# 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 | 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 |
| 2 | 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 |
| 3 | 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 |
| 4 | Elucidating therapeutic molecular targets in premenopausal Asian women with recurrent breast cancers. Npj Breast Cancer, 2018, 4, 19. | 5.2 | 19 |
| 5 | Genomic Analysis of Nasopharyngeal Carcinoma Reveals TME-Based Subtypes. Molecular Cancer Research, 2017, 15, 1722-1732. | 3.4 | 119 |
| 6 | Progress towards molecular patient stratification of hepatocellular carcinoma: Lost in translation?. Journal of Hepatology, 2017, 67, 893-895. | 3.7 | 4 |
| 7 | Integrative biomarker analyses indicate etiological variations in hepatocellular carcinoma. Journal of Hepatology, 2016, 65, 296-304. | 3.7 | 26 |
| 8 | PureCN: copy number calling and SNV classification using targeted short read sequencing. Source Code for Biology and Medicine, 2016, 11, 13. | 1.7 | 101 |
| 9 | Von Hippel-Lindau status influences phenotype of liver cancers arising from PTEN loss. Gastrointestinal Cancer: Targets and Therapy, 2015, 5, 61. | 5.5 | 1 |
| 10 | Co-expression networks identify distinct immune infiltrates in hepatocellular carcinoma. , 2015, 3, . | | 2 |
| 11 | Studying clonal dynamics in response to cancer therapy using high-complexity barcoding. Nature Medicine, 2015, 21, 440-448. | 30.7 | 408 |
| 12 | High-throughput screening using patient-derived tumor xenografts to predict clinical trial drug response. Nature Medicine, 2015, 21, 1318-1325. | 30.7 | 1,065 |
| 13 | Targeted next generation sequencing identifies clinically actionable mutations in patients with melanoma. Pigment Cell and Melanoma Research, 2014, 27, 653-663. | 3.3 | 31 |
| 14 | Mutations of isocitrate dehydrogenase 1 and 2 in intrahepatic cholangiocarcinoma. Current Opinion in Gastroenterology, 2014, 30, 295-302. | 2.3 | 42 |
| 15 | iReckon: Simultaneous isoform discovery and abundance estimation from RNA-seq data. Genome Research, 2013, 23, 519-529. | 5.5 | 123 |
| 16 | A Robust Method for Transcript Quantification with RNA-Seq Data. Journal of Computational Biology, 2013, 20, 167-187. | 1.6 | 13 |
| 17 | Identification of driver genes in hepatocellular carcinoma by exome sequencing. Hepatology, 2013, 58, 1693-1702. | 7.3 | 264 |
| 18 | DiffSplice: the genome-wide detection of differential splicing events with RNA-seq. Nucleic Acids Research, 2013, 41, e39-e39. | 14.5 | 138 |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 19 | Integrating Prior Knowledge in Multiple Testing under Dependence with Applications to Detecting Differential DNA Methylation. Biometrics, 2012, 68, 774-783. | 1.4 | 35 |
| 20 | A Robust Method for Transcript Quantification with RNA-seq Data. Lecture Notes in Computer Science, 2012, , 127-147. | 1.3 | 1 |
| 21 | Nuclear factor I/B is an oncogene in small cell lung cancer. Genes and Development, 2011, 25, 1470-1475. | 5.9 | 142 |
| 22 | MicroRNA-Based Classification of Hepatocellular Carcinoma and Oncogenic Role of miR-517a. Gastroenterology, 2011, 140, 1618-1628.e16. | 1.3 | 205 |
| 23 | Genomic sequencing of colorectal adenocarcinomas identifies a recurrent VTI1A-TCF7L2 fusion. Nature Genetics, 2011, 43, 964-968. | 21.4 | 270 |
| 24 | 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 |
| 25 | Suppression of lung adenocarcinoma progression by Nkx2-1. Nature, 2011, 473, 101-104. | 27.8 | 383 |
| 26 | FDM: a graph-based statistical method to detect differential transcription using RNA-seq data. Bioinformatics, 2011, 27, 2633-2640. | 4.1 | 50 |
| 27 | The landscape of somatic copy-number alteration across human cancers. Nature, 2010, 463, 899-905. | 27.8 | 3,331 |
| 28 | Subtype-specific genomic alterations define new targets for soft-tissue sarcoma therapy. Nature Genetics, 2010, 42, 715-721. | 21.4 | 642 |
| 29 | A probabilistic framework for aligning paired-end RNA-seq data. Bioinformatics, 2010, 26, 1950-1957. | 4.1 | 23 |
| 30 | MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. Nucleic Acids Research, 2010, 38, e178-e178. | 14.5 | 946 |
| 31 | Cancer gene discovery in hepatocellular carcinoma. Journal of Hepatology, 2010, 52, 921-929. | 3.7 | 173 |
| 32 | 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 |
| 33 | Integrative Transcriptome Analysis Reveals Common Molecular Subclasses of Human Hepatocellular Carcinoma. Cancer Research, 2009, 69, 7385-7392. | 0.9 | 978 |
| 34 | A conditional transposon-based insertional mutagenesis screen for genes associated with mouse hepatocellular carcinoma. Nature Biotechnology, 2009, 27, 264-274. | 17.5 | 194 |
| 35 | Mapping duplicated sequences. Nature Biotechnology, 2009, 27, 1001-1002. | 17.5 | 5 |
| 36 | High-resolution mapping of copy-number alterations with massively parallel sequencing. Nature Methods, 2009, 6, 99-103. | 19.0 | 462 |

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|---|---------|-----|-----------|
| 37 | 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 |
| 38 | Pathogenesis of hepatocellular carcinoma and molecular therapies. Current Opinion in Gastroenterology, 2009, 25, 186-194. | 2.3 | 118 |
| 39 | Astrocyte elevated gene-1 regulates hepatocellular carcinoma development and progression. Journal of Clinical Investigation, 2009, 119, 465-477. | 8.2 | 298 |
| 40 | Predicting drug susceptibility of non–small cell lung cancers based on genetic lesions. Journal of Clinical Investigation, 2009, 119, 1727-1740. | 8.2 | 230 |
| 41 | High–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 |
| 42 | Pivotal Role of mTOR Signaling in Hepatocellular Carcinoma. Gastroenterology, 2008, 135, 1972-1983.e11. | 1.3 | 644 |
| 43 | Focal Gains of *VEGFA* and Molecular Classification of Hepatocellular Carcinoma. Cancer Research, 2008, 68, 6779-6788. | 0.9 | 589 |
| 44 | *EML4-ALK* Fusion Gene and Efficacy of an ALK Kinase Inhibitor in Lung Cancer. Clinical Cancer Research, 2008, 14, 4275-4283. | 7.0 | 916 |
| 45 | Gene Expression in Fixed Tissues and Outcome in Hepatocellular Carcinoma. New England Journal of Medicine, 2008, 359, 1995-2004. | 27.0 | 1,148 |
| 46 | Genomics and Signaling Pathways in Hepatocellular Carcinoma. Seminars in Liver Disease, 2007, 27, 055-076. | 3.6 | 491 |
| 47 | Characterizing the cancer genome in lung adenocarcinoma. Nature, 2007, 450, 893-898. | 27.8 | 1,020 |
| 48 | Determining Physical Constraints in Transcriptional Initiation Complexes Using DNA Sequence Analysis. PLoS ONE, 2007, 2, e1199. | 2.5 | 8 |
| 49 | Conservation and Evolution of Cis-Regulatory Systems in Ascomycete Fungi. PLoS Biology, 2004, 2, e398. | 5.6 | 207 |
| 50 | 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 |
| 51 | Position specific variation in the rate of evolution in transcription factor binding sites. BMC Evolutionary Biology, 2003, 3, 19. | 3.2 | 130 |
| 52 | Phylogenetically and spatially conserved word pairs associated with gene-expression changes in yeasts. Genome Biology, 2003, 4, R43. | 9.6 | 44 |
| 53 | Vav2 Is an Activator of Cdc42, Rac1, and RhoA. Journal of Biological Chemistry, 2000, 275, 10141-10149. | 3.4 | 226 |