

# Zhisong He

## List of Publications by Year in descending order

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Version: 2024-02-01

36  
papers

2,299  
citations

361413

20  
h-index

361022

35  
g-index

52  
all docs

52  
docs citations

52  
times ranked

3275  
citing authors

#	ARTICLE	IF	CITATIONS
1	Organoid single-cell genomic atlas uncovers human-specific features of brain development. Nature, 2019, 574, 418-422.	27.8	496
2	Predicting Drug-Target Interaction Networks Based on Functional Groups and Biological Features. PLoS ONE, 2010, 5, e9603.	2.5	241
3	Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. ELife, 2016, 5, .	6.0	200
4	Analysis and Prediction of the Metabolic Stability of Proteins Based on Their Sequential Features, Subcellular Locations and Interaction Networks. PLoS ONE, 2010, 5, e10972.	2.5	123
5	Comprehensive transcriptome analysis of neocortical layers in humans, chimpanzees and macaques. Nature Neuroscience, 2017, 20, 886-895.	14.8	101
6	Lineage recording in human cerebral organoids. Nature Methods, 2022, 19, 90-99.	19.0	93
7	ALYREF mainly binds to the 5' and the 3' regions of the mRNA in vivo. Nucleic Acids Research, 2017, 45, 9640-9653.	14.5	87
8	Exosome cofactor hMTR4 competes with export adaptor ALYREF to ensure balanced nuclear RNA pools for degradation and export. EMBO Journal, 2017, 36, 2870-2886.	7.8	82
9	Charting human development using a multi-endodermal organ atlas and organoid models. Cell, 2021, 184, 3281-3298.e22.	28.9	82
10	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. PLoS ONE, 2010, 5, e11900.	2.5	70
11	Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. Molecular Psychiatry, 2020, 25, 2952-2969.	7.9	66
12	Resolving organoid brain region identities by mapping single-cell genomic data to reference atlases. Cell Stem Cell, 2021, 28, 1148-1159.e8.	11.1	63
13	Conserved expression of lincRNA during human and macaque prefrontal cortex development and maturation. Rna, 2014, 20, 1103-1111.	3.5	59
14	NGN2 induces diverse neuron types from human pluripotency. Stem Cell Reports, 2021, 16, 2118-2127.	4.8	51
15	Evaluating intra- and inter-individual variation in the human placental transcriptome. Genome Biology, 2015, 16, 54.	8.8	45
16	Gene expression reversal toward pre-adult levels in the aging human brain and age-related loss of cellular identity. Scientific Reports, 2017, 7, 5894.	3.3	35
17	Comprehensive investigation of temporal and autism-associated cell type composition-dependent and independent gene expression changes in human brains. Scientific Reports, 2017, 7, 4121.	3.3	34
18	Fluoxetine treatment prevents the inflammatory response in a mouse model of posttraumatic stress disorder. Journal of Psychiatric Research, 2016, 76, 74-83.	3.1	33

#	ARTICLE	IF	CITATIONS
19	CSS: cluster similarity spectrum integration of single-cell genomics data. <i>Genome Biology</i> , 2020, 21, 224.	8.8	30
20	Prediction of interaction between small molecule and enzyme using AdaBoost. <i>Molecular Diversity</i> , 2009, 13, 313-320.	3.9	23
21	Extracellular LGALS3BP regulates neural progenitor position and relates to human cortical complexity. <i>Nature Communications</i> , 2021, 12, 6298.	12.8	21
22	A Sequence-based Approach for Predicting Protein Disordered Regions. <i>Protein and Peptide Letters</i> , 2013, 20, 243-248.	0.9	20
23	Functional association between influenza A (H1N1) virus and human. <i>Biochemical and Biophysical Research Communications</i> , 2009, 390, 1111-1113.	2.1	19
24	Fluoxetine Treatment Rescues Energy Metabolism Pathway Alterations in a Posttraumatic Stress Disorder Mouse Model. <i>Molecular Neuropsychiatry</i> , 2016, 2, 46-59.	2.9	18
25	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. <i>Stem Cell Reports</i> , 2020, 15, 214-225.	4.8	18
26	Suppressing Nodal Signaling Activity Predisposes Ectodermal Differentiation of Epiblast Stem Cells. <i>Stem Cell Reports</i> , 2018, 11, 43-57.	4.8	16
27	Identification and characterization of functional modules reflecting transcriptome transition during human neuron maturation. <i>BMC Genomics</i> , 2018, 19, 262.	2.8	15
28	Characterization of RNA content in individual phase-separated coacervate microdroplets. <i>Nature Communications</i> , 2022, 13, 2626.	12.8	14
29	Cooperativity among Short Amyloid Stretches in Long Amyloidogenic Sequences. <i>PLoS ONE</i> , 2012, 7, e39369.	2.5	10
30	A Novel Sequence-Based Method of Predicting Protein DNA-Binding Residues, Using a Machine Learning Approach. <i>Molecules and Cells</i> , 2010, 30, 99-106.	2.6	7
31	Prediction of Nucleosome Positioning Based on Transcription Factor Binding Sites. <i>PLoS ONE</i> , 2010, 5, e12495.	2.5	7
32	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. <i>Protein and Peptide Letters</i> , 2013, 20, 324-335.	0.9	6
33	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. <i>Protein and Peptide Letters</i> , 2013, 20, 324-335.	0.9	3
34	Gene finding by integrating gene finders. <i>Journal of Biomedical Science and Engineering</i> , 2010, 03, 1061-1068.	0.4	2
35	A committee of NNA classifiers for the prediction of the binding between miRNAs and the target genes using a novel coding method. , 2009, , .		0
36	A novel voting system for the identification of eukaryotic genome promoters. <i>Journal of Biomedical Science and Engineering</i> , 2010, 03, 719-726.	0.4	0