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	Capturing large genomic contexts for accurately predicting enhancer-promoter interactions. Briefings in Bioinformatics, 2022, 23, .	6.5	9
2	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
3	Molecular Correlates of Venous Thromboembolism (VTE) in Ovarian Cancer. Cancers, 2022, 14, 1496.	3.7	6
4	Systematic analysis to identify transcriptome-wide dysregulation of Alzheimerâ€™s disease in genes and isoforms. Human Genetics, 2021, 140, 609-623.	3.8	13
5	Targeting a cytokine checkpoint enhances the fitness of armored cord blood CAR-NK cells. Blood, 2021, 137, 624-636.	1.4	147
6	Sparse Subspace Clustering for Stream Data. IEEE Access, 2021, 9, 57271-57279.	4.2	1
7	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
8	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, 70.	8.8	19
9	An expanded universe of cancer targets. Cell, 2021, 184, 1142-1155.	28.9	135
10	Single-cell RNA-seq analysis reveals compartment-specific heterogeneity and plasticity of microglia. IScience, 2021, 24, 102186.	4.1	31
11	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, 2313.	12.8	12
12	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. Frontiers in Immunology, 2021, 12, 659625.	4.8	6
13	Extended live-cell barcoding approach for multiplexed mass cytometry. Scientific Reports, 2021, 11, 12388.	3.3	10
14	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
15	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	17.5	306
16	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	30.7	134
17	Dynamic Spatio-Temporal Graph-Based CNNs for Traffic Flow Prediction. IEEE Access, 2020, 8, 185136-185145.	4.2	27
18	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	12.8	27

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19	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, 4330.	12.8	60
20	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
21	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	17.5	233
22	Relative Abundance of SARS-CoV-2 Entry Genes in the Enterocytes of the Lower Gastrointestinal Tract. Genes, 2020, 11, 645.	2.4	57
23	Latent periodic process inference from single-cell RNA-seq data. Nature Communications, 2020, 11, 1441.	12.8	23
24	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
25	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
26	Stratified Test Alleviates Batch Effects in Single-Cell Data. Lecture Notes in Computer Science, 2020, , 167-177.	1.3	3
27	Assessing predictions of the impact of variants on splicing in CAGI5. Human Mutation, 2019, 40, 1215-1224.	2.5	18
28	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. Modern Pathology, 2019, 32, 1698-1707.	5.5	35
29	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
30	Elevated Endogenous SDHA Drives Pathological Metabolism in Highly Metastatic Uveal Melanoma. , 2019, 60, 4187.		30
31	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	3.2	30
32	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. European Journal of Cancer, 2019, 120, 54-64.	2.8	18
33	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
34	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
35	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. Cancer Cell, 2019, 35, 851-867.e7.	16.8	156
36	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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37	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
38	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
39	Integrated transcriptomicâ€“genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	19.0	7
40	Prospective Clinical Sequencing of Adult Glioma. Molecular Cancer Therapeutics, 2019, 18, 991-1000.	4.1	15
41	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	28.9	73
42	A novel immature natural killer cell subpopulation predicts relapse after cord blood transplantation. Blood Advances, 2019, 3, 4117-4130.	5.2	23
43	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
44	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
45	Identifying Common Genes, Cell Types and Brain Regions Between Diseases of the Nervous System. Frontiers in Genetics, 2019, 10, 1202.	2.3	4
46	Single-nuclei RNA-seq on human retinal tissue provides improved transcriptome profiling. Nature Communications, 2019, 10, 5743.	12.8	101
47	Use of Targeted Next-Generation Sequencing to Identify Activating Hot Spot Mutations in Cherry Angiomas. JAMA Dermatology, 2019, 155, 211.	4.1	22
48	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
49	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	28.9	1,670
50	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	28.9	620
51	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
52	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	14.3	3,706
53	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
54	Untying the gordion knot of targeting MET in cancer. Cancer Treatment Reviews, 2018, 66, 95-103.	7.7	18

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55	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	16.8	213
56	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
57	Computational approaches for inferring tumor evolution from single-cell genomic data. Current Opinion in Systems Biology, 2018, 7, 16-25.	2.6	36
58	Survival Outcomes by TP53 Mutation Status in Metastatic Breast Cancer. JCO Precision Oncology, 2018, 2018, 1-15.	3.0	43
59	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, 188.	8.8	42
60	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
61	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
62	Structural Variant Breakpoint Detection with novoBreak. Methods in Molecular Biology, 2018, 1833, 129-141.	0.9	3
63	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. Nature Communications, 2018, 9, 2732.	12.8	33
64	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
65	Cancer driver mutation prediction through Bayesian integration of multi-omic data. PLoS ONE, 2018, 13, e0196939.	2.5	23
66	Targeted next generation sequencing of well-differentiated/dedifferentiated liposarcoma reveals novel gene amplifications and mutations. Oncotarget, 2018, 9, 19891-19899.	1.8	28
67	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	5.5	32
68	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
69	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	5.5	15
70	Ph-like acute lymphoblastic leukemia: a high-risk subtype in adults. Blood, 2017, 129, 572-581.	1.4	285
71	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
72	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

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73	Comprehensive Genomic Profiling of Metastatic Squamous Cell Carcinoma of the Anal Canal. Molecular Cancer Research, 2017, 15, 1542-1550.	3.4	59
74	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
75	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
76	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. Genome Biology, 2017, 18, 178.	8.8	152
77	The International Conference on Intelligent Biology and Medicine (ICIBM) 2016: summary and innovation in genomics. BMC Genomics, 2017, 18, 703.	2.8	4
78	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	4.1	5
79	A feasibility study of returning clinically actionable somatic genomic alterations identified in a research laboratory. Oncotarget, 2017, 8, 41806-41814.	1.8	12
80	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
81	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
82	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, 394.	2.8	28
83	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294.	3.3	60
84	Monovar: single-nucleotide variant detection in single cells. Nature Methods, 2016, 13, 505-507.	19.0	150
85	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
86	Functional annotation of rare gene aberration drivers of pancreatic cancer. Nature Communications, 2016, 7, 10500.	12.8	58
87	Genotyping tumor clones from single-cell data. Nature Methods, 2016, 13, 555-556.	19.0	13
88	The degree of intratumor mutational heterogeneity varies by primary tumor sub-site. Oncotarget, 2016, 7, 27185-27198.	1.8	37
89	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, 34.	8.2	13
90	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	3.2	83

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91	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, 7256.	12.8	77
92	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. Cancer Research, 2015, 75, 5341-5354.	0.9	130
93	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
94	Whole Genome Sequencing in Cancer Clinics. EBioMedicine, 2015, 2, 15-16.	6.1	4
95	RET Fusion as a Novel Driver of Medullary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 788-793.	3.6	65
96	Clinical Actionability Enhanced through Deep Targeted Sequencing of Solid Tumors. Clinical Chemistry, 2015, 61, 544-553.	3.2	85
97	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, 6.	8.2	6
98	A Decision Support Framework for Genomically Informed Investigational Cancer Therapy. Journal of the National Cancer Institute, 2015, 107, .	6.3	168
99	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
100	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	19.0	67
101	Characterization of twenty-five ovarian tumour cell lines that phenocopy primary tumours. Nature Communications, 2015, 6, 7419.	12.8	149
102	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
103	Functional consequence of theMET-T1010I polymorphism in breast cancer. Oncotarget, 2015, 6, 2604-2614.	1.8	34
104	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, 299.	2.6	10
105	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	5.5	81
106	BreakDancer: Identification of Genomic Structural Variation from Pairedâ€End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, 15.6.1-11.	25.8	135
107	Bias from removing read duplication in ultra-deep sequencing experiments. Bioinformatics, 2014, 30, 1073-1080.	4.1	39
108	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	27.8	911

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109	Catalytic mTOR inhibitors can overcome intrinsic and acquired resistance to allosteric mTOR inhibitors. Oncotarget, 2014, 5, 8544-8557.	1.8	56
110	BreakTrans: uncovering the genomic architecture of gene fusions. Genome Biology, 2013, 14, R87.	9.6	25
111	Integrated genotyping of structural variation. , 2013, , .		0
112	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
113	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
114	CanDrA: Cancer-Specific Driver Missense Mutation Annotation with Optimized Features. PLoS ONE, 2013, 8, e77945.	2.5	104
115	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	4.1	566
116	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924.	4.1	54
117	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
118	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	27.8	922
119	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	28.9	1,038
120	Massively Parallel Sequencing Approaches for Characterization of Structural Variation. Methods in Molecular Biology, 2012, 838, 369-384.	0.9	49
121	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	27.0	688
122	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	27.8	1,795
123	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	28.9	1,365
124	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	19.0	451
125	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	27.8	991
126	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	7.4	233

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127	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
128	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
129	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	27.8	1,077
130	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
131	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	4.1	1,193
132	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	19.0	1,322
133	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	27.0	2,009
134	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	27.8	2,694
135	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	27.8	1,275
136	PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data. Genome Research, 2007, 17, 659-666.	5.5	76
137	On the detection of functionally coherent groups of protein domains with an extension to protein annotation. BMC Bioinformatics, 2007, 8, 390.	2.6	6
138	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
139	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
140	Simultaneous recognition of words and prosody in the Boston University Radio Speech Corpus. Speech Communication, 2005, 46, 418-439.	2.8	36
141	Landmark-Based Speech Recognition: Report of the 2004 Johns Hopkins Summer Workshop. , 2005, 1, 1213-1216.		52