Barbara M Bakker

List of Publications by Year
in descending order

76 papers	8,352 citations	136740 32 h-index	79541 73 g-index
82 all docs	82 docs citations	82 times ranked	12444 citing authors

#	Article	IF	Citations
1	Pyruvate Dehydrogenase Kinase Inhibition by Dichloroacetate in Melanoma Cells Unveils Metabolic Vulnerabilities. International Journal of Molecular Sciences, 2022, 23, 3745.	1.8	6
2	Inhibition of the succinyl dehydrogenase complex in acute myeloid leukemia leads to a lactate-fuelled respiratory metabolic vulnerability. Nature Communications, 2022, 13, 2013.	5.8	22
3	Full humanization of the glycolytic pathway in Saccharomyces cerevisiae. Cell Reports, 2022, 39, 111010.	2.9	13
4	Butyrate oxidation attenuates the butyrate-induced improvement of insulin sensitivity in myotubes. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2022, 1868, 166476.	1.8	3
5	Shortâ€term protein restriction at advanced age stimulates FGF21 signalling, energy expenditure and browning of white adipose tissue. FEBS Journal, 2021, 288, 2257-2277.	2.2	18
6	A toolbox for the comprehensive analysis of small volume human intestinal samples that can be used with gastrointestinal sampling capsules. Scientific Reports, 2021, 11, 8133.	1.6	9
7	Simultaneous Quantification of the Concentration and Carbon Isotopologue Distribution of Polar Metabolites in a Single Analysis by Gas Chromatography and Mass Spectrometry. Analytical Chemistry, 2021, 93, 8248-8256.	3.2	11
8	Age-related susceptibility to insulin resistance arises from a combination of CPT1B decline and lipid overload. BMC Biology, 2021, 19, 154.	1.7	12
9	Bistability in fatty-acid oxidation resulting from substrate inhibition. PLoS Computational Biology, 2021, 17, e1009259.	1.5	4
10	The Effects of Butyrate on Induced Metabolic-Associated Fatty Liver Disease in Precision-Cut Liver Slices. Nutrients, 2021, 13, 4203.	1.7	10
11	Simultaneous Induction of Glycolysis and Oxidative Phosphorylation during Activation of Hepatic Stellate Cells Reveals Novel Mitochondrial Targets to Treat Liver Fibrosis. Cells, 2020, 9, 2456.	1.8	25
12	Quantitative analysis of amino acid metabolism in liver cancer links glutamate excretion to nucleotide synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 10294-10304.	3.3	45
13	Fibroblastâ€specific genomeâ€scale modelling predicts an imbalance in amino acid metabolism in Refsum disease. FEBS Journal, 2020, 287, 5096-5113.	2.2	8
14	SK channel-mediated metabolic escape to glycolysis inhibits ferroptosis and supports stress resistance in C. elegans. Cell Death and Disease, 2020, 11, 263.	2.7	34
15	Transcriptome analysis suggests a compensatory role of the cofactors coenzyme A and NAD+ in medium-chain acyl-CoA dehydrogenase knockout mice. Scientific Reports, 2019, 9, 14539.	1.6	3
16	Renal temperature reduction progressively favors mitochondrial ROS production over respiration in hypothermic kidney preservation. Journal of Translational Medicine, 2019, 17, 265.	1.8	38
17	CoAâ€dependent activation of mitochondrial acyl carrier protein links four neurodegenerative diseases. EMBO Molecular Medicine, 2019, 11, e10488.	3.3	46
18	Cofactors revisited â€" Predicting the impact of flavoprotein-related diseases on a genome scale. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2019, 1865, 360-370.	1.8	10

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19	A Proinflammatory Gut Microbiota Increases Systemic Inflammation and Accelerates Atherosclerosis. Circulation Research, 2019, 124, 94-100.	2.0	226
20	Targeted Proteomics to Study Mitochondrial Biology. Advances in Experimental Medicine and Biology, 2019, 1158, 101-117.	0.8	1
21	Running wheel access fails to resolve impaired sustainable health in mice feeding a high fat sucrose diet. Aging, 2019, 11, 1564-1579.	1.4	2
22	STRENDA DB: enabling the validation and sharing of enzyme kinetics data. FEBS Journal, 2018, 285, 2193-2204.	2.2	38
23	Runningâ€wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a postâ€transcriptional mechanism. Aging Cell, 2018, 17, e12700.	3.0	31
24	Targeting pathogen metabolism without collateral damage to the host. Scientific Reports, 2017, 7, 40406.	1.6	42
25	SK2 channels regulate mitochondrial respiration and mitochondrial Ca2+ uptake. Cell Death and Differentiation, 2017, 24, 761-773.	5.0	48
26	Male apoE*3-Leiden.CETP mice on high-fat high-cholesterol diet exhibit a biphasic dyslipidemic response, mimicking the changes in plasma lipids observed through life in men. Physiological Reports, 2017, 5, e13376.	0.7	19
27	The promiscuous enzyme medium-chain 3-keto-acyl-CoA thiolase triggers a vicious cycle in fatty-acid beta-oxidation. PLoS Computational Biology, 2017, 13, e1005461.	1.5	23
28	Modeling Distributive Histone Modification by Dot1 Methyltransferases. , 2017, , 117-141.		2
29	Whole-Body Vibration Partially Reverses Aging-Induced Increases in Visceral Adiposity and Hepatic Lipid Storage in Mice. PLoS ONE, 2016, 11, e0149419.	1.1	15
30	Malnutrition-associated liver steatosis and ATP depletion is caused by peroxisomal and mitochondrial dysfunction. Journal of Hepatology, 2016, 65, 1198-1208.	1.8	133
31	Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples. Journal of Proteome Research, 2016, 15, 3204-3213.	1.8	40
32	Living on the edge: substrate competition explains loss of robustness in mitochondrial fatty-acid oxidation disorders. BMC Biology, 2016, 14, 107.	1.7	27
33	Protection against the Metabolic Syndrome by Guar Gum-Derived Short-Chain Fatty Acids Depends on Peroxisome Proliferator-Activated Receptor Î³ and Glucagon-Like Peptide-1. PLoS ONE, 2015, 10, e0136364.	1.1	97
34	Dot1 histone methyltransferases share a distributive mechanism but have highly diverged catalytic properties. Scientific Reports, 2015, 5, 9824.	1.6	15
35	Short-Chain Fatty Acids Protect Against High-Fat Dietâ€"Induced Obesity via a PPARÎ³-Dependent Switch From Lipogenesis to Fat Oxidation. Diabetes, 2015, 64, 2398-2408.	0.3	734
36	Drug target identification through systems biology. Drug Discovery Today: Technologies, 2015, 15, 17-22.	4.0	22

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37	Handling Biological Complexity Using Kron Reduction. Lecture Notes in Control and Information Sciences, 2015, , 73-93.	0.6	2
38	A model reduction method for biochemical reaction networks. BMC Systems Biology, 2014, 8, 52.	3.0	58
39	In or out? On the tightness of glycosomal compartmentalization of metabolites and enzymes in Trypanosoma brucei. Molecular and Biochemical Parasitology, 2014, 198, 18-28.	0.5	18
40	A kinetic model of catabolic adaptation and protein reprofiling in <i>SaccharomycesÂcerevisiae</i> during temperature shifts. FEBS Journal, 2014, 281, 825-841.	2.2	12
41	The Silicon Trypanosome. Advances in Microbial Physiology, 2014, 64, 115-143.	1.0	5
42	The importance and challenges of in vivo-like enzyme kinetics. Perspectives in Science, 2014, 1, 126-130.	0.6	39
43	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. Perspectives in Science, 2014, 1, 131-137.	0.6	65
44	The Short-Chain Fatty Acid Uptake Fluxes by Mice on a Guar Gum Supplemented Diet Associate with Amelioration of Major Biomarkers of the Metabolic Syndrome. PLoS ONE, 2014, 9, e107392.	1.1	63
45	A new regulatory principle for in vivo biochemistry: Pleiotropic low affinity regulation by the adenine nucleotides â€“ Illustrated for the glycolytic enzymes of <i>Saccharomyces cerevisiae</i>. FEBS Letters, 2013, 587, 2860-2867.	1.3	14
46	The role of short-chain fatty acids in the interplay between diet, gut microbiota, and host energy metabolism. Journal of Lipid Research, 2013, 54, 2325-2340.	2.0	3,292
47	Dissecting the Catalytic Mechanism of Trypanosoma brucei Trypanothione Synthetase by Kinetic Analysis and Computational Modeling. Journal of Biological Chemistry, 2013, 288, 23751-23764.	1.6	22
48	Biochemical Competition Makes Fatty-Acid Î²-Oxidation Vulnerable to Substrate Overload. PLoS Computational Biology, 2013, 9, e1003186.	1.5	58
49	Gut-derived short-chain fatty acids are vividly assimilated into host carbohydrates and lipids. American Journal of Physiology - Renal Physiology, 2013, 305, G900-G910.	1.6	401
50	News about old histones: A role for histone age in controlling the epigenome. Cell Cycle, 2012, 11, 11-12.	1.3	16
51	Testing Biochemistry Revisited: How In Vivo Metabolism Can Be Understood from In Vitro Enzyme Kinetics. PLoS Computational Biology, 2012, 8, e1002483.	1.5	88
52	Enzyme Kinetics for Systems Biology. Methods in Enzymology, 2011, 500, 233-257.	0.4	16
53	From Silicon Cell to Silicon Human. , 2011, , 437-458.		4
54	How Molecular Competition Influences Fluxes in Gene Expression Networks. PLoS ONE, 2011, 6, e28494.	1.1	49

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55	Progressive methylation of ageing histones by Dot1 functions as a timer. EMBO Reports, 2011, 12, 956-962.	2.0	56
56	Metabolic regulation rather than <i>de novo</i> enzyme synthesis dominates the osmoâ€adaptation of yeast. Yeast, 2011, 28, 43-53.	0.8	37
57	Quantitative Analysis of Flux Regulation Through Hierarchical Regulation Analysis. Methods in Enzymology, 2011, 500, 571-595.	0.4	12
58	Systems biochemistry in practice: experimenting with modelling and understanding, with regulation and control. Biochemical Society Transactions, 2010, 38, 1189-1196.	1.6	14
59	Systems biology from micro-organisms to human metabolic diseases: the role of detailed kinetic models. Biochemical Society Transactions, 2010, 38, 1294-1301.	1.6	22
60	Integrated multilaboratory systems biology reveals differences in protein metabolism between two reference yeast strains. Nature Communications, 2010, 1, 145.	5.8	100
61	Measuring enzyme activities under standardized <i>inâ€ƒvivo</i>â€like conditions for systems biology. FEBS Journal, 2010, 277, 749-760.	2.2	147
62	The silicon trypanosome. Parasitology, 2010, 137, 1333-1341.	0.7	25
63	Timeâ€dependent regulation analysis dissects shifts between metabolic and geneâ€expression regulation during nitrogen starvation in bakerâ€™s yeast. FEBS Journal, 2009, 276, 5521-5536.	2.2	24
64	Mixed and diverse metabolic and gene-expression regulation of the glycolytic and fermentative pathways in response to a<i>HXK2</i>deletion in<i>Saccharomyces cerevisiae</i>. FEMS Yeast Research, 2008, 8, 155-164.	1.1	12
65	Effect of<i>hxk2</i>deletion and<i>HAP4</i>overexpression on fermentative capacity in<i>Saccharomyces cerevisiae</i>. FEMS Yeast Research, 2008, 8, 195-203.	1.1	13
66	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.	1.6	65
67	Control and Regulation of Gene Expression. Journal of Biological Chemistry, 2008, 283, 2495-2507.	1.6	76
68	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.	3.3	223
69	Unraveling the complexity of flux regulation: A new method demonstrated for nutrient starvation inSaccharomyces cerevisiae. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 2166-2171.	3.3	137
70	Yeast glycolytic oscillations that are not controlled by a single oscillophore: a new definition of oscillophore strength. Journal of Theoretical Biology, 2005, 232, 385-398.	0.8	31
71	Hierarchical and metabolic regulation of glucose influx in starved. FEMS Yeast Research, 2005, 5, 611-619.	1.1	69
72	Network-based selectivity of antiparasitic inhibitors. Molecular Biology Reports, 2002, 29, 1-5.	1.0	25

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73	Stoichiometry and compartmentation of NADH metabolism inSaccharomyces cerevisiae. FEMS Microbiology Reviews, 2001, 25, 15-37.	3.9	410
74	Can yeast glycolysis be understood in terms of in vitro kinetics of the constituent enzymes? Testing biochemistry. FEBS Journal, 2000, 267, 5313-5329.	0.2	587
75	Glycolysis in Bloodstream Form Trypanosoma brucei Can Be Understood in Terms of the Kinetics of the Glycolytic Enzymes. Journal of Biological Chemistry, 1997, 272, 3207-3215.	1.6	194
76	Short-Chain Fatty Acids in the Metabolism of Heart Failure â€“ Rethinking the Fat Stigma. Frontiers in Cardiovascular Medicine, 0, 9, .	1.1	18