Zechen Chong

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/358961/publications.pdf

Version: 2024-02-01

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	An integrated map of structural variation in 2,504 human genomes. Nature, 2015, 526, 75-81.	27.8	1,994
2	Multi-platform discovery of haplotype-resolved structural variation in human genomes. Nature Communications, 2019, 10, 1784.	12.8	636
3	Haplotype-resolved diverse human genomes and integrated analysis of structural variation. Science, 2021, 372, .	12.6	358
4	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	21.4	275
5	Regenerative Potential of Neonatal Porcine Hearts. Circulation, 2018, 138, 2809-2816.	1.6	179
6	Identification of Variant-Specific Functions of PIK3CA by Rapid Phenotyping of Rare Mutations. Cancer Research, 2015, 75, 5341-5354.	0.9	130
7	novoBreak: local assembly for breakpoint detection in cancer genomes. Nature Methods, 2017, 14, 65-67.	19.0	93
8	Megabase Length Hypermutation Accompanies Human Structural Variation at 17p11.2. Cell, 2019, 176, 1310-1324.e10.	28.9	73
9	TransVar: a multilevel variant annotator for precision genomics. Nature Methods, 2015, 12, 1002-1003.	19.0	67
10	An Organismal CNV Mutator Phenotype Restricted to Early Human Development. Cell, 2017, 168, 830-842.e7.	28.9	66
11	Functional annotation of rare gene aberration drivers of pancreatic cancer. Nature Communications, 2016, 7, 10500.	12.8	58
12	Accurate long-read de novo assembly evaluation with Inspector. Genome Biology, 2021, 22, 312.	8.8	46
13	Combining accurate tumor genome simulation with crowdsourcing to benchmark somatic structural variant detection. Genome Biology, 2018, 19, 188.	8.8	42
14	Single-cell isolation by a modular single-cell pipette for RNA-sequencing. Lab on A Chip, 2016, 16, 4742-4748.	6.0	38
15	In vivo screening identifies GATAD2B as a metastasis driver in KRAS-driven lung cancer. Nature Communications, 2018, 9, 2732.	12.8	33
16	Hotspot mutations delineating diverse mutational signatures and biological utilities across cancer types. BMC Genomics, 2016, 17, 394.	2.8	28
17	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
18	ClinSeK: a targeted variant characterization framework for clinical sequencing. Genome Medicine, 2015, 7, 34.	8.2	13

#	Article	IF	Citations
19	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
20	A murine preclinical syngeneic transplantation model for breast cancer precision medicine. Science Advances, 2017, 3, e1600957.	10.3	10
21	MRLR: unraveling high-resolution meiotic recombination by linked reads. Bioinformatics, 2020, 36, 10-16.	4.1	4
22	Structural Variant Breakpoint Detection with novoBreak. Methods in Molecular Biology, 2018, 1833, 129-141.	0.9	3
23	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
24	B-assembler: a circular bacterial genome assembler. BMC Genomics, 2022, 23, 361.	2.8	3
25	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
26	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