	Personal Mutanomes Meet Modern Oncology Drug Discovery and Precision Health. Pharmacological Reviews, 2019, 71, 1-19.	7.1	47
31	Distinct telomere length and molecular signatures in seminoma and non-seminoma of testicular germ cell tumor. Briefings in Bioinformatics, 2019, 20, 1502-1512.	3.2	22
32	Using Reverse Phase Protein Array (RPPA) to Identify and Target Adaptive Resistance. Advances in Experimental Medicine and Biology, 2019, 1188, 251-266.	0.8	17
33	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.	0.8	9
34	A-to-I–edited miRNA-379-5p inhibits cancer cell proliferation through CD97-induced apoptosis. Journal of Clinical Investigation, 2019, 129, 5343-5356.	3.9	46
35	A-to-I RNA Editing Contributes to Proteomic Diversity in Cancer. Cancer Cell, 2018, 33, 817-828.e7.	7.7	172
36	ZRANB1 Is an EZH2 Deubiquitinase and a Potential Therapeutic Target in Breast Cancer. Cell Reports, 2018, 23, 823-837.	2.9	42

#	Article	IF	Citations
37	Prevalent Homozygous Deletions of Type I Interferon and Defensin Genes in Human Cancers Associate with Immunotherapy Resistance. Clinical Cancer Research, 2018, 24, 3299-3308.	3.2	37
38	An Integrated TCGA Pan-Cancer Clinical Data Resource to Drive High-Quality Survival Outcome Analytics. Cell, 2018, 173, 400-416.e11.	13.5	2,277
39	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	13.5	1,670
40	Cell-of-Origin Patterns Dominate the Molecular Classification of 10,000 Tumors from 33 Types of Cancer. Cell, 2018, 173, 291-304.e6.	13.5	1,718
41	A Pan-Cancer Analysis of Enhancer Expression in Nearly 9000 Patient Samples. Cell, 2018, 173, 386-399.e12.	13.5	228
42	Oncogenic Signaling Pathways in The Cancer Genome Atlas. Cell, 2018, 173, 321-337.e10.	13.5	2,111
43	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	2.9	407
44	Pan-Cancer Analysis of lncRNA Regulation Supports Their Targeting of Cancer Genes in Each Tumor Context. Cell Reports, 2018, 23, 297-312.e12.	2.9	205
45	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	6.6	3,706
46	Integrated Genomic Analysis of the Ubiquitin Pathway across Cancer Types. Cell Reports, 2018, 23, 213-226.e3.	2.9	83
47	Molecular Characterization and Clinical Relevance of Metabolic Expression Subtypes in Human Cancers. Cell Reports, 2018, 23, 255-269.e4.	2.9	204
48	When MicroRNAs Meet RNA Editing in Cancer: A Nucleotide Change Can Make a Difference. BioEssays, 2018, 40, 1700188.	1.2	35
49	Credentialing Individual Samples for Proteogenomic Analysis. Molecular and Cellular Proteomics, 2018, 17, 1515-1530.	2.5	5
50	Scalable Open Science Approach for Mutation Calling of Tumor Exomes Using Multiple Genomic Pipelines. Cell Systems, 2018, 6, 271-281.e7.	2.9	605
51	lncRNA Epigenetic Landscape Analysis Identifies EPIC1 as an Oncogenic lncRNA that Interacts with MYC and Promotes Cell-Cycle Progression in Cancer. Cancer Cell, 2018, 33, 706-720.e9.	7.7	400
52	Genomic and Functional Approaches to Understanding Cancer Aneuploidy. Cancer Cell, 2018, 33, 676-689.e3.	7.7	750
53	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	7.7	213
54	The somatic mutation landscape of premalignant colorectal adenoma. Gut, 2018, 67, 1299-1305.	6.1	52

#	Article	IF	Citations
55	The role of A-to-I RNA editing in cancer development. Current Opinion in Genetics and Development, 2018, 48, 51-56.	1.5	67
56	Ventilator‐induced diaphragmatic dysfunction in <i>MDX</i> mice. Muscle and Nerve, 2018, 57, 442-448.	1.0	11
57	NUAK2 is a critical YAP target in liver cancer. Nature Communications, 2018, 9, 4834.	5.8	88
58	RNA editing derived epitopes function as cancer antigens to elicit immune responses. Nature Communications, 2018, 9, 3919.	5.8	120
59	Biosynthetic energy cost for amino acids decreases in cancer evolution. Nature Communications, 2018, 9, 4124.	5.8	27
60	Personalized Integrated Network Modeling of the Cancer Proteome Atlas. Scientific Reports, 2018, 8, 14924.	1.6	14
61	Comprehensive Molecular Characterization of the Hippo Signaling Pathway in Cancer. Cell Reports, 2018, 25, 1304-1317.e5.	2.9	329
62	Long noncoding RNA MALAT1 suppresses breast cancer metastasis. Nature Genetics, 2018, 50, 1705-1715.	9.4	561
63	Fast-Evolving Human-Specific Neural Enhancers Are Associated with Aging-Related Diseases. Cell Systems, 2018, 6, 604-611.e4.	2.9	20
64	A functional genomic screen in vivo identifies CEACAM5 as a clinically relevant driver of breast cancer metastasis. Npj Breast Cancer, 2018, 4, 9.	2.3	32
65	ARID1A deficiency promotes mutability and potentiates therapeutic antitumor immunity unleashed by immune checkpoint blockade. Nature Medicine, 2018, 24, 556-562.	15.2	372
66	SKP2- and OTUD1-regulated non-proteolytic ubiquitination of YAP promotes YAP nuclear localization and activity. Nature Communications, 2018, 9, 2269.	5.8	117
67	A ROR1–HER3–lncRNA signalling axis modulates the Hippo–YAP pathway to regulate bone metastasis. Nature Cell Biology, 2017, 19, 106-119.	4.6	253
68	The LINK-A lncRNA interacts with PtdIns(3,4,5)P3 to hyperactivate AKT and confer resistance to AKT inhibitors. Nature Cell Biology, 2017, 19, 238-251.	4.6	201
69	Immune Microenvironment in Microsatellite-Instable Endometrial Cancers: Hereditary or Sporadic Origin Matters. Clinical Cancer Research, 2017, 23, 4473-4481.	3.2	96
70	Integrated genomic analysis of recurrence-associated small non-coding RNAs in oesophageal cancer. Gut, 2017, 66, 215-225.	6.1	34
71	Characterization of Human Cancer Cell Lines by Reverse-phase Protein Arrays. Cancer Cell, 2017, 31, 225-239.	7.7	190
72	Systematic characterization of A-to-I RNA editing hotspots in microRNAs across human cancers. Genome Research, 2017, 27, 1112-1125.	2.4	144

#	Article	IF	Citations
73	A Pan-Cancer Proteogenomic Atlas of PI3K/AKT/mTOR Pathway Alterations. Cancer Cell, 2017, 31, 820-832.e3.	7.7	433
74	SMARCAD1 Contributes to the Regulation of Naive Pluripotency by Interacting with Histone Citrullination. Cell Reports, 2017, 18, 3117-3128.	2.9	40
75	Energy stress-induced lncRNA FILNC1 represses c-Myc-mediated energy metabolism and inhibits renal tumor development. Nature Communications, 2017, 8, 783.	5.8	157
76	Explore, Visualize, and Analyze Functional Cancer Proteomic Data Using the Cancer Proteome Atlas. Cancer Research, 2017, 77, e51-e54.	0.4	101
77	An integrated bioinformatics platform for investigating the human E3 ubiquitin ligase-substrate interaction network. Nature Communications, 2017, 8, 347.	5.8	151
78	Transcribed ultraconserved region 339 promotes carcinogenesis by modulating tumor suppressor microRNAs. Nature Communications, 2017, 8, 1801.	5.8	36
79	Comparative genomic analysis of esophageal squamous cell carcinoma between Asian and Caucasian patient populations. Nature Communications, 2017, 8, 1533.	5.8	92
80	ILF2 Is a Regulator of RNA Splicing and DNA Damage Response in 1q21-Amplified Multiple Myeloma. Cancer Cell, 2017, 32, 88-100.e6.	7.7	114
81	Ultraconserved long non-coding RNA uc.63 in breast cancer. Oncotarget, 2017, 8, 35669-35680.	0.8	38
82	Clinical and Biologic Significance of *MYC* Genetic Mutations in *De Novo* Diffuse Large B-cell Lymphoma. Clinical Cancer Research, 2016, 22, 3593-3605.	3.2	48
83	Protein profiling identifies mTOR pathway modulation and cytostatic effects of Pim kinase inhibitor, AZD1208, in acute myeloid leukemia. Leukemia and Lymphoma, 2016, 57, 2863-2873.	0.6	19
84	Comprehensive Characterization of Molecular Differences in Cancer between Male and Female Patients. Cancer Cell, 2016, 29, 711-722.	7.7	242
85	Ablation of miR-10b Suppresses Oncogene-Induced Mammary Tumorigenesis and Metastasis and Reactivates Tumor-Suppressive Pathways. Cancer Research, 2016, 76, 6424-6435.	0.4	77
86	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. Breast Cancer Research, 2016, 18, 13.	2.2	41
87	HNF4α is a therapeutic target that links AMPK to WNT signalling in early-stage gastric cancer. Gut, 2016, 65, 19-32.	6.1	91
88	RNA editing in cancer: Mechanistic, prognostic, and therapeutic implications. Molecular and Cellular Oncology, 2016, 3, e1117702.	0.3	7
89	Integrative Protein-Based Prognostic Model for Early-Stage Endometrioid Endometrial Cancer. Clinical Cancer Research, 2016, 22, 513-523.	3.2	25
90	LncRNA NBR2 engages a metabolic checkpoint by regulating AMPK under energy stress. Nature Cell Biology, 2016, 18, 431-442.	4.6	239

#	Article	IF	Citations
91	Allele-Specific Reprogramming of Cancer Metabolism by the Long Non-coding RNA CCAT2. Molecular Cell, 2016, 61, 520-534.	4.5	142
92	The LINK-A lncRNA activates normoxic HIF1α signalling in triple-negative breast cancer. Nature Cell Biology, 2016, 18, 213-224.	4.6	444
93	TANRIC: An Interactive Open Platform to Explore the Function of lncRNAs in Cancer. Cancer Research, 2015, 75, 3728-3737.	0.4	518
94	Telomere Dysfunction Drives Aberrant Hematopoietic Differentiation and Myelodysplastic Syndrome. Cancer Cell, 2015, 27, 644-657.	7.7	85
95	A pathway-based approach for identifying biomarkers of tumor progression to trastuzumab-resistant breast cancer. Cancer Letters, 2015, 356, 880-890.	3.2	31
96	The Genomic Landscape and Clinical Relevance of A-to-I RNA Editing in Human Cancers. Cancer Cell, 2015, 28, 515-528.	7.7	426
97	Epstein–Barr Virus MicroRNAs are Expressed in Patients with Chronic Lymphocytic Leukemia and Correlate with Overall Survival. EBioMedicine, 2015, 2, 572-582.	2.7	43
98	Landscape of dietary factors associated with risk of gastric cancer: A systematic review and dose-response meta-analysis of prospective cohort studies. European Journal of Cancer, 2015, 51, 2820-2832.	1.3	187
99	Next generation sequencing of pancreatic cyst fluid microRNAs from low grade-benign and high grade-invasive lesions. Cancer Letters, 2015, 356, 404-409.	3.2	105
100	PATHOME: an algorithm for accurately detecting differentially expressed subpathways. Oncogene, 2014, 33, 4941-4951.	2.6	70
101	miR-100 Induces Epithelial-Mesenchymal Transition but Suppresses Tumorigenesis, Migration and Invasion. PLoS Genetics, 2014, 10, e1004177.	1.5	110
102	Naturally Occurring Neomorphic PIK3R1 Mutations Activate the MAPK Pathway, Dictating Therapeutic Response to MAPK Pathway Inhibitors. Cancer Cell, 2014, 26, 479-494.	7.7	73
103	miR-205 acts as a tumour radiosensitizer by targeting ZEB1 and Ubc13. Nature Communications, 2014, 5, 5671.	5.8	148
104	α-catenin acts as a tumour suppressor in E-cadherin-negative basal-like breast cancer by inhibiting NF-κB signalling. Nature Cell Biology, 2014, 16, 245-254.	4.6	74
105	Gene co-expression network analysis reveals common system-level properties of prognostic genes across cancer types. Nature Communications, 2014, 5, 3231.	5.8	385
106	ATM-mediated stabilization of ZEB1 promotes DNA damage response and radioresistance through CHK1. Nature Cell Biology, 2014, 16, 864-875.	4.6	367
107	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	13.7	911
108	Assessing the clinical utility of cancer genomic and proteomic data across tumor types. Nature Biotechnology, 2014, 32, 644-652.	9.4	257

#	Article	IF	Citations
109	The Pan-Cancer analysis of pseudogene expression reveals biologically and clinically relevant tumour subtypes. Nature Communications, 2014, 5, 3963.	5.8	143
110	A pan-cancer proteomic perspective on The Cancer Genome Atlas. Nature Communications, 2014, 5, 3887.	5.8	456
111	Identifying molecular drivers of gastric cancer through next-generation sequencing. Cancer Letters, 2013, 340, 241-246.	3.2	36
112	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
113	TCPA: a resource for cancer functional proteomics data. Nature Methods, 2013, 10, 1046-1047.	9.0	446
114	Enabling transparent and collaborative computational analysis of 12 tumor types within The Cancer Genome Atlas. Nature Genetics, 2013, 45, 1121-1126.	9.4	102
115	CanDrA: Cancer-Specific Driver Missense Mutation Annotation with Optimized Features. PLoS ONE, 2013, 8, e77945.	1.1	104
116	SurvNet: a web server for identifying network-based biomarkers that most correlate with patient survival data. Nucleic Acids Research, 2012, 40, W123-W126.	6.5	23
117	Predicting the lethal phenotype of the knockout mouse by integrating comprehensive genomic data. Bioinformatics, 2012, 28, 1246-1252.	1.8	34
118	Whole-exome sequencing combined with functional genomics reveals novel candidate driver cancer genes in endometrial cancer. Genome Research, 2012, 22, 2120-2129.	2.4	206
119	Comparative analysis of somatic copy-number alterations across different human cancer types reveals two distinct classes of breakpoint hotspots. Human Molecular Genetics, 2012, 21, 4957-4965.	1.4	15
120	LIFR is a breast cancer metastasis suppressor upstream of the Hippo-YAP pathway and a prognostic marker. Nature Medicine, 2012, 18, 1511-1517.	15.2	361
121	BM-Map: an efficient software package for accurately allocating multireads of RNA-sequencing data. BMC Genomics, 2012, 13, S9.	1.2	6
122	AMPKα Modulation in Cancer Progression: Multilayer Integrative Analysis of the Whole Transcriptome in Asian Gastric Cancer. Cancer Research, 2012, 72, 2512-2521.	0.4	91
123	BM-Map: Bayesian Mapping of Multireads for Next-Generation Sequencing Data. Biometrics, 2011, 67, 1215-1224.	0.8	23
124	Signalling pathway for RKIP and Let-7 regulates and predicts metastatic breast cancer. EMBO Journal, 2011, 30, 4500-4514.	3.5	175
125	High Frequency of *PIK3R1* and *PIK3R2* Mutations in Endometrial Cancer Elucidates a Novel Mechanism for Regulation of PTEN Protein Stability. Cancer Discovery, 2011, 1, 170-185.	7.7	419
126	Decoding the dual-coding region: key factors influencing the translational potential of a two-ORF-containing transcript. Cell Research, 2010, 20, 508-509.	5.7	3

#	Article	IF	Citations
127	Lowly Expressed Human MicroRNA Genes Evolve Rapidly. Molecular Biology and Evolution, 2009, 26, 1195-1198.	3.5	86
128	Functional compensation by duplicated genes in mouse. Trends in Genetics, 2009, 25, 441-442.	2.9	25
129	Detecting positive selection in the budding yeast genome. Journal of Evolutionary Biology, 2009, 22, 2430-2437.	0.8	19
130	Protein structure protection commits gene expression patterns. Genome Biology, 2008, 9, R107.	13.9	23
131	Fast Evolution of Core Promoters in Primate Genomes. Molecular Biology and Evolution, 2008, 25, 1239-1244.	3.5	15
132	Protein Under-Wrapping Causes Dosage Sensitivity and Decreases Gene Duplicability. PLoS Genetics, 2008, 4, e11.	1.5	53
133	Evolutionary constraints imposed by gene dosage balance. Frontiers in Bioscience - Landmark, 2008, Volume, 4373.	3.0	5
134	Human polymorphism at microRNAs and microRNA target sites. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3300-3305.	3.3	616
135	Hypothesis: RNA editing of microRNA target sites in humans?. Rna, 2007, 13, 463-467.	1.6	80
136	MicroRNA regulation of human protein–protein interaction network. Rna, 2007, 13, 1402-1408.	1.6	153
137	Gene essentiality, gene duplicability and protein connectivity in human and mouse. Trends in Genetics, 2007, 23, 375-378.	2.9	107
138	SWAKK: a web server for detecting positive selection in proteins using a sliding window substitution rate analysis. Nucleic Acids Research, 2006, 34, W382-W384.	6.5	41
139	Decoding the Decoding Region: Analysis of Eukaryotic Release Factor (eRF1) Stop Codon-Binding Residues. Journal of Molecular Evolution, 2005, 60, 337-344.	0.8	26
140	A genome-wide study of dual coding regions in human alternatively spliced genes. Genome Research, 2005, 16, 190-196.	2.4	36
141	Are stop codons recognized by base triplets in the large ribosomal RNA subunit?. Rna, 2005, 11, 1478-1484.	1.6	1
142	Molecular mimicry: Quantitative methods to study structural similarity between protein and RNA. Rna, 2005, 11, 1167-1172.	1.6	8
143	The evolutionary origin of a complex scrambled gene. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 15149-15154.	3.3	47
144	Conservation of tandem stop codons in yeasts. Genome Biology, 2005, 6, R31.	13.9	36