Lasse Ebdrup Pedersen

List of Publications by Year
in descending order

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Version: 2024-02-01

26	1,858	471509	552781
papers	citations	17 h-index	26 g-index

34	34	34	2305
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Multiplex metabolic pathway engineering using CRISPR/Cas9 in Saccharomyces cerevisiae. Metabolic Engineering, 2015, 28, 213-222.	7.0	355
2	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	6.2	205
3	CRMAGE: CRISPR Optimized MAGE Recombineering. Scientific Reports, 2016, 6, 19452.	3.3	180
4	Site-specific integration in CHO cells mediated by CRISPR/Cas9 and homology-directed DNA repair pathway. Scientific Reports, 2015, 5, 8572.	3.3	168
5	Accelerating genome editing in CHO cells using CRISPR Cas9 and CRISPy, a webâ€based target finding tool. Biotechnology and Bioengineering, 2014, 111, 1604-1616.	3.3	167
6	CRISPy-web: An online resource to design sgRNAs for CRISPR applications. Synthetic and Systems Biotechnology, 2016, 1, 118-121.	3.7	117
7	Oneâ€step generation of triple knockout CHO cell lines using CRISPR/Cas9 and fluorescent enrichment. Biotechnology Journal, 2015, 10, 1446-1456.	3.5	108
8	Multiplex secretome engineering enhances recombinant protein production and purity. Nature Communications, 2020, 11, 1908.	12.8	63
9	CasPER, a method for directed evolution in genomic contexts using mutagenesis and CRISPR/Cas9. Metabolic Engineering, 2018, 48, 288-296.	7.0	60
10	Accelerated homologyâ€directed targeted integration of transgenes in Chinese hamster ovary cells via CRISPR/Cas9 and fluorescent enrichment. Biotechnology and Bioengineering, 2016, 113, 2518-2523.	3.3	58
11	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. Scientific Reports, 2017, 7, 40388.	3.3	48
12	Regulation of cell proliferation and cell density by the inorganic phosphate transporter PiT1. Cell Division, 2012, 7, 7.	2.4	39
13	Elucidation of the CHO Super-Ome (CHO-SO) by Proteoinformatics. Journal of Proteome Research, 2015, 14, 4687-4703.	3.7	35
14	Genome-Wide CRISPRi-Based Identification of Targets for Decoupling Growth from Production. ACS Synthetic Biology, 2020, 9, 1030-1040.	3.8	29
15	Awakening dormant glycosyltransferases in CHO cells with CRISPRa. Biotechnology and Bioengineering, 2020, 117, 593-598.	3.3	27
16	Comprehensive Analysis of Genomic Safe Harbors as Target Sites for Stable Expression of the Heterologous Gene in HEK293 Cells. ACS Synthetic Biology, 2020, 9, 1263-1269.	3.8	23
17	Reprogramming AA catabolism in CHO cells with CRISPR/Cas9 genome editing improves cell growth and reduces byproduct secretion. Metabolic Engineering, 2019, 56, 120-129.	7.0	22
18	High levels of the type III inorganic phosphate transporter PiT1 (SLC20A1) can confer faster cell adhesion. Experimental Cell Research, 2014, 326, 57-67.	2.6	20

#	Article	IF	Citations
19	Genome-wide systematic identification of methyltransferase recognition and modification patterns. Nature Communications, 2019, 10, 3311.	12.8	18
20	A synthetic RNA-mediated evolution system in yeast. Nucleic Acids Research, 2021, 49, e88-e88.	14.5	17
21	A metabolic CRISPR-Cas9 screen in Chinese hamster ovary cells identifies glutamine-sensitive genes. Metabolic Engineering, 2021, 66, 114-122.	7.0	17
22	Network reconstruction of the mouse secretory pathway applied on CHO cell transcriptome data. BMC Systems Biology, 2017, 11, 37.	3.0	14
23	An optimized genome-wide, virus-free CRISPR screen for mammalian cells. Cell Reports Methods, 2021, 1, 100062.	2.9	14
24	Synergistic stabilization of a double mutant in chymotrypsin inhibitor 2 from a library screen in E. coli. Communications Biology, 2021, 4, 980.	4.4	13
25	A dual-reporter system for investigating and optimizing protein translation and folding in E. coli. Nature Communications, 2021, 12, 6093.	12.8	12
26	Rational and evolutionary engineering of Saccharomyces cerevisiae for production of dicarboxylic acids from lignocellulosic biomass and exploring genetic mechanisms of the yeast tolerance to the biomass hydrolysate. , 2022, 15, 22.		8