

Jens B Nielsen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

932 papers	61,557 citations	114 h-index	212 g-index
1,010 ext. papers	75,588 ext. citations	8.2 avg, IF	8.23 L-index

#	Paper	IF	Citations
932	Proteomics. Tissue-based map of the human proteome. <i>Science</i> , 2015 , 347, 1260-19	33.3	6576
931	Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 397-406	7.6	1730
930	Gut metagenome in European women with normal, impaired and diabetic glucose control. <i>Nature</i> , 2013 , 498, 99-103	50.4	1715
929	Genome sequencing and analysis of the versatile cell factory <i>Aspergillus niger</i> CBS 513.88. <i>Nature Biotechnology</i> , 2007 , 25, 221-31	44.5	889
928	Genome-scale reconstruction of the <i>Saccharomyces cerevisiae</i> metabolic network. <i>Genome Research</i> , 2003 , 13, 244-53	9.7	775
927	A community-driven global reconstruction of human metabolism. <i>Nature Biotechnology</i> , 2013 , 31, 419-25	44.5	746
926	Fuel ethanol production from lignocellulose: a challenge for metabolic engineering and process integration. <i>Applied Microbiology and Biotechnology</i> , 2001 , 56, 17-34	5.7	701
925	Symptomatic atherosclerosis is associated with an altered gut metagenome. <i>Nature Communications</i> , 2012 , 3, 1245	17.4	666
924	Engineering Cellular Metabolism. <i>Cell</i> , 2016 , 164, 1185-1197	56.2	655
923	Enriching the gene set analysis of genome-wide data by incorporating directionality of gene expression and combining statistical hypotheses and methods. <i>Nucleic Acids Research</i> , 2013 , 41, 4378-91	20.1	505
922	Minimum Information about a Biosynthetic Gene cluster. <i>Nature Chemical Biology</i> , 2015 , 11, 625-31	11.7	498
921	Roux-en-Y Gastric Bypass and Vertical Banded Gastroplasty Induce Long-Term Changes on the Human Gut Microbiome Contributing to Fat Mass Regulation. <i>Cell Metabolism</i> , 2015 , 22, 228-38	24.6	489
920	A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology. <i>Nature Biotechnology</i> , 2008 , 26, 1155-60	44.5	471
919	Mass spectrometry in metabolome analysis. <i>Mass Spectrometry Reviews</i> , 2005 , 24, 613-46	11	456
918	Uncovering transcriptional regulation of metabolism by using metabolic network topology. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 2685-9	11.5	445
917	An interlaboratory comparison of physiological and genetic properties of four <i>Saccharomyces cerevisiae</i> strains. <i>Enzyme and Microbial Technology</i> , 2000 , 26, 706-714	3.8	414
916	Voluntary Running Suppresses Tumor Growth through Epinephrine- and IL-6-Dependent NK Cell Mobilization and Redistribution. <i>Cell Metabolism</i> , 2016 , 23, 554-62	24.6	405

915	Global metabolite analysis of yeast: evaluation of sample preparation methods. <i>Yeast</i> , 2005 , 22, 1155-69	3.4	328
914	Genome-scale metabolic modelling of hepatocytes reveals serine deficiency in patients with non-alcoholic fatty liver disease. <i>Nature Communications</i> , 2014 , 5, 3083	17.4	320
913	Evolutionary programming as a platform for in silico metabolic engineering. <i>BMC Bioinformatics</i> , 2005 , 6, 308	3.6	312
912	Metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>Microbiology and Molecular Biology Reviews</i> , 2000 , 64, 34-50	13.2	311
911	Metabolic engineering of <i>Saccharomyces cerevisiae</i> : a key cell factory platform for future biorefineries. <i>Cellular and Molecular Life Sciences</i> , 2012 , 69, 2671-90	10.3	308
910	<i>Saccharomyces cerevisiae</i> phenotypes can be predicted by using constraint-based analysis of a genome-scale reconstructed metabolic network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 13134-9	11.5	304
909	Flux distributions in anaerobic, glucose-limited continuous cultures of <i>Saccharomyces cerevisiae</i> . <i>Microbiology (United Kingdom)</i> , 1997 , 143 (Pt 1), 203-218	2.9	292
908	Assessing the human gut microbiota in metabolic diseases. <i>Diabetes</i> , 2013 , 62, 3341-9	0.9	289
907	Reconstruction of genome-scale active metabolic networks for 69 human cell types and 16 cancer types using INIT. <i>PLoS Computational Biology</i> , 2012 , 8, e1002518	5	289
906	The RAVEN toolbox and its use for generating a genome-scale metabolic model for <i>Penicillium chrysogenum</i> . <i>PLoS Computational Biology</i> , 2013 , 9, e1002980	5	286
905	Network identification and flux quantification in the central metabolism of <i>Saccharomyces cerevisiae</i> under different conditions of glucose repression. <i>Journal of Bacteriology</i> , 2001 , 183, 1441-51	3.5	284
904	Recon3D enables a three-dimensional view of gene variation in human metabolism. <i>Nature Biotechnology</i> , 2018 , 36, 272-281	44.5	283
903	Biofuels. Altered sterol composition renders yeast thermotolerant. <i>Science</i> , 2014 , 346, 75-8	33.3	279
902	In silico aided metabolic engineering of <i>Saccharomyces cerevisiae</i> for improved bioethanol production. <i>Metabolic Engineering</i> , 2006 , 8, 102-11	9.7	276
901	Quantifying Diet-Induced Metabolic Changes of the Human Gut Microbiome. <i>Cell Metabolism</i> , 2015 , 22, 320-31	24.6	275
900	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011 , 21, 885-97	9.7	266
899	Analysis of gut microbial regulation of host gene expression along the length of the gut and regulation of gut microbial ecology through MyD88. <i>Gut</i> , 2012 , 61, 1124-31	19.2	261
898	OptFlux: an open-source software platform for in silico metabolic engineering. <i>BMC Systems Biology</i> , 2010 , 4, 45	3.5	258

897	Metabolic engineering. <i>Applied Microbiology and Biotechnology</i> , 2001 , 55, 263-83	5.7	258
896	Increasing NADH oxidation reduces overflow metabolism in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 2402-7	11.5	250
895	Modeling isotopomer distributions in biochemical networks using isotopomer mapping matrices. <i>Biotechnology and Bioengineering</i> , 1997 , 55, 831-40	4.9	246
894	Metabolic engineering of yeast for production of fuels and chemicals. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 398-404	11.4	231
893	Characterization of different promoters for designing a new expression vector in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2010 , 27, 955-64	3.4	229
892	Identification of anticancer drugs for hepatocellular carcinoma through personalized genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2014 , 10, 721	12.2	223
891	A comprehensive comparison of RNA-Seq-based transcriptome analysis from reads to differential gene expression and cross-comparison with microarrays: a case study in <i>Saccharomyces cerevisiae</i> . <i>Nucleic Acids Research</i> , 2012 , 40, 10084-97	20.1	222
890	Production of fatty acid-derived oleochemicals and biofuels by synthetic yeast cell factories. <i>Nature Communications</i> , 2016 , 7, 11709	17.4	220
889	Establishing a platform cell factory through engineering of yeast acetyl-CoA metabolism. <i>Metabolic Engineering</i> , 2013 , 15, 48-54	9.7	211
888	Isotopomer analysis using GC-MS. <i>Metabolic Engineering</i> , 1999 , 1, 282-90	9.7	200
887	The gut microbiota modulates host amino acid and glutathione metabolism in mice. <i>Molecular Systems Biology</i> , 2015 , 11, 834	12.2	199
886	The metabolic response of heterotrophic <i>Arabidopsis</i> cells to oxidative stress. <i>Plant Physiology</i> , 2007 , 143, 312-25	6.6	199
885	Genome-scale analysis of <i>Streptomyces coelicolor</i> A3(2) metabolism. <i>Genome Research</i> , 2005 , 15, 820-9	9.7	197
884	Production of plant sesquiterpenes in <i>Saccharomyces cerevisiae</i> : effect of ERG9 repression on sesquiterpene biosynthesis. <i>Biotechnology and Bioengineering</i> , 2008 , 99, 666-77	4.9	195
883	Improving the phenotype predictions of a yeast genome-scale metabolic model by incorporating enzymatic constraints. <i>Molecular Systems Biology</i> , 2017 , 13, 935	12.2	193
882	Modeling <i>Lactococcus lactis</i> using a genome-scale flux model. <i>BMC Microbiology</i> , 2005 , 5, 39	4.5	193
881	Reproducibility of oligonucleotide microarray transcriptome analyses. An interlaboratory comparison using chemostat cultures of <i>Saccharomyces cerevisiae</i> . <i>Journal of Biological Chemistry</i> , 2002 , 277, 37001-8	5.4	191
880	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , 2018 , 27, 559-571.e5	24.6	189

879	Enhancing sesquiterpene production in <i>Saccharomyces cerevisiae</i> through in silico driven metabolic engineering. <i>Metabolic Engineering</i> , 2009 , 11, 328-34	9.7	187
878	It is all about metabolic fluxes. <i>Journal of Bacteriology</i> , 2003 , 185, 7031-5	3.5	185
877	De novo production of resveratrol from glucose or ethanol by engineered <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2015 , 32, 1-11	9.7	184
876	Optimization of ethanol production in <i>Saccharomyces cerevisiae</i> by metabolic engineering of the ammonium assimilation. <i>Metabolic Engineering</i> , 2000 , 2, 69-77	9.7	184
875	Kinetic models in industrial biotechnology - Improving cell factory performance. <i>Metabolic Engineering</i> , 2014 , 24, 38-60	9.7	183
874	De novo sequencing, assembly and analysis of the genome of the laboratory strain <i>Saccharomyces cerevisiae</i> CEN.PK113-7D, a model for modern industrial biotechnology. <i>Microbial Cell Factories</i> , 2012 , 11, 36	6.4	183
873	The next wave in metabolome analysis. <i>Trends in Biotechnology</i> , 2005 , 23, 544-6	15.1	182
872	Growth-rate regulated genes have profound impact on interpretation of transcriptome profiling in <i>Saccharomyces cerevisiae</i> . <i>Genome Biology</i> , 2006 , 7, R107	18.3	177
871	Microbial acetyl-CoA metabolism and metabolic engineering. <i>Metabolic Engineering</i> , 2015 , 28, 28-42	9.7	174
870	Dynamic control of gene expression in <i>Saccharomyces cerevisiae</i> engineered for the production of plant sesquiterpene Bantalone in a fed-batch mode. <i>Metabolic Engineering</i> , 2012 , 14, 91-103	9.7	174
869	The Essence of Metabolic Engineering 1998 , 1-20		174
868	Advances in metabolic engineering of yeast <i>Saccharomyces cerevisiae</i> for production of chemicals. <i>Biotechnology Journal</i> , 2014 , 9, 609-20	5.6	171
867	EasyClone: method for iterative chromosomal integration of multiple genes in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2014 , 14, 238-48	3.1	171
866	Characterization of chromosomal integration sites for heterologous gene expression in <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2009 , 26, 545-51	3.4	171
865	Integration of clinical data with a genome-scale metabolic model of the human adipocyte. <i>Molecular Systems Biology</i> , 2013 , 9, 649	12.2	167
864	Integration of gene expression data into genome-scale metabolic models. <i>Metabolic Engineering</i> , 2004 , 6, 285-93	9.7	166
863	Understanding the interactions between bacteria in the human gut through metabolic modeling. <i>Scientific Reports</i> , 2013 , 3, 2532	4.9	165
862	Diversion of flux toward sesquiterpene production in <i>Saccharomyces cerevisiae</i> by fusion of host and heterologous enzymes. <i>Applied and Environmental Microbiology</i> , 2011 , 77, 1033-40	4.8	164

861	Simultaneous analysis of amino and nonamino organic acids as methyl chloroformate derivatives using gas chromatography-mass spectrometry. <i>Analytical Biochemistry</i> , 2003 , 322, 134-8	3.1	161
860	Glucose control in <i>Saccharomyces cerevisiae</i> : the role of Mig1 in metabolic functions. <i>Microbiology (United Kingdom)</i> , 1998 , 144 (Pt 1), 13-24	2.9	161
859	High-throughput screening for industrial enzyme production hosts by droplet microfluidics. <i>Lab on A Chip</i> , 2014 , 14, 806-13	7.2	158
858	Impact of synthetic biology and metabolic engineering on industrial production of fine chemicals. <i>Biotechnology Advances</i> , 2015 , 33, 1395-402	17.8	153
857	Modelling of microbial kinetics. <i>Chemical Engineering Science</i> , 1992 , 47, 4225-4270	4.4	153
856	Improving production of malonyl coenzyme A-derived metabolites by abolishing Snf1-dependent regulation of Acc1. <i>MBio</i> , 2014 , 5, e01130-14	7.8	152
855	Establishment of a yeast platform strain for production of p-coumaric acid through metabolic engineering of aromatic amino acid biosynthesis. <i>Metabolic Engineering</i> , 2015 , 31, 181-8	9.7	151
854	Increasing galactose consumption by <i>Saccharomyces cerevisiae</i> through metabolic engineering of the GAL gene regulatory network. <i>Nature Biotechnology</i> , 2000 , 18, 1283-6	44.5	149
853	Metabolite profiling of fungi and yeast: from phenotype to metabolome by MS and informatics. <i>Journal of Experimental Botany</i> , 2005 , 56, 273-86	7	147
852	Metabolic flux distributions in <i>Penicillium chrysogenum</i> during fed-batch cultivations. <i>Biotechnology and Bioengineering</i> , 1995 , 46, 117-31	4.9	147
851	Advanced biofuel production by the yeast <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 480-8	9.7	146
850	Metabolic model integration of the bibliome, genome, metabolome and reactome of <i>Aspergillus niger</i> . <i>Molecular Systems Biology</i> , 2008 , 4, 178	12.2	144
849	Production of biopharmaceutical proteins by yeast: advances through metabolic engineering. <i>Bioengineered</i> , 2013 , 4, 207-11	5.7	142
848	Quantitative analysis of metabolic fluxes in <i>Escherichia coli</i> , using two-dimensional NMR spectroscopy and complete isotopomer models. <i>Journal of Biotechnology</i> , 1999 , 71, 175-89	3.7	141
847	Lipid engineering combined with systematic metabolic engineering of <i>Saccharomyces cerevisiae</i> for high-yield production of lycopene. <i>Metabolic Engineering</i> , 2019 , 52, 134-142	9.7	139
846	Use of genome-scale microbial models for metabolic engineering. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 64-9	11.4	138
845	In silico genome-scale reconstruction and validation of the <i>Corynebacterium glutamicum</i> metabolic network. <i>Biotechnology and Bioengineering</i> , 2009 , 102, 583-97	4.9	137
844	Mathematical modelling of metabolism. <i>Current Opinion in Biotechnology</i> , 2000 , 11, 180-6	11.4	137

843	Global analysis of biosynthetic gene clusters reveals vast potential of secondary metabolite production in <i>Penicillium</i> species. <i>Nature Microbiology</i> , 2017 , 2, 17044	26.6	136
842	Establishing a synthetic pathway for high-level production of 3-hydroxypropionic acid in <i>Saccharomyces cerevisiae</i> via <i>β</i> -alanine. <i>Metabolic Engineering</i> , 2015 , 27, 57-64	9.7	136
841	Bioreaction Engineering Principles 1994 ,		136
840	Glucose repression in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015 , 15,	3.1	134
839	Linking high-resolution metabolic flux phenotypes and transcriptional regulation in yeast modulated by the global regulator Gcn4p. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 6477-82	11.5	134
838	High-throughput metabolic state analysis: the missing link in integrated functional genomics of yeasts. <i>Biochemical Journal</i> , 2005 , 388, 669-77	3.8	134
837	Metabolic engineering strategies for microbial synthesis of oleochemicals. <i>Metabolic Engineering</i> , 2015 , 29, 1-11	9.7	133
836	Production of natural products through metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>Current Opinion in Biotechnology</i> , 2015 , 35, 7-15	11.4	132
835	Bioreaction Engineering Principles 2011 ,		132
834	The genome-scale metabolic model iIN800 of <i>Saccharomyces cerevisiae</i> and its validation: a scaffold to query lipid metabolism. <i>BMC Systems Biology</i> , 2008 , 2, 71	3.5	129
833	Reprogramming Yeast Metabolism from Alcoholic Fermentation to Lipogenesis. <i>Cell</i> , 2018 , 174, 1549-1558	58.2	128
832	Metabolic engineering of recombinant protein secretion by <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2012 , 12, 491-510	3.1	128
831	Sampling the solution space in genome-scale metabolic networks reveals transcriptional regulation in key enzymes. <i>PLoS Computational Biology</i> , 2010 , 6, e1000859	5	127
830	Engineering synergy in biotechnology. <i>Nature Chemical Biology</i> , 2014 , 10, 319-22	11.7	126
829	The role of biofuels in the future energy supply. <i>Energy and Environmental Science</i> , 2013 , 6, 1077	35.4	125
828	Industrial systems biology of <i>Saccharomyces cerevisiae</i> enables novel succinic acid cell factory. <i>PLoS ONE</i> , 2013 , 8, e54144	3.7	125
827	Large-scale evaluation of in silico gene deletions in <i>Saccharomyces cerevisiae</i> . <i>OMICS A Journal of Integrative Biology</i> , 2003 , 7, 193-202	3.8	125
826	Systems biology of antibiotic production by microorganisms. <i>Natural Product Reports</i> , 2007 , 24, 1262-87	15.1	123

825	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-276	44.5	121
824	Anaerobic and aerobic batch cultivations of <i>Saccharomyces cerevisiae</i> mutants impaired in glycerol synthesis. <i>Yeast</i> , 2000 , 16, 463-74	3.4	119
823	Measuring enzyme activities under standardized in vivo-like conditions for systems biology. <i>FEBS Journal</i> , 2010 , 277, 749-60	5.7	115
822	Industrial systems biology. <i>Biotechnology and Bioengineering</i> , 2010 , 105, 439-60	4.9	115
821	Antibiotic overproduction in <i>Streptomyces coelicolor</i> A3 2 mediated by phosphofructokinase deletion. <i>Journal of Biological Chemistry</i> , 2008 , 283, 25186-25199	5.4	115
820	Synergies between synthetic biology and metabolic engineering. <i>Nature Biotechnology</i> , 2011 , 29, 693-5	44.5	114
819	Unravelling evolutionary strategies of yeast for improving galactose utilization through integrated systems level analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12179-84	11.5	114
818	Harnessing Yeast Peroxisomes for Biosynthesis of Fatty-Acid-Derived Biofuels and Chemicals with Relieved Side-Pathway Competition. <i>Journal of the American Chemical Society</i> , 2016 , 138, 15368-15377	16.4	113
817	Enhancement of farnesyl diphosphate pool as direct precursor of sesquiterpenes through metabolic engineering of the mevalonate pathway in <i>Saccharomyces cerevisiae</i> . <i>Biotechnology and Bioengineering</i> , 2010 , 106, 86-96	4.9	113
816	Bioreaction Engineering Principles 2003 ,		113
815	On-line and in situ monitoring of biomass in submerged cultivations. <i>Trends in Biotechnology</i> , 1997 , 15, 517-522	15.1	111
814	Impact of systems biology on metabolic engineering of <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2008 , 8, 122-31	3.1	110
813	Integration of metabolome data with metabolic networks reveals reporter reactions. <i>Molecular Systems Biology</i> , 2006 , 2, 50	12.2	110
812	RAVEN 2.0: A versatile toolbox for metabolic network reconstruction and a case study on <i>Streptomyces coelicolor</i> . <i>PLoS Computational Biology</i> , 2018 , 14, e1006541	5	110
811	Combined metabolic engineering of precursor and co-factor supply to increase Santalene production by <i>Saccharomyces cerevisiae</i> . <i>Microbial Cell Factories</i> , 2012 , 11, 117	6.4	108
810	Morphology and physiology of an alpha-amylase producing strain of <i>Aspergillus oryzae</i> during batch cultivations. <i>Biotechnology and Bioengineering</i> , 1996 , 49, 266-76	4.9	108
809	Absolute Quantification of Protein and mRNA Abundances Demonstrate Variability in Gene-Specific Translation Efficiency in Yeast. <i>Cell Systems</i> , 2017 , 4, 495-504.e5	10.6	106
808	Regulation of amino-acid metabolism controls flux to lipid accumulation in. <i>Npj Systems Biology and Applications</i> , 2016 , 2, 16005	5	106

807	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 Suppl 1, S161-S169	3.9	106
806	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, 4387-92	11.5	106
805	Systems Biology of Metabolism. <i>Annual Review of Biochemistry</i> , 2017 , 86, 245-275	29.1	105
804	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016 , 24, 172-84	24.6	105
803	Biobased organic acids production by metabolically engineered microorganisms. <i>Current Opinion in Biotechnology</i> , 2016 , 37, 165-172	11.4	105
802	Architecture of transcriptional regulatory circuits is knitted over the topology of bio-molecular interaction networks. <i>BMC Systems Biology</i> , 2008 , 2, 17	3.5	104
801	Pellet formation and fragmentation in submerged cultures of <i>Penicillium chrysogenum</i> and its relation to penicillin production. <i>Biotechnology Progress</i> , 1995 , 11, 93-8	2.8	104
800	Rapid quantification of yeast lipid using microwave-assisted total lipid extraction and HPLC-CAD. <i>Analytical Chemistry</i> , 2013 , 85, 4912-9	7.8	102
799	Molecular basis for mycophenolic acid biosynthesis in <i>Penicillium brevicompactum</i> . <i>Applied and Environmental Microbiology</i> , 2011 , 77, 3035-43	4.8	102
798	Improvement of galactose uptake in <i>Saccharomyces cerevisiae</i> through overexpression of phosphoglucotransferase: example of transcript analysis as a tool in inverse metabolic engineering. <i>Applied and Environmental Microbiology</i> , 2005 , 71, 6465-72	4.8	102
797	Improved production of fatty acid ethyl esters in <i>Saccharomyces cerevisiae</i> through up-regulation of the ethanol degradation pathway and expression of the heterologous phosphoketolase pathway. <i>Microbial Cell Factories</i> , 2014 , 13, 39	6.4	101
796	Systems medicine and metabolic modelling. <i>Journal of Internal Medicine</i> , 2012 , 271, 142-54	10.8	101
795	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. <i>Nature</i> , 2020 , 581, 310-315	5.4	100
794	Coupled incremental precursor and co-factor supply improves 3-hydroxypropionic acid production in <i>Saccharomyces cerevisiae</i> . <i>Metabolic Engineering</i> , 2014 , 22, 104-9	9.7	100
793	Metabolic engineering: techniques for analysis of targets for genetic manipulations. <i>Biotechnology and Bioengineering</i> , 1998 , 58, 125-32	4.9	100
792	Expression of a cytoplasmic transhydrogenase in <i>Saccharomyces cerevisiae</i> results in formation of 2-oxoglutarate due to depletion of the NADPH pool. <i>Yeast</i> , 2001 , 18, 19-32	3.4	100
791	Microfluidic screening and whole-genome sequencing identifies mutations associated with improved protein secretion by yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4689-96	11.5	99
790	Metabolic footprinting in microbiology: methods and applications in functional genomics and biotechnology. <i>Trends in Biotechnology</i> , 2008 , 26, 490-7	15.1	99

789	Metabolic engineering of beta-lactam production. <i>Metabolic Engineering</i> , 2003 , 5, 56-69	9.7	99
788	The human secretome. <i>Science Signaling</i> , 2019 , 12,	8.8	99
787	Systems Biology of Metabolism: A Driver for Developing Personalized and Precision Medicine. <i>Cell Metabolism</i> , 2017 , 25, 572-579	24.6	98
786	DCEO Biotechnology: Tools To Design, Construct, Evaluate, and Optimize the Metabolic Pathway for Biosynthesis of Chemicals. <i>Chemical Reviews</i> , 2018 , 118, 4-72	68.1	97
785	Human gut microbiota and healthy aging: Recent developments and future prospective. <i>Nutrition and Healthy Aging</i> , 2016 , 4, 3-16	1.3	97
784	Succinate dehydrogenase inhibition leads to epithelial-mesenchymal transition and reprogrammed carbon metabolism. <i>Cancer & Metabolism</i> , 2014 , 2, 21	5.4	97
783	Fifteen years of large scale metabolic modeling of yeast: developments and impacts. <i>Biotechnology Advances</i> , 2012 , 30, 979-88	17.8	97
782	Metabolic network analysis of penicillium chrysogenum using 13c-labeled glucose 2000 , 68, 652-659		97
781	Barriers and opportunities in bio-based production of hydrocarbons. <i>Nature Energy</i> , 2018 , 3, 925-935	62.3	96
780	Chromosome 3p loss of heterozygosity is associated with a unique metabolic network in clear cell renal carcinoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E866-75	11.5	96
779	Mapping the interaction of Snf1 with TORC1 in <i>Saccharomyces cerevisiae</i> . <i>Molecular Systems Biology</i> , 2011 , 7, 545	12.2	95
778	Transcriptomics resources of human tissues and organs. <i>Molecular Systems Biology</i> , 2016 , 12, 862	12.2	95
777	Third-generation biorefineries as the means to produce fuels and chemicals from CO ₂ . <i>Nature Catalysis</i> , 2020 , 3, 274-288	36.5	94
776	Advances in metabolic pathway and strain engineering paving the way for sustainable production of chemical building blocks. <i>Current Opinion in Biotechnology</i> , 2013 , 24, 965-72	11.4	94
775	Characterization of global yeast quantitative proteome data generated from the wild-type and glucose repression <i>saccharomyces cerevisiae</i> strains: the comparison of two quantitative methods. <i>Journal of Proteome Research</i> , 2008 , 7, 266-75	5.6	94
774	Genome-scale metabolic reconstructions of <i>Pichia stipitis</i> and <i>Pichia pastoris</i> and in silico evaluation of their potentials. <i>BMC Systems Biology</i> , 2012 , 6, 24	3.5	93
773	Personal model-assisted identification of NAD and glutathione metabolism as intervention target in NAFLD. <i>Molecular Systems Biology</i> , 2017 , 13, 916	12.2	92
772	Engineering yeast for high-level production of stilbenoid antioxidants. <i>Scientific Reports</i> , 2016 , 6, 36827	4.9	92

771	Metabolic engineering of <i>Saccharomyces cerevisiae</i> for production of fatty acid ethyl esters, an advanced biofuel, by eliminating non-essential fatty acid utilization pathways. <i>Applied Energy</i> , 2014 , 115, 226-232	10.7	92
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