Nongluk Plongthongkum

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/3020319/publications.pdf

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19 papers 2,783 citations

687363 13 h-index 18 g-index

23 all docs 23 docs citations

times ranked

23

6100 citing authors

#	Article	IF	CITATIONS
1	Comparative cellular analysis of motor cortex in human, marmoset and mouse. Nature, 2021, 598, 111-119.	27.8	361
2	Scalable dual-omics profiling with single-nucleus chromatin accessibility and mRNA expression sequencing 2 (SNARE-seq2). Nature Protocols, 2021, 16, 4992-5029.	12.0	18
3	A single-nucleus RNA-sequencing pipeline to decipher the molecular anatomy and pathophysiology of human kidneys. Nature Communications, 2019, 10, 2832.	12.8	206
4	Optimization of trastuzumab production in the cytoplasm of the engineered Esherichia coli SHuffle strains. , 2019, , .		0
5	Reduced graphene oxide and poly(L-methionine) modified screen-printed carbon electrode for determination of yellow azo dye. , 2019, , .		O
6	Large-Scale Targeted DNA Methylation Analysis Using Bisulfite Padlock Probes. Methods in Molecular Biology, 2018, 1708, 365-382.	0.9	1
7	Identification of methylation haplotype blocks aids in deconvolution of heterogeneous tissue samples and tumor tissue-of-origin mapping from plasma DNA. Nature Genetics, 2017, 49, 635-642.	21.4	384
8	Quantitative comparison of DNA methylation assays for biomarker development and clinical applications. Nature Biotechnology, 2016, 34, 726-737.	17.5	270
9	Characterization of Genome-Methylome Interactions in 22 Nuclear Pedigrees. PLoS ONE, 2014, 9, e99313.	2.5	15
10	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2014, 5, 59-68.	11.0	26
11	Advances in the profiling of DNA modifications: cytosine methylation and beyond. Nature Reviews Genetics, 2014, 15, 647-661.	16.3	224
12	Modelling Fanconi anemia pathogenesis and therapeutics using integration-free patient-derived iPSCs. Nature Communications, 2014, 5, 4330.	12.8	102
13	Global DNA methylation and transcriptional analyses of human ESC-derived cardiomyocytes. Protein and Cell, 2013, 5, 59.	11.0	3
14	Library-free methylation sequencing with bisulfite padlock probes. Nature Methods, 2012, 9, 270-272.	19.0	92
15	Identification of a specific reprogramming-associated epigenetic signature in human induced pluripotent stem cells. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 16196-16201.	7.1	152
16	The metabolome of induced pluripotent stem cells reveals metabolic changes occurring in somatic cell reprogramming. Cell Research, 2012, 22, 168-177.	12.0	452
17	Targeted Gene Correction of Laminopathy-Associated LMNA Mutations in Patient-Specific iPSCs. Cell Stem Cell, 2011, 8, 688-694.	11.1	214
18	Ire1 regulated XBP1 mRNA splicing is essential for the unfolded protein response (UPR) in Drosophila melanogaster. Biochemical and Biophysical Research Communications, 2007, 354, 789-794.	2.1	47

#	Article	IF	CITATIONS
19	Therapeutic inhibition of yellow head virus multiplication in infected shrimps by YHV-protease dsRNA. Antiviral Research, 2007, 74, 150-155.	4.1	90