Walter Martin van Gulik

List of Publications by Year
in descending order

109 papers	5,878 citations	61984 43 h-index	79698 73 g-index
111 all docs	111 docs citations	111 times ranked	4946 citing authors

#	Article	IF	Citations
1	Influence of oxygen concentration on the metabolism of <i>Penicillium chrysogenum</i>. Engineering in Life Sciences, 2023, 23, .	3.6	2
2	Fast Sampling of the Cellular Metabolome. Methods in Molecular Biology, 2022, 2349, 11-39.	0.9	0
3	Pathway engineering strategies for improved product yield in yeast-based industrial ethanol production. Synthetic and Systems Biotechnology, 2022, 7, 554-566.	3.7	21
4	Monitoring Intracellular Metabolite Dynamics in Saccharomyces cerevisiae during Industrially Relevant Famine Stimuli. Metabolites, 2022, 12, 263.	2.9	5
5	Genome-wide effect of non-optimal temperatures under anaerobic conditions on gene expression in Saccharomyces cerevisiae. Genomics, 2022, 114, 110386.	2.9	5
6	Continuous production of enzymes under carbon-limited conditions by Trichoderma harzianum P49P11. Fungal Biology, 2021, 125, 177-183.	2.5	4
7	Uncoupling growth and succinic acid production in an industrial <i>Saccharomyces cerevisiae</i> strain. Biotechnology and Bioengineering, 2021, 118, 1557-1567.	3.3	12
8	A possible influence of extracellular polysaccharides on the analysis of intracellular metabolites from Trichoderma harzianum grown under carbon-limited conditions. Fungal Biology, 2021, 125, 368-377.	2.5	4
9	Fedâ€Batch Droplet Nanobioreactor for Controlled Growth of Cyberlindnera (Pichia) jadinii : A Proofâ€Ofâ€Concept Demonstration. Advanced Materials Technologies, 2021, 6, 2100083.	5.8	1
10	Co-fermentation of sugarcane bagasse hydrolysate and molasses by Clostridium saccharoperbutylacetonicum: Effect on sugar consumption and butanol production. Industrial Crops and Products, 2021, 167, 113512.	5.2	11
11	Physiological responses of Saccharomyces cerevisiae to industrially relevant conditions: Slow growth, low pH, and high CO 2 levels. Biotechnology and Bioengineering, 2020, 117, 721-735.	3.3	15
12	Mathematical modelling for the optimization of cellulase production using glycerol for cell growth and cellulose as the inducer substrate. Chemical Engineering Science: X, 2020, 8, 100085.	1.5	3
13	Analysis of the proteins secreted by Trichoderma harzianum P49P11 under carbon-limited conditions. Journal of Proteomics, 2020, 227, 103922.	2.4	3
14	Selection and subsequent physiological characterization of industrial Saccharomyces cerevisiae strains during continuous growth at sub- and- supra optimal temperatures. Biotechnology Reports (Amsterdam, Netherlands), 2020, 26, e00462.	4.4	19
15	Dynamics in redox metabolism, from stoichiometry towards kinetics. Current Opinion in Biotechnology, 2020, 64, 116-123.	6.6	9
16	Scalable microfluidic droplet on-demand generator for non-steady operation of droplet-based assays. Lab on A Chip, 2020, 20, 1398-1409.	6.0	8
17	Differential proteomic analysis by SWATH-MS unravels the most dominant mechanisms underlying yeast adaptation to non-optimal temperatures under anaerobic conditions. Scientific Reports, 2020, 10, 22329.	3.3	22
18	Quantitative Physiology of Non-Energy-Limited Retentostat Cultures of Saccharomyces cerevisiae at Near-Zero Specific Growth Rates. Applied and Environmental Microbiology, 2019, 85, .	3.1	12

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19	Comparative Fluxome and Metabolome Analysis of Formate as an Auxiliary Substrate for Penicillin Production in Glucoseâ€Limited Cultivation of Penicillium chrysogenum. Biotechnology Journal, 2019, 14, 1900009.	3.5	5
20	A dynamic model-based preparation of uniformly-13C-labeled internal standards facilitates quantitative metabolomics analysis of Penicillium chrysogenum. Journal of Biotechnology, 2019, 299, 21-31.	3.8	14
21	Comparative performance of different scaleâ€down simulators of substrate gradients in <i>Penicillium chrysogenum</i> cultures: the need of a biological systems response analysis. Microbial Biotechnology, 2018, 11, 486-497.	4.2	27
22	Computational fluid dynamics simulation of an industrial P. chrysogenum fermentation with a coupled 9-pool metabolic model: Towards rational scale-down and design optimization. Chemical Engineering Science, 2018, 175, 12-24.	3.8	72
23	Power input effects on degeneration in prolonged penicillin chemostat cultures: A systems analysis at flux, residual glucose, metabolite, and transcript levels. Biotechnology and Bioengineering, 2018, 115, 114-125.	3.3	17
24	Stoichiometry and kinetics of single and mixed substrate uptake in Aspergillus niger. Bioprocess and Biosystems Engineering, 2018, 41, 157-170.	3.4	7
25	A 9â€pool metabolic structured kinetic model describing days to seconds dynamics of growth and product formation by <i>Penicillium chrysogenum</i>. Biotechnology and Bioengineering, 2017, 114, 1733-1743.	3.3	41
26	Bioprocess scaleâ€up/down as integrative enabling technology: from fluid mechanics to systems biology and beyond. Microbial Biotechnology, 2017, 10, 1267-1274.	4.2	55
27	Intracellular product recycling in high succinic acid producing yeast at low pH. Microbial Cell Factories, 2017, 16, 90.	4.0	15
28	Transport and metabolism of fumaric acid in <i>Saccharomyces cerevisiae</i> in aerobic glucoseâ€limited chemostat culture. Yeast, 2016, 33, 145-161.	1.7	4
29	Comparative fluxome and metabolome analysis for overproduction of succinate in <i>Escherichia coli</i>. Biotechnology and Bioengineering, 2016, 113, 817-829.	3.3	12
30	Determination of the<i>in vivo</i>NAD:NADH ratio in<i>Saccharomyces cerevisiae</i>under anaerobic conditions, using alcohol dehydrogenase as sensor reaction. Yeast, 2015, 32, 541-557.	1.7	24
31	Growth-rate dependency of de novo resveratrol production in chemostat cultures of an engineered Saccharomyces cerevisiae strain. Microbial Cell Factories, 2015, 14, 133.	4.0	26
32	Integration of microbial kinetics and fluid dynamics toward modelâ€driven scaleâ€up of industrial bioprocesses. Engineering in Life Sciences, 2015, 15, 20-29.	3.6	71
33	Development of tools for quantitative intracellular metabolomics of Aspergillus niger chemostat cultures. Metabolomics, 2015, 11, 1253-1264.	3.0	24
34	In vivo kinetic analysis of the penicillin biosynthesis pathway using PAA stimulus response experiments. Metabolic Engineering, 2015, 32, 155-173.	7.0	12
35	Flux response of glycolysis and storage metabolism during rapid feast/famine conditions in <i>Penicillium chrysogenum</i> using dynamic ¹³C labeling. Biotechnology Journal, 2014, 9, 372-385.	3.5	36
36	Reconstruction of the oxygen uptake and carbon dioxide evolution rates of microbial cultures at near-neutral pH during highly dynamic conditions. Biochemical Engineering Journal, 2014, 83, 42-54.	3.6	11

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37	Towards large scale fermentative production of succinic acid. Current Opinion in Biotechnology, 2014, 30, 190-197.	6.6	196
38	Longâ€term adaptation of <i>Saccharomyces cerevisiae</i> to the burden of recombinant insulin production. Biotechnology and Bioengineering, 2013, 110, 2749-2763.	3.3	29
39	Quantitative analysis of intracellular coenzymes in Saccharomyces cerevisiae using ion pair reversed phase ultra high performance liquid chromatography tandem mass spectrometry. Journal of Chromatography A, 2013, 1311, 115-120.	3.7	52
40	Changes in substrate availability in Escherichia coli lead to rapid metabolite, flux and growth rate responses. Metabolic Engineering, 2013, 16, 115-129.	7.0	35
41	Atypical Glycolysis in Clostridium thermocellum. Applied and Environmental Microbiology, 2013, 79, 3000-3008.	3.1	92
42	pH-Dependent Uptake of Fumaric Acid in Saccharomyces cerevisiae under Anaerobic Conditions. Applied and Environmental Microbiology, 2012, 78, 705-716.	3.1	23
43	Fast Sampling of the Cellular Metabolome. Methods in Molecular Biology, 2012, 881, 279-306.	0.9	28
44	Quantitative metabolomics analysis of amino acid metabolism in recombinant Pichia pastoris under different oxygen availability conditions. Microbial Cell Factories, 2012, 11, 83.	4.0	36
45	Identification of informative metabolic responses using a minibioreactor: a small step change in the glucose supply rate creates a large metabolic response in <i>Saccharomyces cerevisiae</i>. Yeast, 2012, 29, 95-110.	1.7	8
46	Novel insights in transport mechanisms and kinetics of phenylacetic acid and penicillinâ€G in <i>Penicillium chrysogenum</i>. Biotechnology Progress, 2012, 28, 337-348.	2.6	21
47	Development of quantitative metabolomics for Pichia pastoris. Metabolomics, 2012, 8, 284-298.	3.0	45
48	Optimization of cold methanol quenching for quantitative metabolomics of Penicillium chrysogenum. Metabolomics, 2012, 8, 727-735.	3.0	63
49	Determination of Î´â€[<scp>L</scp>â€Î±â€aminoadipyl]â€<scp>L</scp>â€cysteinylâ€<scp>D</scp>â€valine in cell extracts of Penicillium chrysogenum using ion pairâ€RPâ€UPLCâ€MS/MS. Journal of Separation Science, 2012, 35, 225-230.	2.5	4
50	Scaleâ€down of penicillin production in <i>Penicillium chrysogenum</i>. Biotechnology Journal, 2011, 6, 944-958.	3.5	80
51	Cytosolic NADPH balancing in Penicillium chrysogenum cultivated on mixtures of glucose and ethanol. Applied Microbiology and Biotechnology, 2011, 89, 63-72.	3.6	9
52	Degeneration of penicillin production in ethanol-limited chemostat cultivations of Penicillium chrysogenum: A systems biology approach. BMC Systems Biology, 2011, 5, 132.	3.0	27
53	Development of a low pH fermentation strategy for fumaric acid production by Rhizopus oryzae. Enzyme and Microbial Technology, 2011, 48, 39-47.	3.2	77
54	An in vivo data-driven framework for classification and quantification of enzyme kinetics and determination of apparent thermodynamic data. Metabolic Engineering, 2011, 13, 294-306.	7.0	93

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55	Escherichia coli responds with a rapid and large change in growth rate upon a shift from glucose-limited to glucose-excess conditions. Metabolic Engineering, 2011, 13, 307-318.	7.0	45
56	Aerobic batch cultivation in micro bioreactor with integrated electrochemical sensor array. Biotechnology Progress, 2010, 26, 293-300.	2.6	12
57	Fast sampling for quantitative microbial metabolomics. Current Opinion in Biotechnology, 2010, 21, 27-34.	6.6	105
58	Dynamic gene expression regulation model for growth and penicillin production in <i>Penicillium chrysogenum</i>. Biotechnology and Bioengineering, 2010, 106, 608-618.	3.3	49
59	Intracellular metabolite determination in the presence of extracellular abundance: Application to the penicillin biosynthesis pathway in <i>Penicillium chrysogenum</i>. Biotechnology and Bioengineering, 2010, 107, 105-115.	3.3	56
60	Genomeâ€derived minimal metabolic models for <i>Escherichia coli</i> MG1655 with estimated in vivo respiratory ATP stoichiometry. Biotechnology and Bioengineering, 2010, 107, 369-381.	3.3	85
61	Catching prompt metabolite dynamics in Escherichia coli with the BioScope at oxygen rich conditions. Metabolic Engineering, 2010, 12, 477-487.	7.0	30
62	Measuring enzyme activities under standardized <i>inâ€ƒvivo</i>â€like conditions for systems biology. FEBS Journal, 2010, 277, 749-760.	4.7	147
63	Fast dynamic response of the fermentative metabolism of <i>Escherichia coli</i> to aerobic and anaerobic glucose pulses. Biotechnology and Bioengineering, 2009, 104, 1153-1161.	3.3	65
64	Development of a system for the onâ€line measurement of carbon dioxide production in microbioreactors: Application to aerobic batch cultivations of <i>Candida utilis</i>. Biotechnology Progress, 2009, 25, 892-897.	2.6	12
65	Quantitative determination of glucose transfer between cocurrent laminar water streams in a Hâ€shaped microchannel. Biotechnology Progress, 2009, 25, 1826-1832.	2.6	5
66	A system for accurate on-line measurement of total gas consumption or production rates in microbioreactors. Chemical Engineering Science, 2009, 64, 455-458.	3.8	10
67	The Hagenâ€"Poiseuille pump for parallel fed-batch cultivations in microbioreactors. Chemical Engineering Science, 2009, 64, 1877-1884.	3.8	7
68	Development and application of a differential method for reliable metabolome analysis in Escherichia coli. Analytical Biochemistry, 2009, 386, 9-19.	2.4	145
69	Simultaneous quantification of free nucleotides in complex biological samples using ion pair reversed phase liquid chromatography isotope dilution tandem mass spectrometry. Analytical Biochemistry, 2009, 388, 213-219.	2.4	83
70	Conceptual Process Design of Integrated Fermentation, Deacylation, and Crystallization in the Production of Î²-Lactam Antibiotics. Industrial & Engineering Chemistry Research, 2009, 48, 4352-4364.	3.7	7
71	Quantitative Evaluation of Intracellular Metabolite Extraction Techniques for Yeast Metabolomics. Analytical Chemistry, 2009, 81, 7379-7389.	6.5	309
72	An Engineered Yeast Efficiently Secreting Penicillin. PLoS ONE, 2009, 4, e8317.	2.5	73

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73	Leakage-free rapid quenching technique for yeast metabolomics. Metabolomics, 2008, 4, 226-239.	3.0	210
74	Fumaric acid production by fermentation. Applied Microbiology and Biotechnology, 2008, 78, 379-389.	3.6	300
75	Labâ€scale fermentation tests of microchip with integrated electrochemical sensors for pH, temperature, dissolved oxygen and viable biomass concentration. Biotechnology and Bioengineering, 2008, 99, 884-892.	3.3	56
76	Determination of the cytosolic free NAD/NADH ratio in <i>Saccharomyces cerevisiae</i> under steadyâ€state and highly dynamic conditions. Biotechnology and Bioengineering, 2008, 100, 734-743.	3.3	109
77	Quantitative analysis of metabolites in complex biological samples using ion-pair reversed-phase liquid chromatographyâ€“isotope dilution tandem mass spectrometry. Journal of Chromatography A, 2008, 1187, 103-110.	3.7	38
78	A metabolome study of the steady-state relation between central metabolism, amino acid biosynthesis and penicillin production in Penicillium chrysogenum. Metabolic Engineering, 2008, 10, 10-23.	7.0	69
79	Isotopic non-stationary 13C gluconate tracer method for accurate determination of the pentose phosphate pathway split-ratio in Penicillium chrysogenum. Metabolic Engineering, 2008, 10, 178-186.	7.0	31
80	Dynamics of Glycolytic Regulation during Adaptation of <i>Saccharomyces cerevisiae</i> to Fermentative Metabolism. Applied and Environmental Microbiology, 2008, 74, 5710-5723.	3.1	74
81	Quantitative Analysis of the High Temperature-induced Glycolytic Flux Increase in Saccharomyces cerevisiae Reveals Dominant Metabolic Regulation. Journal of Biological Chemistry, 2008, 283, 23524-23532.	3.4	65
82	Control of the Glycolytic Flux in Saccharomyces cerevisiae Grown at Low Temperature. Journal of Biological Chemistry, 2007, 282, 10243-10251.	3.4	59
83	Formate as an Auxiliary Substrate for Glucose-Limited Cultivation of Penicillium chrysogenum : Impact on Penicillin G Production and Biomass Yield. Applied and Environmental Microbiology, 2007, 73, 5020-5025.	3.1	34
84	The fluxes through glycolytic enzymes in <i>Saccharomyces cerevisiae</i> are predominantly regulated at posttranscriptional levels. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15753-15758.	7.1	223
85	Cytosolic NADPH metabolism in penicillin-G producing and non-producing chemostat cultures of Penicillium chrysogenum. Metabolic Engineering, 2007, 9, 112-123.	7.0	48
86	Metabolome dynamic responses of Saccharomyces cerevisiae to simultaneous rapid perturbations in external electron acceptor and electron donor. FEMS Yeast Research, 2007, 7, 48-66.	2.3	36
87	13C-Labeled metabolic flux analysis of a fed-batch culture of elutriatedSaccharomyces cerevisiae. FEMS Yeast Research, 2007, 7, 511-526.	2.3	34
88	Enzymic analysis of NADPH metabolism in Î²-lactam-producing Penicillium chrysogenum: Presence of a mitochondrial NADPH dehydrogenase. Metabolic Engineering, 2006, 8, 91-101.	7.0	42
89	In vivo kinetics of primary metabolism in Saccharomyces cerevisiae studied through prolonged chemostat cultivation. Metabolic Engineering, 2006, 8, 160-171.	7.0	31
90	In vivo kinetics with rapid perturbation experiments in Saccharomyces cerevisiae using a second-generation BioScope. Metabolic Engineering, 2006, 8, 370-383.	7.0	81

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91	Characterization of an experimental miniature bioreactor for cellular perturbation studies. Biotechnology and Bioengineering, 2006, 95, 1032-1042.	3.3	17
92	13 C-Labeled Gluconate Tracing as a Direct and Accurate Method for Determining the Pentose Phosphate Pathway Split Ratio in Penicillium chrysogenum. Applied and Environmental Microbiology, 2006, 72, 4743-4754.	3.1	37
93	Short-Term Metabolome Dynamics and Carbon, Electron, and ATP Balances in Chemostat-Grown Saccharomyces cerevisiae CEN.PK 113-7D following a Glucose Pulse. Applied and Environmental Microbiology, 2006, 72, 3566-3577.	3.1	61
94	Changes in the metabolome of associated with evolution in aerobic glucose-limited chemostats. FEMS Yeast Research, 2005, 5, 419-430.	2.3	80
95	Application of metabolome data in functional genomics: A conceptual strategy. Metabolic Engineering, 2005, 7, 302-310.	7.0	17
96	Quantitative analysis of the microbial metabolome by isotope dilution mass spectrometry using uniformly 13C-labeled cell extracts as internal standards. Analytical Biochemistry, 2005, 336, 164-171.	2.4	375
97	Metabolic-flux analysis of CEN.PK113-7D based on mass isotopomer measurements of C-labeled primary metabolites. FEMS Yeast Research, 2005, 5, 559-568.	2.3	137
98	Revisiting the 13C-label distribution of the non-oxidative branch of the pentose phosphate pathway based upon kinetic and genetic evidence. FEBS Journal, 2005, 272, 4970-4982.	4.7	56
99	Role of Transcriptional Regulation in Controlling Fluxes in Central Carbon Metabolism of Saccharomyces cerevisiae. Journal of Biological Chemistry, 2004, 279, 9125-9138.	3.4	264
100	A new framework for the estimation of control parameters in metabolic pathways using lin-log kinetics. FEBS Journal, 2004, 271, 3348-3359.	0.2	65
101	Analysis of in vivo kinetics of glycolysis in aerobicSaccharomyces cerevisiaeby application of glucose and ethanol pulses. Biotechnology and Bioengineering, 2004, 88, 157-167.	3.3	85
102	Metabolic flux and metabolic network analysis ofPenicillium chrysogenum using 2D [13C,1H] COSY NMR measurements and cumulative bondomer simulation. Biotechnology and Bioengineering, 2003, 83, 75-92.	3.3	36
103	Rapid sampling for analysis of in vivo kinetics using the BioScope: A system for continuous-pulse experiments. Biotechnology and Bioengineering, 2002, 79, 674-681.	3.3	102
104	The coupling between catabolism and anabolism of Methanobacterium thermoautotrophicum in H2- and iron-limited continuous cultures. Enzyme and Microbial Technology, 1999, 25, 784-794.	3.2	16
105	Validation of a Metabolic Network for Saccharomyces cerevisiae Using Mixed Substrate Studies. Biotechnology Progress, 1996, 12, 434-448.	2.6	63
106	Ajmalicine production by cell cultures of Catharanthus roseus: from shake flask to bioreactor. Plant Cell, Tissue and Organ Culture, 1994, 38, 85-91.	2.3	36
107	Effects of carbon dioxide, air flow rate, and inoculation density on the batch growth of Catharanthus roseus cell suspensions in stirred fermentors. Biotechnology Progress, 1994, 10, 335-339.	2.6	18
108	Induction of ajmalicine formation and related enzyme activities in Catharanthus roseus cells: effect of inoculum density. Applied Microbiology and Biotechnology, 1993, 39, 42-47.	3.6	50

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109	Chapter 1 Plant Biotechnology for the Production of Alkaloids: Present Status and Prospects. Alkaloids: Chemistry and Pharmacology, 1991, 40, 1-187.	0.2	24