

Mikael Rasmussen Andersen

List of Publications by Year in descending order

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Version: 2024-02-01

89
papers

6,915
citations

76196

40
h-index

62479

80
g-index

94
all docs

94
docs citations

94
times ranked

6968
citing authors

#	ARTICLE	IF	CITATIONS
1	Use of novel cystine analogs to decrease oxidative stress and control product quality. <i>Journal of Biotechnology</i> , 2021, 327, 1-8.	1.9	8
2	Chemical Diversity of Locked Nucleic Acid-Modified Antisense Oligonucleotides Allows Optimization of Pharmaceutical Properties. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 706-717.	2.3	28
3	Oxidative stress-relieving strategies to improve recombinant protein production in CHO cells. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1172-1186.	1.7	57
4	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. <i>Biotechnology and Bioengineering</i> , 2020, 117, 3448-3458.	1.7	13
5	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020, 11, 1106.	5.8	125
6	Bottlenecks and Future Outlooks for High-Throughput Technologies for Filamentous Fungi. <i>Grand Challenges in Biology and Biotechnology</i> , 2020, , 165-178.	2.4	4
7	Application of a genome-scale model in tandem with enzyme assays for identification of metabolic signatures of high and low CHO cell producers. <i>Metabolic Engineering Communications</i> , 2019, 9, e00097.	1.9	8
8	Reprogramming AA catabolism in CHO cells with CRISPR/Cas9 genome editing improves cell growth and reduces byproduct secretion. <i>Metabolic Engineering</i> , 2019, 56, 120-129.	3.6	22
9	BCAT1 and BCAT2 disruption in CHO cells has cell line-dependent effects. <i>Journal of Biotechnology</i> , 2019, 306, 24-31.	1.9	5
10	Genetic engineering approaches to improve posttranslational modification of biopharmaceuticals in different production platforms. <i>Biotechnology and Bioengineering</i> , 2019, 116, 2778-2796.	1.7	34
11	Strategies to establish the link between biosynthetic gene clusters and secondary metabolites. <i>Fungal Genetics and Biology</i> , 2019, 130, 107-121.	0.9	64
12	Resistance Gene-Directed Genome Mining of 50 <i>Aspergillus</i> Species. <i>MSystems</i> , 2019, 4, .	1.7	29
13	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. <i>ACS Synthetic Biology</i> , 2019, 8, 758-774.	1.9	32
14	Genus level analysis of PKS-NRPS and NRPS-PKS hybrids reveals their origin in <i>Aspergilli</i> . <i>BMC Genomics</i> , 2019, 20, 847.	1.2	15
15	Application of a curated genome-scale metabolic model of CHO DG44 to an industrial fed-batch process. <i>Metabolic Engineering</i> , 2019, 51, 9-19.	3.6	49
16	Glyco-engineered CHO cell lines producing alpha-1-antitrypsin and C1 esterase inhibitor with fully humanized N-glycosylation profiles. <i>Metabolic Engineering</i> , 2019, 52, 143-152.	3.6	42
17	Impact of CHO Metabolism on Cell Growth and Protein Production: An Overview of Toxic and Inhibiting Metabolites and Nutrients. <i>Biotechnology Journal</i> , 2018, 13, e1700499.	1.8	134
18	Using Titer and Titer Normalized to Confluence Are Complementary Strategies for Obtaining Chinese Hamster Ovary Cell Lines with High Volumetric Productivity of Etanercept. <i>Biotechnology Journal</i> , 2018, 13, e1700216.	1.8	16

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19	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E753-E761.	3.3	126
20	Glycoengineering in CHO Cells: Advances in Systems Biology. Biotechnology Journal, 2018, 13, e1700234.	1.8	51
21	Pros and cons of different therapeutic antibody formats for recombinant antivenom development. Toxicon, 2018, 146, 151-175.	0.8	125
22	Fed-Batch CHO Cell Culture for Lab-Scale Antibody Production. Methods in Molecular Biology, 2018, 1674, 147-161.	0.4	11
23	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. Scientific Reports, 2018, 8, 17957.	1.6	33
24	A community-driven reconstruction of the <i>Aspergillus niger</i> metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	2.5	20
25	Antibody Cross-Reactivity in Antivenom Research. Toxins, 2018, 10, 393.	1.5	33
26	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . Nature Genetics, 2018, 50, 1688-1695.	9.4	160
27	An Online Compendium of CHO RNA-Seq Data Allows Identification of CHO Cell Line-Specific Transcriptomic Signatures. Biotechnology Journal, 2018, 13, e1800070.	1.8	21
28	Novofumigatonin biosynthesis involves a non-heme iron-dependent endoperoxide isomerase for orthoester formation. Nature Communications, 2018, 9, 2587.	5.8	85
29	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. ACS Synthetic Biology, 2018, 7, 2148-2159.	1.9	51
30	CRISPR/Cas9-Multiplexed Editing of Chinese Hamster Ovary B4Galactin 1, 2, 3, and 4 Tailors N-Glycan Profiles of Therapeutics and Secreted Host Cell Proteins. Biotechnology Journal, 2018, 13, e1800111.	1.8	27
31	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. Scientific Reports, 2017, 7, 40388.	1.6	48
32	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . Genome Biology, 2017, 18, 28.	3.8	417
33	Engineer Medium and Feed for Modulating N-Glycosylation of Recombinant Protein Production in CHO Cell Culture. Methods in Molecular Biology, 2017, 1603, 209-226.	0.4	3
34	Cell Factory Engineering. Cell Systems, 2017, 4, 262-275.	2.9	96
35	Pitfalls to avoid when using phage display for snake toxins. Toxicon, 2017, 126, 79-89.	0.8	14
36	<i>Aspergilli</i> : Models for systems biology in filamentous fungi. Current Opinion in Systems Biology, 2017, 6, 67-73.	1.3	20

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37	Network reconstruction of the mouse secretory pathway applied on CHO cell transcriptome data. BMC Systems Biology, 2017, 11, 37.	3.0	14
38	Model-based analysis of N-glycosylation in Chinese hamster ovary cells. PLoS ONE, 2017, 12, e0175376.	1.1	39
39	Recombinant snakebite antivenoms: A cost-competitive solution to a neglected tropical disease?. PLoS Neglected Tropical Diseases, 2017, 11, e0005361.	1.3	64
40	Cross-recognition of a pit viper (Crotalinae) polyspecific antivenom explored through high-density peptide microarray epitope mapping. PLoS Neglected Tropical Diseases, 2017, 11, e0005768.	1.3	17
41	Linker Flexibility Facilitates Module Exchange in Fungal Hybrid PKS-NRPS Engineering. PLoS ONE, 2016, 11, e0161199.	1.1	30
42	Glycoprofiling effects of media additives on IgG produced by CHO cells in fed-batch bioreactors. Biotechnology and Bioengineering, 2016, 113, 359-366.	1.7	38
43	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	2.9	205
44	Endoplasmic reticulum-directed recombinant mRNA displays subcellular localization equal to endogenous mRNA during transient expression in CHO cells. Biotechnology Journal, 2016, 11, 1362-1367.	1.8	6
45	Current challenges of research on filamentous fungi in relation to human welfare and a sustainable bio-economy: a white paper. Fungal Biology and Biotechnology, 2016, 3, 6.	2.5	208
46	High-throughput immuno-profiling of mamba (Dendroaspis) venom toxin epitopes using high-density peptide microarrays. Scientific Reports, 2016, 6, 36629.	1.6	33
47	An Integrated Metabolomic and Genomic Mining Workflow To Uncover the Biosynthetic Potential of Bacteria. MSystems, 2016, 1, .	1.7	55
48	Alcohol dehydrogenase gene ADH3 activates glucose alcoholic fermentation in genetically engineered Dekkera bruxellensis yeast. Applied Microbiology and Biotechnology, 2016, 100, 3219-3231.	1.7	16
49	FunGeneClusterS: Predicting fungal gene clusters from genome and transcriptome data. Synthetic and Systems Biotechnology, 2016, 1, 122-129.	1.8	47
50	Novel Centromeric Loci of the Wine and Beer Yeast Dekkera bruxellensis CEN1 and CEN2. PLoS ONE, 2016, 11, e0161741.	1.1	15
51	Approaches for Comparative Genomics in Aspergillus and Penicillium. , 2016, , 43-74.		0
52	Multi-omic profiling of EPO-producing Chinese hamster ovary cell panel reveals metabolic adaptation to heterologous protein production. Biotechnology and Bioengineering, 2015, 112, 2373-2387.	1.7	20
53	Versatile microscale screening platform for improving recombinant protein productivity in Chinese hamster ovary cells. Scientific Reports, 2015, 5, 18016.	1.6	23
54	Deciphering the signaling mechanisms of the plant cell wall degradation machinery in Aspergillus oryzae. BMC Systems Biology, 2015, 9, 77.	3.0	5

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55	Glycoengineering of Chinese hamster ovary cells for enhanced erythropoietin N-glycan branching and sialylation. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2343-2351.	1.7	75
56	Deep sequencing reveals different compositions of mRNA transcribed from the <i>F8</i> gene in a panel of FVIII-producing CHO cell lines. <i>Biotechnology Journal</i> , 2015, 10, 1081-1089.	1.8	4
57	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 13.	2.0	30
58	Current state of genome-scale modeling in filamentous fungi. <i>Biotechnology Letters</i> , 2015, 37, 1131-1139.	1.1	25
59	Combining Stable Isotope Labeling and Molecular Networking for Biosynthetic Pathway Characterization. <i>Analytical Chemistry</i> , 2015, 87, 6520-6526.	3.2	51
60	A multi-pronged investigation into the effect of glucose starvation and culture duration on fed-batch CHO cell culture. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2172-2184.	1.7	54
61	Sequencing the CHO DXB11 genome reveals regional variations in genomic stability and haploidy. <i>BMC Genomics</i> , 2015, 16, 160.	1.2	75
62	Amino acid and glucose metabolism in fed-batch CHO cell culture affects antibody production and glycosylation. <i>Biotechnology and Bioengineering</i> , 2015, 112, 521-535.	1.7	152
63	Toward genome-scale models of the Chinese hamster ovary cells: incentives, status and perspectives. <i>Pharmaceutical Bioprocessing</i> , 2014, 2, 437-448.	0.8	13
64	Elucidation of primary metabolic pathways in <i>Aspergillus</i> species: Orphaned research in characterizing orphan genes. <i>Briefings in Functional Genomics</i> , 2014, 13, 451-455.	1.3	24
65	Aggressive dereplication using UHPLC-DAD-QTOF: screening extracts for up to 3000 fungal secondary metabolites. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 1933-1943.	1.9	126
66	A Versatile System for USER Cloning-Based Assembly of Expression Vectors for Mammalian Cell Engineering. <i>PLoS ONE</i> , 2014, 9, e96693.	1.1	26
67	Full transcriptome analysis of Chinese Hamster Ovary cell lines producing a dynamic range of Coagulation Factor VIII. <i>BMC Proceedings</i> , 2013, 7, .	1.8	0
68	Supercluster takes a walk on the wild side. <i>Trends in Microbiology</i> , 2013, 21, 617-618.	3.5	0
69	Integrated Approaches for Assessment of Cellular Performance in Industrially Relevant Filamentous Fungi. <i>Industrial Biotechnology</i> , 2013, 9, 337-344.	0.5	15
70	Accurate prediction of secondary metabolite gene clusters in filamentous fungi. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E99-107.	3.3	211
71	<i>Aspergillus nidulans</i> Synthesize Insect Juvenile Hormones upon Expression of a Heterologous Regulatory Protein and in Response to Grazing by <i>Drosophila melanogaster</i> Larvae. <i>PLoS ONE</i> , 2013, 8, e73369.	1.1	21
72	Mapping the polysaccharide degradation potential of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2012, 13, 313.	1.2	35

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73	Identification of a Transcription Factor Controlling pH-Dependent Organic Acid Response in <i>Aspergillus niger</i> . PLoS ONE, 2012, 7, e50596.	1.1	22
74	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. Genome Research, 2011, 21, 885-897.	2.4	329
75	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	9.4	699
76	Hydrophobins from <i>Aspergillus</i> species cannot be clearly divided into two classes. BMC Research Notes, 2010, 3, 344.	0.6	70
77	Studies of the Production of Fungal Polyketides in <i>Aspergillus nidulans</i> by Using Systems Biology Tools. Applied and Environmental Microbiology, 2009, 75, 2212-2220.	1.4	31
78	Proteome analysis of <i>Aspergillus niger</i> : Lactate added in starch-containing medium can increase production of the mycotoxin fumonisin B2 by modifying acetyl-CoA metabolism. BMC Microbiology, 2009, 9, 255.	1.3	47
79	Uncovering transcriptional regulation of glycerol metabolism in <i>Aspergilli</i> through genome-wide gene expression data analysis. Molecular Genetics and Genomics, 2009, 282, 571-86.	1.0	56
80	Overexpression of isocitrate lyase"glyoxylate bypass influence on metabolism in <i>Aspergillus niger</i> . Metabolic Engineering, 2009, 11, 107-116.	3.6	37
81	Current status of systems biology in <i>Aspergilli</i> . Fungal Genetics and Biology, 2009, 46, S180-S190.	0.9	43
82	Post-genomic insights into the plant polysaccharide degradation potential of <i>Aspergillus nidulans</i> and comparison to <i>Aspergillus niger</i> and <i>Aspergillus oryzae</i> . Fungal Genetics and Biology, 2009, 46, S161-S169.	0.9	133
83	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99
84	Systemic analysis of the response of <i>Aspergillus niger</i> to ambient pH. Genome Biology, 2009, 10, R47.	13.9	99
85	Essential pathway identification: from <i>in silico</i> analysis to potential antifungal targets in <i>Aspergillus fumigatus</i> . Medical Mycology, 2009, 47, S80-S87.	0.3	20
86	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i> . Molecular Systems Biology, 2008, 4, 178.	3.2	190
87	A trispecies <i>Aspergillus</i> microarray: Comparative transcriptomics of three <i>Aspergillus</i> species. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 4387-4392.	3.3	152
88	Systems Analysis Unfolds the Relationship between the Phosphoketolase Pathway and Growth in <i>Aspergillus nidulans</i> . PLoS ONE, 2008, 3, e3847.	1.1	40
89	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	9.4	1,047