Ken Chen

List of Articles by Year
in descending order

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120 peer-reviewed articles	33,865 peer-reviewed citations	25260 57 peer-reviewed h-index	12996 7.83 score
137 documents	38786 doc citations	23147 63 h-index	73093 citing authors

#	Article	IF	Citations
1	Self-supervised learning on millions of primary RNA sequences from 72 vertebrates improves sequence-based RNA splicing prediction. Briefings in Bioinformatics, 2024, 25, .	4.0	68
2	Prioritizing genomic variants pathogenicity via DNA, RNA, and protein-level features based on extreme gradient boosting. Human Genetics, 2024, 144, 253-263.	1.8	2
3	Deciphering cell types by integrating scATAC-seq data with genome sequences. Nature Computational Science, 2024, 4, 285-298.	8.9	29
4	VCAT: an integrated variant function annotation tools. Human Genetics, 2024, 143, 1311-1322.	1.8	0
5	Enhanced soluble expression and characterization of human N-acetylglucosaminyltransferase IVa in Escherichia coli. Enzyme and Microbial Technology, 2024, 181, 110524.	2.7	1
6	Fast and accurate protein intrinsic disorder prediction by using a pretrained language model. Briefings in Bioinformatics, 2023, 24, .	4.0	20
7	Capturing large genomic contexts for accurately predicting enhancer-promoter interactions. Briefings in Bioinformatics, 2022, 23, .	4.0	32
8	Cardiac ISL1-Interacting Protein, a Cardioprotective Factor, Inhibits the Transition From Cardiac Hypertrophy to Heart Failure. Frontiers in Cardiovascular Medicine, 2022, 9, .	1.6	4
9	Molecular Correlates of Venous Thromboembolism (VTE) in Ovarian Cancer. Cancers, 2022, 14, 1496.	2.7	24
10	Profiling human pathogenic repeat expansion regions by synergistic and multi-level impacts on molecular connections. Human Genetics, 2022, 142, 245-274.	1.8	1
11	Ab initio spillover compensation in mass cytometry data. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2021, 99, 899-909.	1.6	19
12	Targeting a cytokine checkpoint enhances the fitness of armored cord blood CAR-NK cells. Blood, 2021, 137, 624-636.	3.6	280
13	Sparse Subspace Clustering for Stream Data. IEEE Access, 2021, 9, 57271-57279.	2.4	4
14	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, .	3.3	51
15	MEDALT: single-cell copy number lineage tracing enabling gene discovery. Genome Biology, 2021, 22, .	4.8	39
16	Single-cell RNA-seq analysis reveals compartment-specific heterogeneity and plasticity of microglia. IScience, 2021, 24, 102186.	2.4	60
17	Spatially interacting phosphorylation sites and mutations in cancer. Nature Communications, 2021, 12, .	10.8	20
18	Response to Hypomethylating Agents in Myelodysplastic Syndrome Is Associated With Emergence of Novel TCR Clonotypes. Frontiers in Immunology, 2021, 12, .	3.3	17

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19	Extended live-cell barcoding approach for multiplexed mass cytometry. Scientific Reports, 2021, 11, .	2.7	21
20	Identification of Novel Single-Nucleotide Variants With Potential of Mediating Malfunction of MicroRNA in Congenital Heart Disease. Frontiers in Cardiovascular Medicine, 2021, 8, .	1.6	5
21	Delineating copy number and clonal substructure in human tumors from single-cell transcriptomes. Nature Biotechnology, 2021, 39, 599-608.	19.7	848
22	Single-cell dissection of intratumoral heterogeneity and lineage diversity in metastatic gastric adenocarcinoma. Nature Medicine, 2021, 27, 141-151.	22.6	249
23	Dynamic Spatio-Temporal Graph-Based CNNs for Traffic Flow Prediction. IEEE Access, 2020, 8, 185136-185145.	2.4	77
24	Sex differences in oncogenic mutational processes. Nature Communications, 2020, 11, .	10.8	96
25	A robust benchmark for detection of germline large deletions and insertions. Nature Biotechnology, 2020, 38, 1347-1355.	19.7	410
26	Latent periodic process inference from single-cell RNA-seq data. Nature Communications, 2020, 11, .	10.8	56
27	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	14.1	464
28	Systematic analysis to identify transcriptome-wide dysregulation of Alzheimer's disease in genes and isoforms. Human Genetics, 2020, 140, 609-623.	1.8	20
29	Hybrid oncocytic/chromophobe renal tumors are molecularly distinct from oncocytoma and chromophobe renal cell carcinoma. Modern Pathology, 2019, 32, 1698-1707.	3.8	50
30	SiCloneFit: Bayesian inference of population structure, genotype, and phylogeny of tumor clones from single-cell genome sequencing data. Genome Research, 2019, 29, 1847-1859.	3.3	123
31	Elevated Endogenous SDHA Drives Pathological Metabolism in Highly Metastatic Uveal Melanoma. , 2019, 60, 4187.		51
32	SCMarker: Ab initio marker selection for single cell transcriptome profiling. PLoS Computational Biology, 2019, 15, e1007445.	1.9	40
33	Dynamic clonal remodelling in breast cancer metastases is associated with subtype conversion. European Journal of Cancer, 2019, 120, 54-64.	2.8	20
34	Sequential Therapy with PARP and WEE1 Inhibitors Minimizes Toxicity while Maintaining Efficacy. Cancer Cell, 2019, 35, 851-867.e7.	28.4	215
35	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, .	10.8	849
36	Comparison of different functional prediction scores using a gene-based permutation model for identifying cancer driver genes. BMC Medical Genomics, 2019, 12, .	1.3	12

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37	Integrated transcriptomic–genomic tool Texomer profiles cancer tissues. Nature Methods, 2019, 16, 401-404.	13.1	12
38	Prospective Clinical Sequencing of Adult Glioma. Molecular Cancer Therapeutics, 2019, 18, 991-1000.	1.2	18
39	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	23.4	91
40	A novel immature natural killer cell subpopulation predicts relapse after cord blood transplantation. Blood Advances, 2019, 3, 4117-4130.	3.7	34
41	Identifying Common Genes, Cell Types and Brain Regions Between Diseases of the Nervous System. Frontiers in Genetics, 2019, 10, .	1.6	6
42	Single-nuclei RNA-seq on human retinal tissue provides improved transcriptome profiling. Nature Communications, 2019, 10, .	10.8	129
43	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.	4.5	56
44	Comprehensive Characterization of Cancer Driver Genes and Mutations. Cell, 2018, 173, 371-385.e18.	23.4	2,168
45	Pathogenic Germline Variants in 10,389 Adult Cancers. Cell, 2018, 173, 355-370.e14.	23.4	831
46	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	4.4	596
47	The Immune Landscape of Cancer. Immunity, 2018, 48, 812-830.e14.	16.6	5,243
48	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	4.4	235
49	Untying the gordion knot of targeting MET in cancer. Cancer Treatment Reviews, 2018, 66, 95-103.	6.0	22
50	Systematic Functional Annotation of Somatic Mutations in Cancer. Cancer Cell, 2018, 33, 450-462.e10.	28.4	316
51	Variants with a low allele frequency detected in genomic DNA affect the accuracy of mutation detection in cell-free DNA by next-generation sequencing. Cancer, 2018, 124, 1061-1069.	2.7	14
52	Computational approaches for inferring tumor evolution from single-cell genomic data. Current Opinion in Systems Biology, 2018, 7, 16-25.	1.2	42
53	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, .	4.8	50
54	Hypervirulent group A Streptococcus emergence in an acaspular background is associated with marked remodeling of the bacterial cell surface. PLoS ONE, 2018, 13, e0207897.	1.5	13

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55	Genetic biomarkers of sensitivity and resistance to venetoclax monotherapy in patients with relapsed acute myeloid leukemia. American Journal of Hematology, 2018, 93, .	5.2	139
56	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. Nature Communications, 2018, 9, .	10.8	45
57	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.	2.6	3
58	Cancer driver mutation prediction through Bayesian integration of multi-omic data. PLoS ONE, 2018, 13, e0196939.	1.5	26
59	HySA: a Hybrid Structural variant Assembly approach using next-generation and single-molecule sequencing technologies. Genome Research, 2017, 27, 793-800.	3.3	33
60	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	23.4	113
61	GenomeVIP: a cloud platform for genomic variant discovery and interpretation. Genome Research, 2017, 27, 1450-1459.	3.3	19
62	Ph-like acute lymphoblastic leukemia: a high-risk subtype in adults. Blood, 2017, 129, 572-581.	3.6	364
63	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.	4.5	67
64	Sarcomatoid Renal Cell Carcinoma Has a Distinct Molecular Pathogenesis, Driver Mutation Profile, and Transcriptional Landscape. Clinical Cancer Research, 2017, 23, 6686-6696.	4.5	92
65	Comprehensive Genomic Profiling of Metastatic Squamous Cell Carcinoma of the Anal Canal. Molecular Cancer Research, 2017, 15, 1542-1550.	2.0	74
66	Active Disclosure of Secondary Germline Findings to Deceased Research Participants' Personal Representatives: Process and Outcomes. JCO Precision Oncology, 2017, , 1-5.	1.1	4
67	SiFit: inferring tumor trees from single-cell sequencing data under finite-sites models. Genome Biology, 2017, 18, .	4.8	185
68	BreakPoint Surveyor: a pipeline for structural variant visualization. Bioinformatics, 2017, 33, 3121-3122.	3.2	5
69	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, .	2.1	33
70	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, .	2.7	67
71	Monovar: single-nucleotide variant detection in single cells. Nature Methods, 2016, 13, 505-507.	13.1	178
72	Novel algorithmic approach predicts tumor mutation load and correlates with immunotherapy clinical outcomes using a defined gene mutation set. BMC Medicine, 2016, 14, .	4.4	111

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73	Functional annotation of rare gene aberration drivers of pancreatic cancer. Nature Communications, 2016, 7, .	10.8	84
74	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2016, 14, 65-67.	13.1	108
75	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, .	5.9	13
76	Genome Modeling System: A Knowledge Management Platform for Genomics. PLoS Computational Biology, 2015, 11, e1004274.	1.9	87
77	Analysis of deletion breakpoints from 1,092 humans reveals details of mutation mechanisms. Nature Communications, 2015, 6, .	10.8	94
78	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. Cancer Research, 2015, 75, 5341-5354.	2.6	160
79	Gene mutations in primary tumors and corresponding patient-derived xenografts derived from non-small cell lung cancer. Cancer Letters, 2015, 357, 179-185.	6.5	90
80	RET Fusion as a Novel Driver of Medullary Thyroid Carcinoma. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 788-793.	3.1	79
81	Clinical Actionability Enhanced through Deep Targeted Sequencing of Solid Tumors. Clinical Chemistry, 2015, 61, 544-553.	0.6	91
82	Ploidy-Seq: inferring mutational chronology by sequencing polyploid tumor subpopulations. Genome Medicine, 2015, 7, .	5.9	6
83	A Decision Support Framework for Genomically Informed Investigational Cancer Therapy. Journal of the National Cancer Institute, 2015, 107, .	3.2	189
84	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	30.7	2,453
85	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	13.1	98
86	Characterization of twenty-five ovarian tumour cell lines that phenocopy primary tumours. Nature Communications, 2015, 6, .	10.8	178
87	Ability to Generate Patient-Derived Breast Cancer Xenografts Is Enhanced in Chemoresistant Disease and Predicts Poor Patient Outcomes. PLoS ONE, 2015, 10, e0136851.	1.5	67
88	Towards accurate characterization of clonal heterogeneity based on structural variation. BMC Bioinformatics, 2014, 15, .	2.5	10
89	TIGRA: A targeted iterative graph routing assembler for breakpoint assembly. Genome Research, 2014, 24, 310-317.	3.3	90
90	BreakDancer: Identification of Genomic Structural Variation from Paired-End Read Mapping. Current Protocols in Bioinformatics, 2014, 45, .	3.3	156

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91	Bias from removing read duplication in ultra-deep sequencing experiments. Bioinformatics, 2014, 30, 1073-1080.	3.2	46
92	Clonal evolution in breast cancer revealed by single nucleus genome sequencing. Nature, 2014, 512, 155-160.	30.7	1,013
93	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	26.4	4,888
94	A survey of intragenic breakpoints in glioblastoma identifies a distinct subset associated with poor survival. Genes and Development, 2013, 27, 1462-1472.	2.8	83
95	CanDrA: Cancer-Specific Driver Missense Mutation Annotation with Optimized Features. PLoS ONE, 2013, 8, e77945.	1.5	117
96	SomaticSniper: identification of somatic point mutations in whole genome sequencing data. Bioinformatics, 2012, 28, 311-317.	3.2	657
97	BreakFusion: targeted assembly-based identification of gene fusions in whole transcriptome paired-end sequencing data. Bioinformatics, 2012, 28, 1923-1924.	3.2	57
98	Background Mutations in Parental Cells Account for Most of the Genetic Heterogeneity of Induced Pluripotent Stem Cells. Cell Stem Cell, 2012, 10, 570-582.	11.6	207
99	Whole-genome analysis informs breast cancer response to aromatase inhibition. Nature, 2012, 486, 353-360.	30.7	994
100	Genomic Landscape of Non-Small Cell Lung Cancer in Smokers and Never-Smokers. Cell, 2012, 150, 1121-1134.	23.4	1,117
101	Clonal Architecture of Secondary Acute Myeloid Leukemia. New England Journal of Medicine, 2012, 366, 1090-1098.	26.4	738
102	Clonal evolution in relapsed acute myeloid leukaemia revealed by whole-genome sequencing. Nature, 2012, 481, 506-510.	30.7	1,937
103	The Origin and Evolution of Mutations in Acute Myeloid Leukemia. Cell, 2012, 150, 264-278.	23.4	1,512
104	CREST maps somatic structural variation in cancer genomes with base-pair resolution. Nature Methods, 2011, 8, 652-654.	13.1	476
105	Mapping copy number variation by population-scale genome sequencing. Nature, 2011, 470, 59-65.	30.7	1,079
106	Use of Whole-Genome Sequencing to Diagnose a Cryptic Fusion Oncogene. JAMA - Journal of the American Medical Association, 2011, 305, 1577.	14.4	239
107	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.	14.4	150
108	Sequencing a mouse acute promyelocytic leukemia genome reveals genetic events relevant for disease progression. Journal of Clinical Investigation, 2011, 121, 1445-1455.	6.6	92

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109	Genome remodelling in a basal-like breast cancer metastasis and xenograft. Nature, 2010, 464, 999-1005.	30.7	1,116
110	CMDS: a population-based method for identifying recurrent DNA copy number aberrations in cancer from high-resolution data. Bioinformatics, 2010, 26, 464-469.	3.2	60
111	VarScan: variant detection in massively parallel sequencing of individual and pooled samples. Bioinformatics, 2009, 25, 2283-2285.	3.2	1,376
112	BreakDancer: an algorithm for high-resolution mapping of genomic structural variation. Nature Methods, 2009, 6, 677-681.	13.1	1,466
113	Recurring Mutations Found by Sequencing an Acute Myeloid Leukemia Genome. New England Journal of Medicine, 2009, 361, 1058-1066.	26.4	2,143
114	Somatic mutations affect key pathways in lung adenocarcinoma. Nature, 2008, 455, 1069-1075.	30.7	2,804
115	DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome. Nature, 2008, 456, 66-72.	30.7	1,343
116	PolyScan: An automatic indel and SNP detection approach to the analysis of human resequencing data. Genome Research, 2007, 17, 659-666.	3.3	77
117	On the detection of functionally coherent groups of protein domains with an extension to protein annotation. BMC Bioinformatics, 2007, 8, .	2.5	6
118	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.	2.2	73
119	Computational Analysis and Prediction of the Binding Motif and Protein Interacting Partners of the Abl SH3 Domain. PLoS Computational Biology, 2006, 2, e1.	1.9	158
120	Simultaneous recognition of words and prosody in the Boston University Radio Speech Corpus. Speech Communication, 2005, 46, 418-439.	1.7	36