Zechen Chong

List of Publications by Year
in descending order

26 papers	4,237 citations	471509 17 h-index	610901 24 g-index
30 all docs	30 docs citations	30 times ranked	9781 citing authors

#	Article	IF	Citations
1	B-assembler: a circular bacterial genome assembler. BMC Genomics, 2022, 23, 361.	2.8	3
2	ClipSV: improving structural variation detection by read extension, spliced alignment and tree-based decision rules. NAR Genomics and Bioinformatics, 2021, 3, lqab003.	3.2	0
3	Ozone and Particulate Matter Exposure and Alzheimerâ€™s Disease: A Review of Human and Animal Studies. Advances in Alzheimer's Disease, 2021, , .	0.2	0
4	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
5	RNF2 ablation reprograms the tumor-immune microenvironment and stimulates durable NK and CD4+ T-cell-dependent antitumor immunity. Nature Cancer, 2021, 2, 1018-1038.	13.2	11
6	Accurate long-read de novo assembly evaluation with Inspector. Genome Biology, 2021, 22, 312.	8.8	46
7	MRLR: unraveling high-resolution meiotic recombination by linked reads. Bioinformatics, 2020, 36, 10-16.	4.1	4
8	Ozone and Particulate Matter Exposure and Alzheimerâ€™s Disease: A Review of Human and Animal Studies. Journal of Alzheimer's Disease, 2020, 76, 807-824.	2.6	3
9	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
10	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
11	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	28.9	73
12	Marker chromosome genomic structure and temporal origin implicate a chromoanasynthesis event in a family with pleiotropic psychiatric phenotypes. Human Mutation, 2018, 39, 939-946.	2.5	26
13	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, 188.	8.8	42
14	Structural Variant Breakpoint Detection with novoBreak. Methods in Molecular Biology, 2018, 1833, 129-141.	0.9	3
15	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. Nature Communications, 2018, 9, 2732.	12.8	33
16	Regenerative Potential of Neonatal Porcine Hearts. Circulation, 2018, 138, 2809-2816.	1.6	179
17	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
18	A murine preclinical syngeneic transplantation model for breast cancer precision medicine. Science Advances, 2017, 3, e1600957.	10.3	10

#	Article	IF	Citations
19	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
20	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, 394.	2.8	28
21	Single-cell isolation by a modular single-cell pipette for RNA-sequencing. Lab on A Chip, 2016, 16, 4742-4748.	6.0	38
22	Functional annotation of rare gene aberration drivers of pancreatic cancer. Nature Communications, 2016, 7, 10500.	12.8	58
23	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, 34.	8.2	13
24	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. Cancer Research, 2015, 75, 5341-5354.	0.9	130
25	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
26	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	19.0	67