Ken Chen

List of Publications by Year
in descending order

141	39,752	19657 61	10445 139
papers	citations	h-index	g-index

147	147	147	54663
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
2	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
3	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	27.8	2,694
4	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
5	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
6	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
7	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
8	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
9	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	19.0	1,322
10	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
11	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	4.1	1,193
12	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
13	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
14	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
15	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
16	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	27.8	911
17	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
18	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636

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19	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
20	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
21	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
22	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
23	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
24	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	17.5	306
25	Ph-like acute lymphoblastic leukemia: a high-risk subtype in adults. Blood, 2017, 129, 572-581.	1.4	285
26	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
27	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233
28	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
29	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	16.8	213
30	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.1	199
31	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
32	A Decision Support Framework for Genomically Informed Investigational Cancer Therapy. Journal of the National Cancer Institute, 2015, 107, .	6.3	168
33	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. Cancer Cell, 2019, 35, 851-867.e7.	16.8	156
34	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. Genome Biology, 2017, 18, 178.	8.8	152
35	Monovar: single-nucleotide variant detection in single cells. Nature Methods, 2016, 13, 505-507.	19.0	150
36	Characterization of twenty-five ovarian tumour cell lines that phenocopy primary tumours. Nature Communications, 2015, 6, 7419.	12.8	149

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37	Targeting a cytokine checkpoint enhances the fitness of armored cord blood CAR-NK cells. Blood, 2021, 137, 624-636.	1.4	147
38	Identification of a Novel <emph type="ital">TP53</emph> Cancer Susceptibility Mutation Through Whole-Genome Sequencing of a Patient With Therapy-Related AML. JAMA - Journal of the American Medical Association, 2011, 305, 1568.	7.4	146
39	Computational Analysis and Prediction of the Binding Motif and Protein Interacting Partners of the Abl SH3 Domain. PLoS Computational Biology, 2006, 2, e1.	3.2	145
40	BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11.	25.8	135
41	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
42	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	30.7	134
43	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. Cancer Research, 2015, 75, 5341-5354.	0.9	130
44	Genetic biomarkers of sensitivity and resistance to venetoclax monotherapy in patients with relapsed acute myeloid leukemia. American Journal of Hematology, 2018, 93, E202.	4.1	116
45	Novel algorithmic approach predicts tumor mutation load and correlates with immunotherapy clinical outcomes using a defined gene mutation set. BMC Medicine, 2016, 14, 168.	5.5	106
46	CanDrA: Cancer-Specific Driver Missense Mutation Annotation with Optimized Features. PLoS ONE, 2013, 8, e77945.	2.5	104
47	Single-nuclei RNA-seq on human retinal tissue provides improved transcriptome profiling. Nature Communications, 2019, 10, 5743.	12.8	101
48	SiCloneFit: Bayesian inference of population structure, genotype, and phylogeny of tumor clones from single-cell genome sequencing data. Genome Research, 2019, 29, 1847-1859.	5.5	97
49	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
50	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	8.2	91
51	Clinical Actionability Enhanced through Deep Targeted Sequencing of Solid Tumors. Clinical Chemistry, 2015, 61, 544-553.	3.2	85
52	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83
53	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	5.5	81
54	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. Cancer Letters, 2015, 357, 179-185.	7.2	81

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55	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	12.8	77
56	PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data. Genome Research, 2007, 17, 659-666.	5.5	76
57	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. Genes and Development, 2013, 27, 1462-1472.	5.9	74
58	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	28.9	73
59	Prediction of Binding Affinities between the Human Amphiphysin-1 SH3 Domain and Its Peptide Ligands Using Homology Modeling, Molecular Dynamics and Molecular Field Analysis. Journal of Proteome Research, 2006, 5, 32-43.	3.7	70
60	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	19.0	67
61	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
62	Sarcomatoid Renal Cell Carcinoma Has a Distinct Molecular Pathogenesis, Driver Mutation Profile, and Transcriptional Landscape. Clinical Cancer Research, 2017, 23, 6686-6696.	7.0	66
63	RET Fusion as a Novel Driver of Medullary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 788-793.	3.6	65
64	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294.	3.3	60
65	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	12.8	60
66	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. Bioinformatics, 2010, 26, 464-469.	4.1	59
67	Comprehensive Genomic Profiling of Metastatic Squamous Cell Carcinoma of the Anal Canal. Molecular Cancer Research, 2017, 15, 1542-1550.	3.4	59
68	Functional annotation of rare gene aberration drivers of pancreatic cancer. Nature Communications, 2016, 7, 10500.	12.8	58
69	Relative Abundance of SARS-CoV-2 Entry Genes in the Enterocytes of the Lower Gastrointestinal Tract. Genes, 2020, 11, 645.	2.4	57
70	Catalytic mTOR inhibitors can overcome intrinsic and acquired resistance to allosteric mTOR inhibitors. Oncotarget, 2014, 5, 8544-8557.	1.8	56
71	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924.	4.1	54
72	Ability to Generate Patient-Derived Breast Cancer Xenografts Is Enhanced in Chemoresistant Disease and Predicts Poor Patient Outcomes. PLoS ONE, 2015, 10, e0136851.	2.5	54

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73	MET amplification in metastatic colorectal cancer: an acquired response to EGFR inhibition, not a de novo phenomenon. Oncotarget, 2016, 7, 54627-54631.	1.8	53
74	Landmark-Based Speech Recognition: Report of the 2004 Johns Hopkins Summer Workshop. , 2005, 1, 1213-1216.		52
75	Massively Parallel Sequencing Approaches for Characterization of Structural Variation. Methods in Molecular Biology, 2012, 838, 369-384.	0.9	49
76	A Population of Heterogeneous Breast Cancer Patient-Derived Xenografts Demonstrate Broad Activity of PARP Inhibitor in BRCA1/2 Wild-Type Tumors. Clinical Cancer Research, 2017, 23, 6468-6477.	7.0	48
77	Validation of HER2 Amplification as a Predictive Biomarker for Antiâ€“Epidermal Growth Factor Receptor Antibody Therapy in Metastatic Colorectal Cancer. JCO Precision Oncology, 2019, 3, 1-13.	3.0	46
78	Survival Outcomes by TP53 Mutation Status in Metastatic Breast Cancer. JCO Precision Oncology, 2018, 2018, 1-15.	3.0	43
79	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, 188.	8.8	42
80	Bias from removing read duplication in ultra-deep sequencing experiments. Bioinformatics, 2014, 30, 1073-1080.	4.1	39
81	Distinct Biological Types of Ocular Adnexal Sebaceous Carcinoma: HPV-Driven and Virus-Negative Tumors Arise through Nonoverlapping Molecular-Genetic Alterations. Clinical Cancer Research, 2019, 25, 1280-1290.	7.0	39
82	The degree of intratumor mutational heterogeneity varies by primary tumor sub-site. Oncotarget, 2016, 7, 27185-27198.	1.8	37
83	Simultaneous recognition of words and prosody in the Boston University Radio Speech Corpus. Speech Communication, 2005, 46, 418-439.	2.8	36
84	Computational approaches for inferring tumor evolution from single-cell genomic data. Current Opinion in Systems Biology, 2018, 7, 16-25.	2.6	36
85	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. Modern Pathology, 2019, 32, 1698-1707.	5.5	35
86	Functional consequence of theMET-T1010I polymorphism in breast cancer. Oncotarget, 2015, 6, 2604-2614.	1.8	34
87	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. Nature Communications, 2018, 9, 2732.	12.8	33
88	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	5.5	32
89	Single-cell RNA-seq analysis reveals compartment-specific heterogeneity and plasticity of microglia. IScience, 2021, 24, 102186.	4.1	31
90	Elevated Endogenous SDHA Drives Pathological Metabolism in Highly Metastatic Uveal Melanoma. , 2019, 60, 4187.		30

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91	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	3.2	30
92	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, 394.	2.8	28
93	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. Oncotarget, 2018, 9, 19891-19899.	1.8	28
94	Dynamic Spatio-Temporal Graph-Based CNNs for Traffic Flow Prediction. IEEE Access, 2020, 8, 185136-185145.	4.2	27
95	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27
96	BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87.	9.6	25
97	Cancer driver mutation prediction through Bayesian integration of multi-omic data. PLoS ONE, 2018, 13, e0196939.	2.5	23
98	A novel immature natural killer cell subpopulation predicts relapse after cord blood transplantation. Blood Advances, 2019, 3, 4117-4130.	5.2	23
99	Latent periodic process inference from single-cell RNA-seq data. Nature Communications, 2020, 11, 1441.	12.8	23
100	Use of Targeted Next-Generation Sequencing to Identify Activating Hot Spot Mutations in Cherry Angiomas. JAMA Dermatology, 2019, 155, 211.	4.1	22
101	GMP-Compliant Universal Antigen Presenting Cells (uAPC) Promote the Metabolic Fitness and Antitumor Activity of Armored Cord Blood CAR-NK Cells. Frontiers in Immunology, 2021, 12, 626098.	4.8	21
102	Adaptive responses in a PARP inhibitor window of opportunity trial illustrate limited functional interlesional heterogeneity and potential combination therapy options. Oncotarget, 2019, 10, 3533-3546.	1.8	19
103	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19
104	Untying the gordion knot of targeting MET in cancer. Cancer Treatment Reviews, 2018, 66, 95-103.	7.7	18
105	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	2.5	18
106	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. European Journal of Cancer, 2019, 120, 54-64.	2.8	18
107	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	5.5	15
108	Prospective Clinical Sequencing of Adult Glioma. Molecular Cancer Therapeutics, 2019, 18, 991-1000.	4.1	15

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109	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, 34.	8.2	13
110	Genotyping tumor clones from single-cell data. Nature Methods, 2016, 13, 555-556.	19.0	13
111	Hypervirulent group A Streptococcus emergence in an acaspular background is associated with marked remodeling of the bacterial cell surface. PLoS ONE, 2018, 13, e0207897.	2.5	13
112	Systematic analysis to identify transcriptome-wide dysregulation of Alzheimerâ€™s disease in genes and isoforms. Human Genetics, 2021, 140, 609-623.	3.8	13
113	Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. BMC Medical Genomics, 2019, 12, 22.	1.5	12
114	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, 2313.	12.8	12
115	A feasibility study of returning clinically actionable somatic genomic alterations identified in a research laboratory. Oncotarget, 2017, 8, 41806-41814.	1.8	12
116	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cellâ€free DNA by nextâ€generation sequencing. Cancer, 2018, 124, 1061-1069.	4.1	11
117	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299.	2.6	10
118	Ab initio spillover compensation in mass cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2020, 99, 899-909.	1.5	10
119	Extended live-cell barcoding approach for multiplexed mass cytometry. Scientific Reports, 2021, 11, 12388.	3.3	10
120	Genomic analysis of exceptional responder to regorafenib in treatment-refractory metastatic rectal cancer: a case report and review of the literature. Oncotarget, 2017, 8, 57882-57888.	1.8	10
121	Expanded Analysis of Secondary Germline Findings From Matched Tumor/Normal Sequencing Identifies Additional Clinically Significant Mutations. JCO Precision Oncology, 2019, 3, 1-11.	3.0	9
122	Capturing large genomic contexts for accurately predicting enhancer-promoter interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	9
123	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	19.0	7
124	On the detection of functionally coherent groups of protein domains with an extension to protein annotation. BMC Bioinformatics, 2007, 8, 390.	2.6	6
125	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
126	Predicting the change of exon splicing caused by genetic variant using support vector regression. Human Mutation, 2019, 40, 1235-1242.	2.5	6

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127	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. Frontiers in Immunology, 2021, 12, 659625.	4.8	6
128	Molecular Correlates of Venous Thromboembolism (VTE) in Ovarian Cancer. Cancers, 2022, 14, 1496.	3.7	6
129	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	4.1	5
130	Whole Genome Sequencing in Cancer Clinics. EBioMedicine, 2015, 2, 15-16.	6.1	4
131	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. BMC Genomics, 2017, 18, 703.	2.8	4
132	Identifying Common Genes, Cell Types and Brain Regions Between Diseases of the Nervous System. Frontiers in Genetics, 2019, 10, 1202.	2.3	4
133	Active Disclosure of Secondary Germline Findings to Deceased Research Participantsâ€™ Personal Representatives: Process and Outcomes. JCO Precision Oncology, 2017, 1, 1-5.	3.0	3
134	Structural Variant Breakpoint Detection with novoBreak. Methods in Molecular Biology, 2018, 1833, 129-141.	0.9	3
135	Stratified Test Alleviates Batch Effects in Single-Cell Data. Lecture Notes in Computer Science, 2020, , 167-177.	1.3	3
136	Metachronous Medulloblastoma in a Child With Successfully Treated Neuroblastoma: Case Report and Novel Findings of DNA Sequencing. Journal of the National Comprehensive Cancer Network: JNCCN, 2018, 16, 683-691.	4.9	2
137	Comments on the model parameters in â€œSiFit: inferring tumor trees from single-cell sequencing data under finite-sites modelsâ€• Genome Biology, 2019, 20, 95.	8.8	1
138	Sparse Subspace Clustering for Stream Data. IEEE Access, 2021, 9, 57271-57279.	4.2	1
139	Integrated genotyping of structural variation. , 2013, , .		0
140	Identification of Novel Single-Nucleotide Variants With Potential of Mediating Malfunction of MicroRNA in Congenital Heart Disease. Frontiers in Cardiovascular Medicine, 2021, 8, 739598.	2.4	0
141	Cardiac ISL1-Interacting Protein, a Cardioprotective Factor, Inhibits the Transition From Cardiac Hypertrophy to Heart Failure. Frontiers in Cardiovascular Medicine, 2022, 9, 857049.	2.4	0