Cheng-Zhong Zhang

List of Publications by Year
in descending order

30	7,953	304743 22	434195 31
papers	citations	h-index	g-index

38	38	38	15229
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Pan-cancer patterns of somatic copy number alteration. Nature Genetics, 2013, 45, 1134-1140.	21.4	1,616
2	Chromothripsis from DNA damage inÂmicronuclei. Nature, 2015, 522, 179-184.	27.8	924
3	Whole-exome sequencing of circulating tumor cells provides a window into metastatic prostate cancer. Nature Biotechnology, 2014, 32, 479-484.	17.5	495
4	Genomic Copy Number Dictates a Gene-Independent Cell Response to CRISPR/Cas9 Targeting. Cancer Discovery, 2016, 6, 914-929.	9.4	485
5	Mechanoenzymatic Cleavage of the Ultralarge Vascular Protein von Willebrand Factor. Science, 2009, 324, 1330-1334.	12.6	484
6	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	21.4	431
7	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	27.8	424
8	Breaching Self-Tolerance to Alu Duplex RNA Underlies MDA5-Mediated Inflammation. Cell, 2018, 172, 797-810.e13.	28.9	306
9	Chromothripsis as an on-target consequence of CRISPRâ€“Cas9 genome editing. Nature Genetics, 2021, 53, 895-905.	21.4	305
10	Mechanisms generating cancer genome complexity from a single cell division error. Science, 2020, 368, .	12.6	298
11	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	5.5	288
12	Structural Alterations Driving Castration-Resistant Prostate Cancer Revealed by Linked-Read Genome Sequencing. Cell, 2018, 174, 433-447.e19.	28.9	258
13	A mechanically stabilized receptorâ€“ligand flex-bond important in the vasculature. Nature, 2010, 466, 992-995.	27.8	251
14	EGFR Variant Heterogeneity in Glioblastoma Resolved through Single-Nucleus Sequencing. Cancer Discovery, 2014, 4, 956-971.	9.4	251
15	Chromothripsis and beyond: rapid genome evolution from complex chromosomal rearrangements. Genes and Development, 2013, 27, 2513-2530.	5.9	220
16	Structural specializations of A2, a force-sensing domain in the ultralarge vascular protein von Willebrand factor. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 9226-9231.	7.1	167
17	Chromothripsis: A New Mechanism for Rapid Karyotype Evolution. Annual Review of Genetics, 2015, 49, 183-211.	7.6	155
18	Genetic interrogation of circulating multiple myeloma cells at single-cell resolution. Science Translational Medicine, 2016, 8, 363ra147.	12.4	126

#	Article	IF	Citations
19	Exome sequencing of lymphomas from three dog breeds reveals somatic mutation patterns reflecting genetic background. Genome Research, 2015, 25, 1634-1645.	5.5	96
20	Calibrating genomic and allelic coverage bias in single-cell sequencing. Nature Communications, 2015, 6, 6822.	12.8	74
21	Whole chromosome loss and genomic instability in mouse embryos after CRISPR-Cas9 genome editing. Nature Communications, 2021, 12, 5855.	12.8	72
22	Integrated single-cell genetic and transcriptional analysis suggests novel drivers of chronic lymphocytic leukemia. Genome Research, 2017, 27, 1300-1311.	5.5	67
23	Polymer-Tethered Ligand-Receptor Interactions between Surfaces II. Langmuir, 2007, 23, 13024-13039.	3.5	18
24	Determination of complete chromosomal haplotypes by bulk DNA sequencing. Genome Biology, 2021, 22, 139.	8.8	16
25	Polymer-tethered ligand-receptor interactions between surfaces. Journal of Polymer Science, Part B: Polymer Physics, 2006, 44, 2621-2637.	2.1	12
26	From Mutational Mechanisms in Single Cells to Mutational Patterns in Cancer Genomes. Cold Spring Harbor Symposia on Quantitative Biology, 2015, 80, 117-137.	1.1	11
27	Cancer Genomic Rearrangements and Copy Number Alterations from Errors in Cell Division. Annual Review of Cancer Biology, 2022, 6, 245-268.	4.5	10
28	Using whole genome scores to compare three clinical phenotyping methods in complex diseases. Scientific Reports, 2018, 8, 11360.	3.3	9
29	Decoding complex patterns of oncogene amplification. Nature Genetics, 2021, 53, 1626-1627.	21.4	2
30	No pains, no gains: how chromosome fragmentation promotes gene amplification. Molecular Cell, 2021, 81, 901-904.	9.7	1