Charles Lee

List of Publications by Year in descending order

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58 papers	26,928 citations	159358 30 h-index	143772 57 g-index
64 all docs	64 docs citations	64 times ranked	44994 citing authors

#	Article	IF	Citations
1	A global reference for human genetic variation. Nature, 2015, 526, 68-74.	13.7	13,998
2	Global variation in copy number in the human genome. Nature, 2006, 444, 444-454.	13.7	3,831
3	Detection of large-scale variation in the human genome. Nature Genetics, 2004, 36, 949-951.	9.4	2,602
4	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	13.7	1,994
5	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	13.7	991
6	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	5.8	636
7	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	6.0	358
8	Diverse Mechanisms of Somatic Structural Variations in Human Cancer Genomes. Cell, 2013, 153, 919-929.	13.5	308
9	Mutation spectrum revealed by breakpoint sequencing of human germline CNVs. Nature Genetics, 2010, 42, 385-391.	9.4	211
10	Completing the map of human genetic variation. Nature, 2007, 447, 161-165.	13.7	178
11	Bifidobacterium bifidum strains synergize with immune checkpoint inhibitors to reduce tumour burden in mice. Nature Microbiology, 2021, 6, 277-288.	5.9	130
12	Fully phased human genome assembly without parental data using single-cell strand sequencing and long reads. Nature Biotechnology, 2021, 39, 302-308.	9.4	127
13	Conservation of copy number profiles during engraftment and passaging of patient-derived cancer xenografts. Nature Genetics, 2021, 53, 86-99.	9.4	118
14	An Integrative Approach to Precision Cancer Medicine Using Patient-Derived Xenografts. Molecules and Cells, 2016, 39, 77-86.	1.0	110
15	Clonal Evolution Enhances Leukemia-Propagating Cell Frequency in T Cell Acute Lymphoblastic Leukemia through Akt/mTORC1 Pathway Activation. Cancer Cell, 2014, 25, 366-378.	7.7	98
16	Studying cancer immunotherapy using patient-derived xenografts (PDXs) in humanized mice. Experimental and Molecular Medicine, 2018, 50, 1-9.	3.2	85
17	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	5.8	77
18	Survival of Del17p CLL Depends on Genomic Complexity and Somatic Mutation. Clinical Cancer Research, 2017, 23, 735-745.	3.2	74

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19	Engineering microdeletions and microduplications by targeting segmental duplications with CRISPR. Nature Neuroscience, 2016, 19, 517-522.	7.1	72
20	Expectations and blind spots for structural variation detection from long-read assemblies and short-read genome sequencing technologies. American Journal of Human Genetics, 2021, 108, 919-928.	2.6	72
21	Recurrent inversion polymorphisms in humans associate with genetic instability and genomic disorders. Cell, 2022, 185, 1986-2005.e26.	13.5	67
22	Perspective of mesenchymal transformation in glioblastoma. Acta Neuropathologica Communications, 2021, 9, 50.	2.4	63
23	COVID-19 preclinical models: human angiotensin-converting enzyme 2 transgenic mice. Human Genomics, 2020, 14, 20.	1.4	59
24	One reference genome is not enough. Genome Biology, 2019, 20, 104.	3.8	58
25	Molecular pathogenesis of congenital diaphragmatic hernia revealed by exome sequencing, developmental data, and bioinformatics. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 12450-12455.	3.3	49
26	Genomic alterations in BCL2L1 and DLC1 contribute to drug sensitivity in gastric cancer. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 12492-12497.	3.3	46
27	FusorSV: an algorithm for optimally combining data from multiple structural variation detection methods. Genome Biology, 2018, 19, 38.	3.8	46
28	Cryptic and Complex Chromosomal Aberrations in Early-Onset Neuropsychiatric Disorders. American Journal of Human Genetics, 2014, 95, 454-461.	2.6	45
29	Whole-exome sequencing identifies recurrent AKT1 mutations in sclerosing hemangioma of lung. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10672-10677.	3.3	42
30	High prevalence of TP53 mutations is associated with poor survival and an EMT signature in gliosarcoma patients. Experimental and Molecular Medicine, 2017, 49, e317-e317.	3.2	37
31	Comprehensive Molecular Characterization of Adenocarcinoma of the Gastroesophageal Junction Between Esophageal and Gastric Adenocarcinomas. Annals of Surgery, 2022, 275, 706-717.	2.1	30
32	Seroprevalence of SARS-CoV-2-Specific IgG Antibodies Among Adults Living in Connecticut: Post-Infection Prevalence (PIP) Study. American Journal of Medicine, 2021, 134, 526-534.e11.	0.6	28
33	Predictive biomarkers for 5-fluorouracil and oxaliplatin-based chemotherapy in gastric cancers via profiling of patient-derived xenografts. Nature Communications, 2021, 12, 4840.	5.8	27
34	Systematic analysis of copy number variation associated with congenital diaphragmatic hernia. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 5247-5252.	3.3	26
35	TeXP: Deconvolving the effects of pervasive and autonomous transcription of transposable elements. PLoS Computational Biology, 2019, 15, e1007293.	1.5	24
36	Development of a Novel Orthotopic Gastric Cancer Mouse Model. Biological Procedures Online, 2021, 23, 1.	1.4	19

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37	A Novel Combination Treatment Targeting BCL-XL and MCL1 for KRAS/BRAF-mutated and BCL2L1-amplified Colorectal Cancers. Molecular Cancer Therapeutics, 2017, 16, 2178-2190.	1.9	17
38	Association of CNVs with methylation variation. Npj Genomic Medicine, 2020, 5, 41.	1.7	17
39	Spermidine-induced recovery of human dermal structure and barrier function by skin microbiome. Communications Biology, 2021, 4, 231.	2.0	17
40	Genomic Alterations in the RB Pathway Indicate Prognostic Outcomes of Early-Stage Lung Adenocarcinoma. Clinical Cancer Research, 2015, 21, 2613-2623.	3.2	16
41	High-resolution deconstruction of evolution induced by chemotherapy treatments in breast cancer xenografts. Scientific Reports, 2018, 8, 17937.	1.6	15
42	Genomeâ€scale CRISPR screening identifies cell cycle and protein ubiquitination processes as druggable targets for erlotinibâ€resistant lung cancer. Molecular Oncology, 2021, 15, 487-502.	2.1	15
43	Comprehensive Analysis of Alternative Splicing in Gastric Cancer Identifies Epithelialâ€“Mesenchymal Transition Subtypes Associated with Survival. Cancer Research, 2022, 82, 543-555.	0.4	12
44	A novel treatment strategy for lapatinib resistance in a subset of HER2-amplified gastric cancer. BMC Cancer, 2021, 21, 923.	1.1	11
45	Sex-specific phenotypic effects and evolutionary history of an ancient polymorphic deletion of the human growth hormone receptor. Science Advances, 2021, 7, eabi4476.	4.7	11
46	Targeting antioxidant enzymes enhances the therapeutic efficacy of the BCL-XL inhibitor ABT-263 in KRAS-mutant colorectal cancers. Cancer Letters, 2021, 497, 123-136.	3.2	8
47	Alterations in the Rho pathway contribute to Epstein-Barr virusâ€“induced lymphomagenesis in immunosuppressed environments. Blood, 2018, 131, 1931-1941.	0.6	7
48	SvAnna: efficient and accurate pathogenicity prediction of coding and regulatory structural variants in long-read genome sequencing. Genome Medicine, 2022, 14, 44.	3.6	7
49	Mako: A Graph-based Pattern Growth Approach to Detect Complex Structural Variants. Genomics, Proteomics and Bioinformatics, 2022, 20, 205-218.	3.0	6
50	Employeesâ€™ Views and Ethical, Legal, and Social Implications Assessment of Voluntary Workplace Genomic Testing. Frontiers in Genetics, 2021, 12, 643304.	1.1	4
51	Three decades of the Human Genome Organization. American Journal of Medical Genetics, Part A, 2021, 185, 3314-3321.	0.7	4
52	JAX-CNV: A Whole-genome Sequencing-based Algorithm for Copy Number Detection at Clinical Grade Level. Genomics, Proteomics and Bioinformatics, 2022, 20, 1197-1206.	3.0	3
53	Glucose metabolic profiles evaluated by PET associated with molecular characteristic landscape of gastric cancer. Gastric Cancer, 2021, , 1.	2.7	2
54	Voluntary workplace genomic testing: wellness benefit or Pandoraâ€™s box?. Npj Genomic Medicine, 2022, 7, 5.	1.7	2

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55	The X Chromosome from Telomere to Telomere: Key Achievements and Future Opportunities. Faculty Reviews, 2021, 10, 63.	1.7	1
56	Standard personalized medicine platform integrating clinical genomics and patient-derived xenograft models for gastric cancer.. Journal of Clinical Oncology, 2017, 35, 120-120.	0.8	0
57	Molecular profiling of adenocarcinoma of esophagogastric junction.. Journal of Clinical Oncology, 2017, 35, 65-65.	0.8	0
58	TMOD-13. IDENTIFYING DRIVERS IN THE CONVERGING SYNTENIC REGIONS OF SPONTANEOUS CANINE AND PEDIATRIC HIGH-GRADE GLIOMA USING IMAGING BASED CRISPR-CAS9 ARRAY SCREEN. Neuro-Oncology, 2021, 23, vi218-vi218.	0.6	0