Zhisong He

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3114753/publications.pdf

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36	2,299	20	35
papers	citations	h-index	g-index
		361413	361022

52	52	52	3275
all docs	docs citations	times ranked	citing authors

#	ARTICLE	IF	CITATIONS
1	Lineage recording in human cerebral organoids. Nature Methods, 2022, 19, 90-99.	19.0	93
2	Characterization of RNA content in individual phase-separated coacervate microdroplets. Nature Communications, 2022, 13, 2626.	12.8	14
3	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
4	Charting human development using a multi-endodermal organ atlas and organoid models. Cell, 2021, 184, 3281-3298.e22.	28.9	82
5	NGN2 induces diverse neuron types from human pluripotency. Stem Cell Reports, 2021, 16, 2118-2127.	4.8	51
6	Extracellular LGALS3BP regulates neural progenitor position and relates to human cortical complexity. Nature Communications, 2021, 12, 6298.	12.8	21
7	Lipidome alterations in human prefrontal cortex during development, aging, and cognitive disorders. Molecular Psychiatry, 2020, 25, 2952-2969.	7.9	66
8	Human Stem Cell Resources Are an Inroad to Neandertal DNA Functions. Stem Cell Reports, 2020, 15, 214-225.	4.8	18
9	CSS: cluster similarity spectrum integration of single-cell genomics data. Genome Biology, 2020, 21, 224.	8.8	30
10	Organoid single-cell genomic atlas uncovers human-specific features of brain development. Nature, 2019, 574, 418-422.	27.8	496
11	Suppressing Nodal Signaling Activity Predisposes Ectodermal Differentiation of Epiblast Stem Cells. Stem Cell Reports, 2018, 11, 43-57.	4.8	16
12	Identification and characterization of functional modules reflecting transcriptome transition during human neuron maturation. BMC Genomics, 2018, 19, 262.	2.8	15
13	Comprehensive transcriptome analysis of neocortical layers in humans, chimpanzees and macaques. Nature Neuroscience, 2017, 20, 886-895.	14.8	101
14	ALYREF mainly binds to the 5â€² and the 3â€² regions of the mRNA in vivo. Nucleic Acids Research, 2017, 45, 9640-9653.	14.5	87
15	Exosome cofactor <scp>hMTR</scp>4 competes with export adaptor <scp>ALYREF</scp> to ensure balanced nuclear <scp>RNA</scp> pools for degradation and export. EMBO Journal, 2017, 36, 2870-2886.	7.8	82
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 Rescues Energy Metabolism Pathway Alterations in a Posttraumatic Stress Disorder Mouse Model. Molecular Neuropsychiatry, 2016, 2, 46-59.	2.9	18

#	ARTICLE	IF	CITATIONS
19	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
20	Differences and similarities between human and chimpanzee neural progenitors during cerebral cortex development. ELife, 2016, 5, .	6.0	200
21	Evaluating intra- and inter-individual variation in the human placental transcriptome. Genome Biology, 2015, 16, 54.	8.8	45
22	Conserved expression of lincRNA during human and macaque prefrontal cortex development and maturation. Rna, 2014, 20, 1103-1111.	3.5	59
23	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. Protein and Peptide Letters, 2013, 20, 324-335.	0.9	3
24	A Sequence-based Approach for Predicting Protein Disordered Regions. Protein and Peptide Letters, 2013, 20, 243-248.	0.9	20
25	Inter- and Intra-Chain Disulfide Bond Prediction Based on Optimal Feature Selection. Protein and Peptide Letters, 2013, 20, 324-335.	0.9	6
26	Cooperativity among Short Amyloid Stretches in Long Amyloidogenic Sequences. PLoS ONE, 2012, 7, e39369.	2.5	10
27	A Novel Sequence-Based Method of Predicting Protein DNA-Binding Residues, Using a Machine Learning Approach. Molecules and Cells, 2010, 30, 99-106.	2.6	7
28	Prediction of Nucleosome Positioning Based on Transcription Factor Binding Sites. PLoS ONE, 2010, 5, e12495.	2.5	7
29	Predicting Drug-Target Interaction Networks Based on Functional Groups and Biological Features. PLoS ONE, 2010, 5, e9603.	2.5	241
30	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
31	Prediction of Deleterious Non-Synonymous SNPs Based on Protein Interaction Network and Hybrid Properties. PLoS ONE, 2010, 5, e11900.	2.5	70
32	Gene finding by integrating gene finders. Journal of Biomedical Science and Engineering, 2010, 03, 1061-1068.	0.4	2
33	A novel voting system for the identification of eukaryotic genome promoters. Journal of Biomedical Science and Engineering, 2010, 03, 719-726.	0.4	0
34	A committee of NNA classifiers for the prediction of the binding between miRNAs and the target genes using a novel coding method. , 2009, , .		0
35	Prediction of interaction between small molecule and enzyme using AdaBoost. Molecular Diversity, 2009, 13, 313-320.	3.9	23
36	Functional association between influenza A (H1N1) virus and human. Biochemical and Biophysical Research Communications, 2009, 390, 1111-1113.	2.1	19