Derek Y Chiang

List of Publications by Year
in descending order

53 papers	17,045 citations	87888 38 h-index	175258 52 g-index
54 all docs	54 docs citations	54 times ranked	27922 citing authors

#	Article	IF	Citations
1	The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905.	27.8	3,331
2	Gene Expression in Fixed Tissues and Outcome in Hepatocellular Carcinoma. New England Journal of Medicine, 2008, 359, 1995-2004.	27.0	1,148
3	High-throughput screening using patient-derived tumor xenografts to predict clinical trial drug response. Nature Medicine, 2015, 21, 1318-1325.	30.7	1,065
4	Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898.	27.8	1,020
5	Integrative Transcriptome Analysis Reveals Common Molecular Subclasses of Human Hepatocellular Carcinoma. Cancer Research, 2009, 69, 7385-7392.	0.9	978
6	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. Nucleic Acids Research, 2010, 38, e178-e178.	14.5	946
7	*EML4-ALK* Fusion Gene and Efficacy of an ALK Kinase Inhibitor in Lung Cancer. Clinical Cancer Research, 2008, 14, 4275-4283.	7.0	916
8	Pivotal Role of mTOR Signaling in Hepatocellular Carcinoma. Gastroenterology, 2008, 135, 1972-1983.e11.	1.3	644
9	Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721.	21.4	642
10	Focal Gains of *VEGFA* and Molecular Classification of Hepatocellular Carcinoma. Cancer Research, 2008, 68, 6779-6788.	0.9	589
11	Genomics and Signaling Pathways in Hepatocellular Carcinoma. Seminars in Liver Disease, 2007, 27, 055-076.	3.6	491
12	High-resolution mapping of copy-number alterations with massively parallel sequencing. Nature Methods, 2009, 6, 99-103.	19.0	462
13	Studying clonal dynamics in response to cancer therapy using high-complexity barcoding. Nature Medicine, 2015, 21, 440-448.	30.7	408
14	Suppression of lung adenocarcinoma progression by Nkx2-1. Nature, 2011, 473, 101-104.	27.8	383
15	Astrocyte elevated gene-1 regulates hepatocellular carcinoma development and progression. Journal of Clinical Investigation, 2009, 119, 465-477.	8.2	298
16	Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968.	21.4	270
17	Identification of driver genes in hepatocellular carcinoma by exome sequencing. Hepatology, 2013, 58, 1693-1702.	7.3	264
18	Predicting drug susceptibility of non–small cell lung cancers based on genetic lesions. Journal of Clinical Investigation, 2009, 119, 1727-1740.	8.2	230

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19	Vav2 Is an Activator of Cdc42, Rac1, and RhoA. Journal of Biological Chemistry, 2000, 275, 10141-10149.	3.4	226
20	IGF activation in a molecular subclass of hepatocellular carcinoma and pre-clinical efficacy of IGF-1R blockage. Journal of Hepatology, 2010, 52, 550-559.	3.7	211
21	Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. PLoS Biology, 2004, 2, e398.	5.6	207
22	Ras pathway activation in hepatocellular carcinoma and anti-tumoral effect of combined sorafenib and rapamycin in vivo. Journal of Hepatology, 2009, 51, 725-733.	3.7	206
23	MicroRNA-Based Classification of Hepatocellular Carcinoma and Oncogenic Role of miR-517a. Gastroenterology, 2011, 140, 1618-1628.e16.	1.3	205
24	A conditional transposon-based insertional mutagenesis screen for genes associated with mouse hepatocellular carcinoma. Nature Biotechnology, 2009, 27, 264-274.	17.5	194
25	Cancer gene discovery in hepatocellular carcinoma. Journal of Hepatology, 2010, 52, 921-929.	3.7	173
26	Nuclear factor I/B is an oncogene in small cell lung cancer. Genes and Development, 2011, 25, 1470-1475.	5.9	142
27	DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. Nucleic Acids Research, 2013, 41, e39-e39.	14.5	138
28	MONKEY: identifying conserved transcription-factor binding sites in multiple alignments using a binding site-specific evolutionary model. Genome Biology, 2004, 5, R98.	9.6	134
29	Position specific variation in the rate of evolution in transcription factor binding sites. BMC Evolutionary Biology, 2003, 3, 19.	3.2	130
30	iReckon: Simultaneous isoform discovery and abundance estimation from RNA-seq data. Genome Research, 2013, 23, 519-529.	5.5	123
31	Genomic Analysis of Nasopharyngeal Carcinoma Reveals TME-Based Subtypes. Molecular Cancer Research, 2017, 15, 1722-1732.	3.4	119
32	Pathogenesis of hepatocellular carcinoma and molecular therapies. Current Opinion in Gastroenterology, 2009, 25, 186-194.	2.3	118
33	Highâ€resolution analysis of genetic alterations in small bowel carcinoid tumors reveals areas of recurrent amplification and loss. Genes Chromosomes and Cancer, 2008, 47, 591-603.	2.8	101
34	PureCN: copy number calling and SNV classification using targeted short read sequencing. Source Code for Biology and Medicine, 2016, 11, 13.	1.7	101
35	Glioblastoma-Derived Epidermal Growth Factor Receptor Carboxyl-Terminal Deletion Mutants Are Transforming and Are Sensitive to EGFR-Directed Therapies. Cancer Research, 2011, 71, 7587-7596.	0.9	70
36	FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. Bioinformatics, 2011, 27, 2633-2640.	4.1	50

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37	Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. Genome Biology, 2003, 4, R43.	9.6	44
38	Mutations of isocitrate dehydrogenase 1 and 2 in intrahepatic cholangiocarcinoma. Current Opinion in Gastroenterology, 2014, 30, 295-302.	2.3	42
39	Integrating Prior Knowledge in Multiple Testing under Dependence with Applications to Detecting Differential DNA Methylation. Biometrics, 2012, 68, 774-783.	1.4	35
40	ILT3 (LILRB4) Promotes the Immunosuppressive Function of Tumor-Educated Human Monocytic Myeloid-Derived Suppressor Cells. Molecular Cancer Research, 2021, 19, 702-716.	3.4	32
41	Targeted next generation sequencing identifies clinically actionable mutations in patients with melanoma. Pigment Cell and Melanoma Research, 2014, 27, 653-663.	3.3	31
42	Integrative biomarker analyses indicate etiological variations in hepatocellular carcinoma. Journal of Hepatology, 2016, 65, 296-304.	3.7	26
43	A probabilistic framework for aligning paired-end RNA-seq data. Bioinformatics, 2010, 26, 1950-1957.	4.1	23
44	Elucidating therapeutic molecular targets in premenopausal Asian women with recurrent breast cancers. Npj Breast Cancer, 2018, 4, 19.	5.2	19
45	A Robust Method for Transcript Quantification with RNA-Seq Data. Journal of Computational Biology, 2013, 20, 167-187.	1.6	13
46	A community‐based lung cancer rapid tissue donation protocol provides high‐quality drug‐resistant specimens for proteogenomic analyses. Cancer Medicine, 2020, 9, 225-237.	2.8	11
47	Reverse Translating Molecular Determinants of Anti–Programmed Death 1 Immunotherapy Response in Mouse Syngeneic Tumor Models. Molecular Cancer Therapeutics, 2022, 21, 427-439.	4.1	10
48	Determining Physical Constraints in Transcriptional Initiation Complexes Using DNA Sequence Analysis. PLoS ONE, 2007, 2, e1199.	2.5	8
49	Mapping duplicated sequences. Nature Biotechnology, 2009, 27, 1001-1002.	17.5	5
50	Progress towards molecular patient stratification of hepatocellular carcinoma: Lost in translation?. Journal of Hepatology, 2017, 67, 893-895.	3.7	4
51	Co-expression networks identify distinct immune infiltrates in hepatocellular carcinoma. , 2015, 3, .		2
52	Von Hippel-Lindau status influences phenotype of liver cancers arising from PTEN loss. Gastrointestinal Cancer: Targets and Therapy, 2015, 5, 61.	5.5	1
53	A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147.	1.3	1