

Mikael Rasmussen Andersen

List of Publications by Year in descending order

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89
papers

6,915
citations

76326

40
h-index

62596

80
g-index

94
all docs

94
docs citations

94
times ranked

6968
citing authors

#	ARTICLE	IF	CITATIONS
1	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007, 25, 221-231.	17.5	1,047
2	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. <i>Nature Biotechnology</i> , 2011, 29, 735-741.	17.5	699
3	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus <i>Aspergillus</i> . <i>Genome Biology</i> , 2017, 18, 28.	8.8	417
4	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	5.5	329
5	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.	7.1	211
6	Current challenges of research on filamentous fungi in relation to human welfare and a sustainable bio-economy: a white paper. <i>Fungal Biology and Biotechnology</i> , 2016, 3, 6.	5.1	208
7	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. <i>Cell Systems</i> , 2016, 3, 434-443.e8.	6.2	205
8	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i> . <i>Molecular Systems Biology</i> , 2008, 4, 178.	7.2	190
9	Investigation of inter- and intraspecies variation through genome sequencing of <i>Aspergillus</i> section <i>Nigri</i> . <i>Nature Genetics</i> , 2018, 50, 1688-1695.	21.4	160
10	A trispecies <i>Aspergillus</i> microarray: Comparative transcriptomics of three <i>Aspergillus</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 4387-4392.	7.1	152
11	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.	3.3	152
12	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.	3.5	134
13	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> . <i>Fungal Genetics and Biology</i> , 2009, 46, S161-S169.	2.1	133
14	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.	3.7	126
15	Linking secondary metabolites to gene clusters through genome sequencing of six diverse <i>Aspergillus</i> species. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E753-E761.	7.1	126
16	Pros and cons of different therapeutic antibody formats for recombinant antivenom development. <i>Toxicon</i> , 2018, 146, 151-175.	1.6	125
17	A comparative genomics study of 23 <i>Aspergillus</i> species from section <i>Flavi</i> . <i>Nature Communications</i> , 2020, 11, 1106.	12.8	125
18	The 2008 update of the <i>Aspergillus nidulans</i> genome annotation: A community effort. <i>Fungal Genetics and Biology</i> , 2009, 46, S2-S13.	2.1	99

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19	Systemic analysis of the response of <i>Aspergillus niger</i> to ambient pH. <i>Genome Biology</i> , 2009, 10, R47.	9.6	99
20	Cell Factory Engineering. <i>Cell Systems</i> , 2017, 4, 262-275.	6.2	96
21	Novofumigatonin biosynthesis involves a non-heme iron-dependent endoperoxide isomerase for orthoester formation. <i>Nature Communications</i> , 2018, 9, 2587.	12.8	85
22	Glycoengineering of Chinese hamster ovary cells for enhanced erythropoietin N-glycan branching and sialylation. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2343-2351.	3.3	75
23	Sequencing the CHO DXB11 genome reveals regional variations in genomic stability and haploidy. <i>BMC Genomics</i> , 2015, 16, 160.	2.8	75
24	Hydrophobins from <i>Aspergillus</i> species cannot be clearly divided into two classes. <i>BMC Research Notes</i> , 2010, 3, 344.	1.4	70
25	Strategies to establish the link between biosynthetic gene clusters and secondary metabolites. <i>Fungal Genetics and Biology</i> , 2019, 130, 107-121.	2.1	64
26	Recombinant snakebite antivenoms: A cost-competitive solution to a neglected tropical disease?. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005361.	3.0	64
27	Oxidative stress-alleviating strategies to improve recombinant protein production in CHO cells. <i>Biotechnology and Bioengineering</i> , 2020, 117, 1172-1186.	3.3	57
28	Uncovering transcriptional regulation of glycerol metabolism in <i>Aspergilli</i> through genome-wide gene expression data analysis. <i>Molecular Genetics and Genomics</i> , 2009, 282, 571-86.	2.1	56
29	An Integrated Metabolomic and Genomic Mining Workflow To Uncover the Biosynthetic Potential of Bacteria. <i>MSystems</i> , 2016, 1, .	3.8	55
30	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.	3.3	54
31	Combining Stable Isotope Labeling and Molecular Networking for Biosynthetic Pathway Characterization. <i>Analytical Chemistry</i> , 2015, 87, 6520-6526.	6.5	51
32	Glycoengineering in CHO Cells: Advances in Systems Biology. <i>Biotechnology Journal</i> , 2018, 13, e1700234.	3.5	51
33	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. <i>ACS Synthetic Biology</i> , 2018, 7, 2148-2159.	3.8	51
34	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.	7.0	49
35	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. <i>Scientific Reports</i> , 2017, 7, 40388.	3.3	48
36	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. <i>BMC Microbiology</i> , 2009, 9, 255.	3.3	47

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37	FunGeneClusterS: Predicting fungal gene clusters from genome and transcriptome data. <i>Synthetic and Systems Biotechnology</i> , 2016, 1, 122-129.	3.7	47
38	Current status of systems biology in <i>Aspergilli</i> . <i>Fungal Genetics and Biology</i> , 2009, 46, S180-S190.	2.1	43
39	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.	7.0	42
40	Systems Analysis Unfolds the Relationship between the Phosphoketolase Pathway and Growth in <i>Aspergillus nidulans</i> . <i>PLoS ONE</i> , 2008, 3, e3847.	2.5	40
41	Model-based analysis of N-glycosylation in Chinese hamster ovary cells. <i>PLoS ONE</i> , 2017, 12, e0175376.	2.5	39
42	Glycoprofiling effects of media additives on IgG produced by CHO cells in fed-batch bioreactors. <i>Biotechnology and Bioengineering</i> , 2016, 113, 359-366.	3.3	38
43	Overexpression of isocitrate lyase-glyoxylate bypass influence on metabolism in <i>Aspergillus niger</i> . <i>Metabolic Engineering</i> , 2009, 11, 107-116.	7.0	37
44	Mapping the polysaccharide degradation potential of <i>Aspergillus niger</i> . <i>BMC Genomics</i> , 2012, 13, 313.	2.8	35
45	Genetic engineering approaches to improve posttranslational modification of biopharmaceuticals in different production platforms. <i>Biotechnology and Bioengineering</i> , 2019, 116, 2778-2796.	3.3	34
46	High-throughput immuno-profiling of mamba (<i>Dendroaspis</i>) venom toxin epitopes using high-density peptide microarrays. <i>Scientific Reports</i> , 2016, 6, 36629.	3.3	33
47	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. <i>Scientific Reports</i> , 2018, 8, 17957.	3.3	33
48	Antibody Cross-Reactivity in Antivenom Research. <i>Toxins</i> , 2018, 10, 393.	3.4	33
49	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. <i>ACS Synthetic Biology</i> , 2019, 8, 758-774.	3.8	32
50	Studies of the Production of Fungal Polyketides in <i>Aspergillus nidulans</i> by Using Systems Biology Tools. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2212-2220.	3.1	31
51	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. <i>Frontiers in Bioengineering and Biotechnology</i> , 2015, 3, 13.	4.1	30
52	Linker Flexibility Facilitates Module Exchange in Fungal Hybrid PKS-NRPS Engineering. <i>PLoS ONE</i> , 2016, 11, e0161199.	2.5	30
53	Resistance Gene-Directed Genome Mining of 50 <i>Aspergillus</i> Species. <i>MSystems</i> , 2019, 4, .	3.8	29
54	Chemical Diversity of Locked Nucleic Acid-Modified Antisense Oligonucleotides Allows Optimization of Pharmaceutical Properties. <i>Molecular Therapy - Nucleic Acids</i> , 2020, 19, 706-717.	5.1	28

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55	CRISPR/Cas9-Multiplexed Editing of Chinese Hamster Ovary B4Gal1, 2, 3, and 4 Tailors Glycan Profiles of Therapeutics and Secreted Host Cell Proteins. <i>Biotechnology Journal</i> , 2018, 13, e1800111.	3.5	27
56	A Versatile System for USER Cloning-Based Assembly of Expression Vectors for Mammalian Cell Engineering. <i>PLoS ONE</i> , 2014, 9, e96693.	2.5	26
57	Current state of genome-scale modeling in filamentous fungi. <i>Biotechnology Letters</i> , 2015, 37, 1131-1139.	2.2	25
58	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.	2.7	24
59	Versatile microscale screening platform for improving recombinant protein productivity in Chinese hamster ovary cells. <i>Scientific Reports</i> , 2015, 5, 18016.	3.3	23
60	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.	7.0	22
61	Identification of a Transcription Factor Controlling pH-Dependent Organic Acid Response in <i>Aspergillus niger</i> . <i>PLoS ONE</i> , 2012, 7, e50596.	2.5	22
62	An Online Compendium of CHO RNA-Seq Data Allows Identification of CHO Cell Line-Specific Transcriptomic Signatures. <i>Biotechnology Journal</i> , 2018, 13, e1800070.	3.5	21
63	<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.	2.5	21
64	Essential pathway identification: from <i>in silico</i> analysis to potential antifungal targets in <i>Aspergillus fumigatus</i> . <i>Medical Mycology</i> , 2009, 47, S80-S87.	0.7	20
65	Multi-omic profiling of EPO-producing Chinese hamster ovary cell panel reveals metabolic adaptation to heterologous protein production. <i>Biotechnology and Bioengineering</i> , 2015, 112, 2373-2387.	3.3	20
66	<i>Aspergilli</i> : Models for systems biology in filamentous fungi. <i>Current Opinion in Systems Biology</i> , 2017, 6, 67-73.	2.6	20
67	A community-driven reconstruction of the <i>Aspergillus niger</i> metabolic network. <i>Fungal Biology and Biotechnology</i> , 2018, 5, 16.	5.1	20
68	Cross-recognition of a pit viper (<i>Crotalinae</i>) polyspecific antivenom explored through high-density peptide microarray epitope mapping. <i>PLoS Neglected Tropical Diseases</i> , 2017, 11, e0005768.	3.0	17
69	Alcohol dehydrogenase gene ADH3 activates glucose alcoholic fermentation in genetically engineered <i>Dekkera bruxellensis</i> yeast. <i>Applied Microbiology and Biotechnology</i> , 2016, 100, 3219-3231.	3.6	16
70	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.	3.5	16
71	Integrated Approaches for Assessment of Cellular Performance in Industrially Relevant Filamentous Fungi. <i>Industrial Biotechnology</i> , 2013, 9, 337-344.	0.8	15
72	Genus level analysis of PKS-NRPS and NRPS-PKS hybrids reveals their origin in <i>Aspergilli</i> . <i>BMC Genomics</i> , 2019, 20, 847.	2.8	15

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73	Novel Centromeric Loci of the Wine and Beer Yeast <i>Dekkera bruxellensis</i> CEN1 and CEN2. PLoS ONE, 2016, 11, e0161741.	2.5	15
74	Pitfalls to avoid when using phage display for snake toxins. Toxicon, 2017, 126, 79-89.	1.6	14
75	Network reconstruction of the mouse secretory pathway applied on CHO cell transcriptome data. BMC Systems Biology, 2017, 11, 37.	3.0	14
76	Toward genome-scale models of the Chinese hamster ovary cells: incentives, status and perspectives. Pharmaceutical Bioprocessing, 2014, 2, 437-448.	0.8	13
77	Characterization of glutathione proteome in CHO cells and its relationship with productivity and cholesterol synthesis. Biotechnology and Bioengineering, 2020, 117, 3448-3458.	3.3	13
78	Fed-Batch CHO Cell Culture for Lab-Scale Antibody Production. Methods in Molecular Biology, 2018, 1674, 147-161.	0.9	11
79	Application of a genome-scale model in tandem with enzyme assays for identification of metabolic signatures of high and low CHO cell producers. Metabolic Engineering Communications, 2019, 9, e00097.	3.6	8
80	Use of novel cystine analogs to decrease oxidative stress and control product quality. Journal of Biotechnology, 2021, 327, 1-8.	3.8	8
81	Endoplasmic reticulum-directed recombinant mRNA displays subcellular localization equal to endogenous mRNA during transient expression in CHO cells. Biotechnology Journal, 2016, 11, 1362-1367.	3.5	6
82	Deciphering the signaling mechanisms of the plant cell wall degradation machinery in <i>Aspergillus oryzae</i> . BMC Systems Biology, 2015, 9, 77.	3.0	5
83	BCAT1 and BCAT2 disruption in CHO cells has cell line-dependent effects. Journal of Biotechnology, 2019, 306, 24-31.	3.8	5
84	Deep sequencing reveals different compositions of mRNA transcribed from the <i>F8</i> gene in a panel of FVIII-producing CHO cell lines. Biotechnology Journal, 2015, 10, 1081-1089.	3.5	4
85	Bottlenecks and Future Outlooks for High-Throughput Technologies for Filamentous Fungi. Grand Challenges in Biology and Biotechnology, 2020, , 165-178.	2.4	4
86	Engineer Medium and Feed for Modulating N-Glycosylation of Recombinant Protein Production in CHO Cell Culture. Methods in Molecular Biology, 2017, 1603, 209-226.	0.9	3
87	Full transcriptome analysis of Chinese Hamster Ovary cell lines producing a dynamic range of Coagulation Factor VIII. BMC Proceedings, 2013, 7, .	1.6	0
88	Supercluster takes a walk on the wild side. Trends in Microbiology, 2013, 21, 617-618.	7.7	0
89	Approaches for Comparative Genomics in <i>Aspergillus</i> and <i>Penicillium</i> . , 2016, , 43-74.		0