He Zhang

List of Publications by Year
in descending order

25 papers	5,297 citations	361413 20 h-index	610901 24 g-index
28 all docs	28 docs citations	28 times ranked	15758 citing authors

#	Article	IF	Citations
1	Abstract P5-17-09: A genome-wide CRISPR screen identifies PRMT5 as a novel therapeutic target in ER+/RB1-deficient breast cancer. Cancer Research, 2022, 82, P5-17-09-P5-17-09.	0.9	0
2	RBM33 directs the nuclear export of transcripts containing GC-rich elements. Genes and Development, 2022, 36, 550-565.	5.9	12
3	Serial genomic analysis of endometrium supports the existence of histologically indistinct endometrial cancer precursors. Journal of Pathology, 2021, 254, 20-30.	4.5	9
4	Discovery of rare variants associated with blood pressure regulation through meta-analysis of 1.3 million individuals. Nature Genetics, 2020, 52, 1314-1332.	21.4	91
5	A ubiquitin ligase mediates target-directed microRNA decay independently of tailing and trimming. Science, 2020, 370, .	12.6	135
6	Ribosome Recycling by ABCE1 Links Lysosomal Function and Iron Homeostasis to 3Ê¹ UTR-Directed Regulation and Nonsense-Mediated Decay. Cell Reports, 2020, 32, 107895.	6.4	36
7	Loss-of-function genomic variants highlight potential therapeutic targets for cardiovascular disease. Nature Communications, 2020, 11, 6417.	12.8	39
8	A PoleP286R mouse model of endometrial cancer recapitulates high mutational burden and immunotherapy response. JCI Insight, 2020, 5, .	5.0	25
9	miR-26 suppresses adipocyte progenitor differentiation and fat production by targeting Fbxl19. Genes and Development, 2019, 33, 1367-1380.	5.9	50
10	DEFOR: depth- and frequency-based somatic copy number alteration detector. Bioinformatics, 2019, 35, 3824-3825.	4.1	4
11	Suppression of Ribosomal Pausing by eIF5A Is Necessary to Maintain the Fidelity of Start Codon Selection. Cell Reports, 2019, 29, 3134-3146.e6.	6.4	44
12	Fbxw7 is a driver of uterine carcinosarcoma by promoting epithelial-mesenchymal transition. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 25880-25890.	7.1	47
13	PUMILIO hyperactivity drives premature aging of Norad-deficient mice. ELife, 2019, 8, .	6.0	65
14	Loss of Dis3l2 partially phenocopies Perlman syndrome in mice and results in up-regulation of Igf2 in nephron progenitor cells. Genes and Development, 2018, 32, 903-908.	5.9	34
15	Polymerase-mediated ultramutagenesis in mice produces diverse cancers with high mutational load. Journal of Clinical Investigation, 2018, 128, 4179-4191.	8.2	56
16	Systematic Evaluation of Pleiotropy Identifies 6 Further Loci Associated WithÂCoronary ArteryÂDisease. Journal of the American College of Cardiology, 2017, 69, 823-836.	2.8	214
17	Exome-wide association study of plasma lipids in >300,000 individuals. Nature Genetics, 2017, 49, 1758-1766.	21.4	470
18	Exome chip meta-analysis identifies novel loci and East Asianâ€"specific coding variants that contribute to lipid levels and coronary artery disease. Nature Genetics, 2017, 49, 1722-1730.	21.4	129

#	Article	IF	Citations
19	Targeting renal cell carcinoma with a HIF-2 antagonist. Nature, 2016, 539, 112-117.	27.8	521
20	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
21	Trans-ancestry meta-analyses identify rare and common variants associated with blood pressure and hypertension. Nature Genetics, 2016, 48, 1151-1161.	21.4	261
22	Exome-wide association analysis reveals novel coding sequence variants associated with lipid traits in Chinese. Nature Communications, 2015, 6, 10206.	12.8	86
23	Whole-Exome Sequencing Identifies Rare and Low-Frequency Coding Variants Associated with LDL Cholesterol. American Journal of Human Genetics, 2014, 94, 233-245.	6.2	193
24	Systematic evaluation of coding variation identifies a candidate causal variant in TM6SF2 influencing total cholesterol and myocardial infarction risk. Nature Genetics, 2014, 46, 345-351.	21.4	268
25	Effects of Long-Term Averaging of Quantitative Blood Pressure Traits on the Detection of Genetic Associations. American Journal of Human Genetics, 2014, 95, 49-65.	6.2	73