Mikael RÃ¸rdam Andersen

List of Publications by Year
in descending order

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89	6,915	40	80
papers	citations	h-index	g-index
		76196	62479

94	94	94	6968
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genome sequencing and analysis of the versatile cell factory Aspergillus niger CBS 513.88. Nature Biotechnology, 2007, 25, 221-231.	9.4	1,047
2	The genomic sequence of the Chinese hamster ovary (CHO)-K1 cell line. Nature Biotechnology, 2011, 29, 735-741.	9.4	699
3	Comparative genomics reveals high biological diversity and specific adaptations in the industrially and medically important fungal genus Aspergillus. Genome Biology, 2017, 18, 28.	3.8	417
4	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
5	Accurate prediction of secondary metabolite gene clusters in filamentous fungi. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E99-107.	3.3	211
6	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
7	A Consensus Genome-scale Reconstruction of Chinese Hamster Ovary Cell Metabolism. Cell Systems, 2016, 3, 434-443.e8.	2.9	205
8	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i>. Molecular Systems Biology, 2008, 4, 178.	3.2	190
9	Investigation of inter- and intraspecies variation through genome sequencing of Aspergillus section Nigri. Nature Genetics, 2018, 50, 1688-1695.	9.4	160
10	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
11	Amino acid and glucose metabolism in fedâ€batch CHO cell culture affects antibody production and glycosylation. Biotechnology and Bioengineering, 2015, 112, 521-535.	1.7	152
12	Impact of CHO Metabolism on Cell Growth and Protein Production: An Overview of Toxic and Inhibiting Metabolites and Nutrients. Biotechnology Journal, 2018, 13, e1700499.	1.8	134
13	Post-genomic insights into the plant polysaccharide degradation potential of Aspergillus nidulans and comparison to Aspergillus niger and Aspergillus oryzae. Fungal Genetics and Biology, 2009, 46, S161-S169.	0.9	133
14	Aggressive dereplication using UHPLCâ€"DADâ€"QTOF: screening extracts for up to 3000 fungal secondary metabolites. Analytical and Bioanalytical Chemistry, 2014, 406, 1933-1943.	1.9	126
15	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
16	Pros and cons of different therapeutic antibody formats for recombinant antivenom development. Toxicon, 2018, 146, 151-175.	0.8	125
17	A comparative genomics study of 23 Aspergillus species from section Flavi. Nature Communications, 2020, 11, 1106.	5.8	125
18	The 2008 update of the Aspergillus nidulans genome annotation: A community effort. Fungal Genetics and Biology, 2009, 46, S2-S13.	0.9	99

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19	Systemic analysis of the response of Aspergillus niger to ambient pH. Genome Biology, 2009, 10, R47.	13.9	99
20	Cell Factory Engineering. Cell Systems, 2017, 4, 262-275.	2.9	96
21	Novofumigatonin biosynthesis involves a non-heme iron-dependent endoperoxide isomerase for orthoester formation. Nature Communications, 2018, 9, 2587.	5.8	85
22	Glycoengineering of Chinese hamster ovary cells for enhanced erythropoietin Nâ€glycan branching and sialylation. Biotechnology and Bioengineering, 2015, 112, 2343-2351.	1.7	75
23	Sequencing the CHO DXB11 genome reveals regional variations in genomic stability and haploidy. BMC Genomics, 2015, 16, 160.	1.2	75
24	Hydrophobins from Aspergillus species cannot be clearly divided into two classes. BMC Research Notes, 2010, 3, 344.	0.6	70
25	Strategies to establish the link between biosynthetic gene clusters and secondary metabolites. Fungal Genetics and Biology, 2019, 130, 107-121.	0.9	64
26	Recombinant snakebite antivenoms: A cost-competitive solution to a neglected tropical disease?. PLoS Neglected Tropical Diseases, 2017, 11, e0005361.	1.3	64
27	Oxidative stressâ€alleviating strategies to improve recombinant protein production in CHO cells. Biotechnology and Bioengineering, 2020, 117, 1172-1186.	1.7	57
28	Uncovering transcriptional regulation of glycerol metabolism in Aspergilli through genome-wide gene expression data analysis. Molecular Genetics and Genomics, 2009, 282, 571-86.	1.0	56
29	An Integrated Metabolomic and Genomic Mining Workflow To Uncover the Biosynthetic Potential of Bacteria. MSystems, 2016, 1, .	1.7	55
30	A multiâ€pronged investigation into the effect of glucose starvation and culture duration on fedâ€batch CHO cell culture. Biotechnology and Bioengineering, 2015, 112, 2172-2184.	1.7	54
31	Combining Stable Isotope Labeling and Molecular Networking for Biosynthetic Pathway Characterization. Analytical Chemistry, 2015, 87, 6520-6526.	3.2	51
32	Glycoengineering in CHO Cells: Advances in Systems Biology. Biotechnology Journal, 2018, 13, e1700234.	1.8	51
33	Minimizing Clonal Variation during Mammalian Cell Line Engineering for Improved Systems Biology Data Generation. ACS Synthetic Biology, 2018, 7, 2148-2159.	1.9	51
34	Application of a curated genome-scale metabolic model of CHO DG44 to an industrial fed-batch process. Metabolic Engineering, 2019, 51, 9-19.	3.6	49
35	Ribosome profiling-guided depletion of an mRNA increases cell growth rate and protein secretion. Scientific Reports, 2017, 7, 40388.	1.6	48
36	Proteome analysis of Aspergillus niger: 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

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37	FunGeneClusterS: Predicting fungal gene clusters from genome and transcriptome data. Synthetic and Systems Biotechnology, 2016, 1, 122-129.	1.8	47
38	Current status of systems biology in Aspergilli. Fungal Genetics and Biology, 2009, 46, S180-S190.	0.9	43
39	Glyco-engineered CHO cell lines producing alpha-1-antitrypsin and C1 esterase inhibitor with fully humanized N-glycosylation profiles. Metabolic Engineering, 2019, 52, 143-152.	3.6	42
40	Systems Analysis Unfolds the Relationship between the Phosphoketolase Pathway and Growth in Aspergillus nidulans. PLoS ONE, 2008, 3, e3847.	1.1	40
41	Model-based analysis of N-glycosylation in Chinese hamster ovary cells. PLoS ONE, 2017, 12, e0175376.	1.1	39
42	Glycoprofiling effects of media additives on IgG produced by CHO cells in fedâ€batch bioreactors. Biotechnology and Bioengineering, 2016, 113, 359-366.	1.7	38
43	Overexpression of isocitrate lyaseâ€”glyoxylate bypass influence on metabolism in Aspergillus niger. Metabolic Engineering, 2009, 11, 107-116.	3.6	37
44	Mapping the polysaccharide degradation potential of Aspergillus niger. BMC Genomics, 2012, 13, 313.	1.2	35
45	Genetic engineering approaches to improve posttranslational modification of biopharmaceuticals in different production platforms. Biotechnology and Bioengineering, 2019, 116, 2778-2796.	1.7	34
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	Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. Scientific Reports, 2018, 8, 17957.	1.6	33
48	Antibody Cross-Reactivity in Antivenom Research. Toxins, 2018, 10, 393.	1.5	33
49	Systematic Evaluation of Site-Specific Recombinant Gene Expression for Programmable Mammalian Cell Engineering. ACS Synthetic Biology, 2019, 8, 758-774.	1.9	32
50	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
51	Analysis of genetic variation and potential applications in genome-scale metabolic modeling. Frontiers in Bioengineering and Biotechnology, 2015, 3, 13.	2.0	30
52	Linker Flexibility Facilitates Module Exchange in Fungal Hybrid PKS-NRPS Engineering. PLoS ONE, 2016, 11, e0161199.	1.1	30
53	Resistance Gene-Directed Genome Mining of 50 <i>Aspergillus</i> Species. MSystems, 2019, 4, .	1.7	29
54	Chemical Diversity of Locked Nucleic Acid-Modified Antisense Oligonucleotides Allows Optimization of Pharmaceutical Properties. Molecular Therapy - Nucleic Acids, 2020, 19, 706-717.	2.3	28

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55	CRISPR/Cas9â€Multiplexed Editing of Chinese Hamster Ovary B4Galâ€T1, 2, 3, and 4 Tailors <i>N</i>â€Glycan Profiles of Therapeutics and Secreted Host Cell Proteins. Biotechnology Journal, 2018, 13, e1800111.	1.8	27
56	A Versatile System for USER Cloning-Based Assembly of Expression Vectors for Mammalian Cell Engineering. PLoS ONE, 2014, 9, e96693.	1.1	26
57	Current state of genome-scale modeling in filamentous fungi. Biotechnology Letters, 2015, 37, 1131-1139.	1.1	25
58	Elucidation of primary metabolic pathways in Aspergillus species: Orphaned research in characterizing orphan genes. Briefings in Functional Genomics, 2014, 13, 451-455.	1.3	24
59	Versatile microscale screening platform for improving recombinant protein productivity in Chinese hamster ovary cells. Scientific Reports, 2015, 5, 18016.	1.6	23
60	Reprogramming AA catabolism in CHO cells with CRISPR/Cas9 genome editing improves cell growth and reduces byproduct secretion. Metabolic Engineering, 2019, 56, 120-129.	3.6	22
61	Identification of a Transcription Factor Controlling pH-Dependent Organic Acid Response in Aspergillus niger. PLoS ONE, 2012, 7, e50596.	1.1	22
62	An Online Compendium of CHO RNAâ€Seq Data Allows Identification of CHO Cell Lineâ€Specific Transcriptomic Signatures. Biotechnology Journal, 2018, 13, e1800070.	1.8	21
63	Aspergillus nidulans Synthesize Insect Juvenile Hormones upon Expression of a Heterologous Regulatory Protein and in Response to Grazing by Drosophila melanogaster Larvae. PLoS ONE, 2013, 8, e73369.	1.1	21
64	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
65	Multiâ€omic profiling Âof EPOâ€producing Chinese hamster ovary cell panel reveals metabolic adaptation to heterologous protein production. Biotechnology and Bioengineering, 2015, 112, 2373-2387.	1.7	20
66	Aspergilli: Models for systems biology in filamentous fungi. Current Opinion in Systems Biology, 2017, 6, 67-73.	1.3	20
67	A community-driven reconstruction of the Aspergillus niger metabolic network. Fungal Biology and Biotechnology, 2018, 5, 16.	2.5	20
68	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
69	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
70	Using Titer and Titer Normalized to Confluence Are Complementary Strategies for Obtaining Chinese Hamster Ovary Cell Lines with High Volumetric Productivity of Etanercept. Biotechnology Journal, 2018, 13, e1700216.	1.8	16
71	Integrated Approaches for Assessment of Cellular Performance in Industrially Relevant Filamentous Fungi. Industrial Biotechnology, 2013, 9, 337-344.	0.5	15
72	Genus level analysis of PKS-NRPS and NRPS-PKS hybrids reveals their origin in Aspergilli. BMC Genomics, 2019, 20, 847.	1.2	15

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73	Novel Centromeric Loci of the Wine and Beer Yeast Dekkera bruxellensis CEN1 and CEN2. PLoS ONE, 2016, 11, e0161741.	1.1	15
74	Pitfalls to avoid when using phage display for snake toxins. Toxicon, 2017, 126, 79-89.	0.8	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.	1.7	13
78	Fed-Batch CHO Cell Culture for Lab-Scale Antibody Production. Methods in Molecular Biology, 2018, 1674, 147-161.	0.4	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.	1.9	8
80	Use of novel cystine analogs to decrease oxidative stress and control product quality. Journal of Biotechnology, 2021, 327, 1-8.	1.9	8
81	Endoplasmic reticulumâ€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
82	Deciphering the signaling mechanisms of the plant cell wall degradation machinery in Aspergillus oryzae. 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.	1.9	5
84	Deep sequencing reveals different compositions of mRNA transcribed from the <i>F8</i> gene in a panel of FVIIIâ€producing CHO cell lines. Biotechnology Journal, 2015, 10, 1081-1089.	1.8	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.	0.4	3
87	Full transcriptome analysis of Chinese Hamster Ovary cell lines producing a dynamic range of Coagulation Factor VIII. BMC Proceedings, 2013, 7, .	1.8	0
88	Supercluster takes a walk on the wild side. Trends in Microbiology, 2013, 21, 617-618.	3.5	0
89	Approaches for Comparative Genomics in Aspergillus and Penicillium. , 2016, , 43-74.		0