Hermann-Georg HolzhÃ¼tter

List of Publications by Year
in descending order

127 papers	6,200 citations	81900 39 h-index	76900 74 g-index
132 all docs	132 docs citations	132 times ranked	8712 citing authors

#	Article	IF	Citations
1	Functional Consequences of Metabolic Zonation in Murine Livers: Insights for an Old Story. Hepatology, 2021, 73, 795-810.	7.3	35
2	Metabolic heterogeneity of human hepatocellular carcinoma: implications for personalized pharmacological treatment. FEBS Journal, 2021, 288, 2332-2346.	4.7	12
3	Regulation of the cytochrome P450 epoxyeicosanoid pathway is associated with distinct histologic features in pediatric non-alcoholic fatty liver disease. Prostaglandins Leukotrienes and Essential Fatty Acids, 2021, 164, 102229.	2.2	6
4	Computational Hypothesis: How Intra-Hepatic Functional Heterogeneity May Influence the Cascading Progression of Free Fatty Acid-Induced Non-Alcoholic Fatty Liver Disease (NAFLD). Cells, 2021, 10, 578.	4.1	4
5	How histopathologic changes in pediatric nonalcoholic fatty liver disease influence in vivo liver stiffness. Acta Biomaterialia, 2021, 123, 178-186.	8.3	13
6	Low neuronal metabolism during isoflurane-induced burst suppression is related to synaptic inhibition while neurovascular coupling and mitochondrial function remain intact. Journal of Cerebral Blood Flow and Metabolism, 2021, 41, 2640-2655.	4.3	23
7	In vitro proteasome processing of neo-splicetopes does not predict their presentation in vivo. ELife, 2021, 10, .	6.0	10
8	Effect of Post-mortem Interval and Perfusion on the Biophysical Properties of ex vivo Liver Tissue Investigated Longitudinally by MRE and DWI. Frontiers in Physiology, 2021, 12, 696304.	2.8	4
9	CARDIOKIN1: Computational Assessment of Myocardial Metabolic Capability in Healthy Controls and Patients With Valve Diseases. Circulation, 2021, 144, 1926-1939.	1.6	11
10	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. British Journal of Cancer, 2020, 122, 233-244.	6.4	16
11	Changes in Liver Mechanical Properties and Water Diffusivity During Normal Pregnancy Are Driven by Cellular Hypertrophy. Frontiers in Physiology, 2020, 11, 605205.	2.8	6
12	Functional consequences of metabolic zonation in murine livers: new insights for an old story. Journal of Hepatology, 2020, 73, S293-S294.	3.7	2
13	A novel variant of the 13C-methacetin liver function breath test that eliminates the confounding effect of individual differences in systemic CO2 kinetics. Archives of Toxicology, 2020, 94, 401-415.	4.2	12
14	The Axonal Membrane Protein PRG2 Inhibits PTEN and Directs Growth to Branches. Cell Reports, 2019, 29, 2028-2040.e8.	6.4	25
15	Metabolic modelling of kidney diseases: Lessons learned from the liver. Acta Physiologica, 2019, 227, e13350.	3.8	2
16	Characterization of Lipid and Lipid Droplet Metabolism in Human HCC. Cells, 2019, 8, 512.	4.1	60
17	Tomoelastography for the Evaluation of Pediatric Nonalcoholic Fatty Liver Disease. Investigative Radiology, 2019, 54, 198-203.	6.2	28
18	Genetic determinants of steatosis and fibrosis progression in paediatric nonâ€alcoholic fatty liver disease. Liver International, 2019, 39, 540-556.	3.9	54

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19	Local oxygen homeostasis during various neuronal network activity states in the mouse hippocampus. Journal of Cerebral Blood Flow and Metabolism, 2019, 39, 859-873.	4.3	26
20	The importance of membrane microdomains for bile salt-dependent biliary lipid secretion. Journal of Cell Science, 2018, 131, .	2.0	4
21	Dynamic Metabolic Zonation of the Hepatic Glucose Metabolism Is Accomplished by Sinusoidal Plasma Gradients of Nutrients and Hormones. Frontiers in Physiology, 2018, 9, 1786.	2.8	21
22	US Time-Harmonic Elastography: Detection of Liver Fibrosis in Adolescents with Extreme Obesity with Nonalcoholic Fatty Liver Disease. Radiology, 2018, 288, 99-106.	7.3	38
23	HEPATOKIN1 is a biochemistry-based model of liver metabolism for applications in medicine and pharmacology. Nature Communications, 2018, 9, 2386.	12.8	44
24	Possible neurotoxicity of the anesthetic propofol: evidence for the inhibition of complex II of the respiratory chain in area CA3 of rat hippocampal slices. Archives of Toxicology, 2018, 92, 3191-3205.	4.2	33
25	Crystal structure and functional characterization of selenocysteine-containing glutathione peroxidase 4 suggests an alternative mechanism of peroxide reduction. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2018, 1863, 1095-1107.	2.4	45
26	A multiscale modelling approach to assess the impact of metabolic zonation and microperfusion on the hepatic carbohydrate metabolism. PLoS Computational Biology, 2018, 14, e1006005.	3.2	31
27	The crystal structure of Pseudomonas aeruginosa lipoxygenase Ala420Gly mutant explains the improved oxygen affinity and the altered reaction specificity. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2017, 1862, 463-473.	2.4	26
28	Targeting pathogen metabolism without collateral damage to the host. Scientific Reports, 2017, 7, 40406.	3.3	42
29	A unifying mathematical model of lipid droplet metabolism reveals key molecular players in the development of hepatic steatosis. FEBS Journal, 2017, 284, 3245-3261.	4.7	21
30	Renal oncocytoma characterized by the defective complex I of the respiratory chain boosts the synthesis of the ROS scavenger glutathione. Oncotarget, 2017, 8, 105882-105904.	1.8	32
31	Mathematical Modeling of Cellular Metabolism. Recent Results in Cancer Research, 2016, 207, 221-232.	1.8	5
32	The relative importance of kinetic mechanisms and variable enzyme abundances for the regulation of hepatic glucose metabolism â€“ insights from mathematical modeling. BMC Biology, 2016, 14, 15.	3.8	34
33	On the Influence of Growth in Perfusion Dependent Biological Systems â€“ at the Example of the Human Liver. Proceedings in Applied Mathematics and Mechanics, 2015, 15, 119-120.	0.2	1
34	Joint Effect of Unlinked Genotypes: Application to Type 2 Diabetes in the EPICâ€Potsdam Caseâ€Cohort Study. Annals of Human Genetics, 2015, 79, 253-263.	0.8	5
35	Pathobiochemical signatures of cholestatic liver disease in bile duct ligated mice. BMC Systems Biology, 2015, 9, 83.	3.0	51
36	Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892.	6.4	47

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37	Computer Simulations Suggest a Key Role of Membranous Nanodomains in Biliary Lipid Secretion. PLoS Computational Biology, 2015, 11, e1004033.	3.2	6
38	Physiology-Based Kinetic Modeling of Neuronal Energy Metabolism Unravels the Molecular Basis of NAD(P)H Fluorescence Transients. Journal of Cerebral Blood Flow and Metabolism, 2015, 35, 1494-1506.	4.3	38
39	Sequential Metabolic Phases as a Means to Optimize Cellular Output in a Constant Environment. PLoS ONE, 2015, 10, e0118347.	2.5	2
40	Quantitative time-resolved analysis reveals intricate, differential regulation of standard- and immuno-proteasomes. ELife, 2015, 4, e07545.	6.0	39
41	The virtual liver: state of the art and future perspectives. Archives of Toxicology, 2014, 88, 2071-2075.	4.2	41
42	Modelling Proteasome and Proteasome Regulator Activities. Biomolecules, 2014, 4, 585-599.	4.0	10
43	SEE: structured representation of scientific evidence in the biomedical domain using Semantic Web techniques. Journal of Biomedical Semantics, 2014, 5, S1.	1.6	5
44	On growth effects in the human liver. Proceedings in Applied Mathematics and Mechanics, 2014, 14, 105-106.	0.2	0
45	The High Energy Demand of Neuronal Cells Caused by Passive Leak Currents is Not a Waste of Energy. Cell Biochemistry and Biophysics, 2013, 67, 527-535.	1.8	15
46	Recent advances in 2D and 3D in vitro systems using primary hepatocytes, alternative hepatocyte sources and non-parenchymal liver cells and their use in investigating mechanisms of hepatotoxicity, cell signaling and ADME. Archives of Toxicology, 2013, 87, 1315-1530.	4.2	1,089
47	Rapid degradation of solidâ€phase bound peptides by the 20S proteasome. Journal of Peptide Science, 2013, 19, 588-597.	1.4	0
48	Oxygen Consumption Rates during Three Different Neuronal Activity States in the Hippocampal CA3 Network. Journal of Cerebral Blood Flow and Metabolism, 2013, 33, 263-271.	4.3	63
49	Metabolic gradients as key regulators in zonation of tumor energy metabolism: A tissueâ€scale modelâ€based study. Biotechnology Journal, 2013, 8, 1058-1069.	3.5	13
50	Implications of enzyme deficiencies on mitochondrial energy metabolism and reactive oxygen species formation of neurons involved in rotenoneâ€induced Parkinson's disease: a modelâ€based analysis. FEBS Journal, 2013, 280, 5080-5093.	4.7	19
51	Evaluation of 41 Candidate Gene Variants for Obesity in the EPIC-Potsdam Cohort by Multi-Locus Stepwise Regression. PLoS ONE, 2013, 8, e68941.	2.5	18
52	Assessment of Hepatic Detoxification Activity: Proposal of an Improved Variant of the 13C-Methacetin Breath Test. PLoS ONE, 2013, 8, e70780.	2.5	8
53	Kinetic Modeling of the Mitochondrial Energy Metabolism of Neuronal Cells: The Impact of Reduced<mml:math xmlns:mml="http://www.w3.org/1998/Math/MathML"><mml:mi>Î±</mml:mi></mml:math>-Ketoglutarate Dehydrogenase Activities on ATP Production and Generation of Reactive Oxygen Species. International Journal of Cell Biology, 2012, 2012, 1-11.	2.5	28
54	Quantifying the Contribution of the Liver to Glucose Homeostasis: A Detailed Kinetic Model of Human Hepatic Glucose Metabolism. PLoS Computational Biology, 2012, 8, e1002577.	3.2	166

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55	CySBML: a Cytoscape plugin for SBML. Bioinformatics, 2012, 28, 2402-2403.	4.1	49
56	Kinetic Modeling of Human Hepatic Glucose Metabolism in Type 2 Diabetes Mellitus Predicts Higher Risk of Hypoglycemic Events in Rigorous Insulin Therapy. Journal of Biological Chemistry, 2012, 287, 36978-36989.	3.4	20
57	Network-based assessment of the selectivity of metabolic drug targets in Plasmodium falciparum with respect to human liver metabolism. BMC Systems Biology, 2012, 6, 118.	3.0	28
58	CardioNet: A human metabolic network suited for the study of cardiomyocyte metabolism. BMC Systems Biology, 2012, 6, 114.	3.0	58
59	Metabolic Consequences of TGFb Stimulation in CulturedPrimary Mouse Hepatocytes Screened from Transcript Data with ModeScore. Metabolites, 2012, 2, 983-1003.	2.9	2
60	The virtual liver: a multidisciplinary, multilevel challenge for systems biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 221-235.	6.6	93
61	A Hypothetical Model of Cargo-Selective Rab Recruitment During Organelle Maturation. Cell Biochemistry and Biophysics, 2012, 63, 59-71.	1.8	9
62	Multi-locus stepwise regression: a haplotype-based algorithm for finding genetic associations applied to atopic dermatitis. BMC Medical Genetics, 2012, 13, 8.	2.1	11
63	Enzymatic features of the glucose metabolism in tumor cells. FEBS Journal, 2011, 278, 2436-2459.	4.7	56
64	The influence of the chloride currents on action potential firing and volume regulation of excitable cells studied by a kinetic model. Journal of Theoretical Biology, 2011, 276, 42-49.	1.7	10
65	FASIMU: flexible software for flux-balance computation series in large metabolic networks. BMC Bioinformatics, 2011, 12, 28.	2.6	55
66	Infrared spectroscopic ellipsometry (IRSE) and Xâ€ray photoelectron spectroscopy (XPS) monitoring the preparation of maleimideâ€functionalized surfaces: from Au towards Si (111). Surface and Interface Analysis, 2011, 43, 1203-1210.	1.8	16
67	Enzyme maintenance effort as criterion for the characterization of alternative pathways and length distribution of isofunctional enzymes. BioSystems, 2011, 105, 122-129.	2.0	2
68	Metannogen: annotation of biological reaction networks. Bioinformatics, 2011, 27, 2763-2764.	4.1	3
69	Antimalarial drug targets in Plasmodium falciparum predicted by stage-specific metabolic network analysis. BMC Systems Biology, 2010, 4, 120.	3.0	101
70	FLUXVIZ â€" CYTOSCAPE PLUG-IN FOR VISUALIZATION OF FLUX DISTRIBUTIONS IN NETWORKS. , 2010, , .		7
71	Fluxviz - Cytoscape plug-in for visualization of flux distributions in networks. Genome Informatics, 2010, 24, 96-103.	0.4	16
72	A Conceptual Mathematical Model of the Dynamic Self-Organisation of Distinct Cellular Organelles. PLoS ONE, 2009, 4, e8295.	2.5	25

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73	Finding one's way in proteomics: a protein species nomenclature. Chemistry Central Journal, 2009, 3, 11.	2.6	229
74	Polyubiquitin substrates allosterically activate their own degradation by the 26S proteasome. Nature Structural and Molecular Biology, 2009, 16, 219-225.	8.2	64
75	Uncovering Metabolic Objectives Pursued by Changes of Enzyme Levels. Annals of the New York Academy of Sciences, 2009, 1158, 57-70.	3.8	9
76	A computational analysis of protein interactions in metabolic networks reveals novel enzyme pairs potentially involved in metabolic channeling. Journal of Theoretical Biology, 2008, 252, 456-464.	1.7	27
77	Modeling the in Vitro 20S Proteasome Activity: The Effect of PA28â€“Î±Î² and of the Sequence and Length of Polypeptides on the Degradation Kinetics. Journal of Molecular Biology, 2008, 377, 1607-1617.	4.2	28
78	Characterizing the N-Terminal Processing Motif of MHC Class I Ligands. Journal of Immunology, 2008, 180, 3210-3217.	0.8	39
79	Computational Lipidology: Predicting Lipoprotein Density Profiles in Human Blood Plasma. PLoS Computational Biology, 2008, 4, e1000079.	3.2	27
80	COMPUTER AIDED OPTIMIZATION OF CARBON ATOM LABELING FOR TRACER EXPERIMENTS. , 2008, , .		0
81	Molecular dioxygen enters the active site of 12/15-lipoxygenase via dynamic oxygen access channels. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 13319-13324.	7.1	134
82	The stability and robustness of metabolic states: identifying stabilizing sites in metabolic networks. Molecular Systems Biology, 2007, 3, 146.	7.2	97
83	PRUNING GENOME-SCALE METABOLIC MODELS TO CONSISTENT <i>AD FUNCTIONEM</i> NETWORKS. , 2007, , .		1
84	Including metabolite concentrations into flux balance analysis: thermodynamic realizability as a constraint on flux distributions in metabolic networks. BMC Systems Biology, 2007, 1, 23.	3.0	124
85	METANNOGEN: compiling features of biochemical reactions needed for the reconstruction of metabolic networks. BMC Systems Biology, 2007, 1, 5.	3.0	13
86	Pruning genome-scale metabolic models to consistent ad functionem networks. Genome Informatics, 2007, 18, 308-19.	0.4	5
87	The generalized flux-minimization method and its application to metabolic networks affected by enzyme deficiencies. BioSystems, 2006, 83, 98-107.	2.0	27
88	Composition of metabolic flux distributions by functionally interpretable minimal flux modes (MinModes). Genome Informatics, 2006, 17, 195-207.	0.4	10
89	Dual role of oxygen during lipoxygenase reactions. FEBS Journal, 2005, 272, 2523-2535.	4.7	31
90	Quantifying the Contribution of Defective Ribosomal Products to Antigen Production: A Model-Based Computational Analysis. Journal of Immunology, 2005, 175, 7957-7964.	0.8	15

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91	Structural biology of mammalian lipoxygenases: Enzymatic consequences of targeted alterations of the protein structure. Biochemical and Biophysical Research Communications, 2005, 338, 93-101.	2.1	113
92	Both lysine-clusters of the NH2-terminal prion-protein fragment PrP23-110 are essential for t-PA mediated plasminogen activation. Thrombosis and Haemostasis, 2004, 91, 465-472.	3.4	21
93	The principle of flux minimization and its application to estimate stationary fluxes in metabolic networks. FEBS Journal, 2004, 271, 2905-2922.	0.2	265
94	Computational Design of Reduced Metabolic Networks. ChemBioChem, 2004, 5, 1401-1422.	2.6	15
95	Stochastic Model of Influenza Virus Fusion. , 2004, , 411-420.		0
96	Dermal and inhalation acute toxic class methods: test procedures and biometric evaluations for the Globally Harmonized Classification System. Archives of Toxicology, 2003, 77, 243-254.	4.2	12
97	Hepatitis B Virus HBx Peptide 116â€"138 and Proteasome Activator PA28 Compete for Binding to the Proteasome Î±4/MC6 Subunit. Biological Chemistry, 2003, 384, 39-49.	2.5	29
98	Identifying MHC Class I Epitopes by Predicting the TAP Transport Efficiency of Epitope Precursors. Journal of Immunology, 2003, 171, 1741-1749.	0.8	290
99	Stimulation of plasminogen activation by recombinant cellular prion protein is conserved in the NH2-terminal fragment PrP23-110. Thrombosis and Haemostasis, 2003, 89, 812-819.	3.4	30
100	Assessment of Proteasomal Cleavage Probabilities from Kinetic Analysis of Time-dependent Product Formation. Journal of Molecular Biology, 2002, 318, 847-862.	4.2	43
101	<i>In Vitro</i> Phototoxicity Testing: Development and Validation of a New Concentration Response Analysis Software and Biostatistical Analyses Related to the Use of Various Prediction Models. ATLA Alternatives To Laboratory Animals, 2002, 30, 415-432.	1.0	45
102	Prediction of temporal gene expression. FEBS Journal, 2002, 269, 5406-5413.	0.2	98
103	Stochastic Simulation of Hemagglutinin-Mediated Fusion Pore Formation. Biophysical Journal, 2001, 81, 1360-1372.	0.5	7
104	A Compartment Model to Calculate Time-dependent Concentration Profiles of Topically Applied Chemical Compounds in the Anterior Compartments of the Rabbit Eye. ATLA Alternatives To Laboratory Animals, 2001, 29, 347-365.	1.0	7
105	Human T cell responses to endogenously presented HLA-A*0201 restricted peptides of simian virus 40 large T antigen. Journal of Cellular Biochemistry, 2001, 82, 155-162.	2.6	11
106	Identification of HLA-B27-Restricted Peptides from the <i>Chlamydia trachomatis</i> Proteome with Possible Relevance to HLA-B27-Associated Diseases. Journal of Immunology, 2001, 167, 4738-4746.	0.8	125
107	Kinetic evidences for facilitation of peptide channelling by the proteasome activator PA28. FEBS Journal, 2000, 267, 6221-6230.	0.2	67
108	Evidence for the Existence of a Non-catalytic Modifier Site of Peptide Hydrolysis by the 20 S Proteasome. Journal of Biological Chemistry, 2000, 275, 22056-22063.	3.4	84

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109	A Kinetic Model of Vertebrate 20S Proteasome Accounting for the Generation of Major Proteolytic Fragments from Oligomeric Peptide Substrates. Biophysical Journal, 2000, 79, 1196-1205.	0.5	75
110	Rapid Flip-Flop of Phospholipids in Endoplasmic Reticulum Membranes Studied by a Stopped-Flow Approach. Biophysical Journal, 2000, 78, 2628-2640.	0.5	85
111	Macrophage cholesteryl ester hydrolases and hormone-sensitive lipase prefer specifically oxidized cholesteryl esters as substrates over their non-oxidized counterparts. Biochemical Journal, 2000, 352, 125-133.	3.7	15
112	How an Inhibitor of the HIV-I Protease Modulates Proteasome Activity. Journal of Biological Chemistry, 1999, 274, 35734-35740.	3.4	138
113	A theoretical approach towards the identification of cleavage-determining amino acid motifs of the 20s proteasome 1 1Edited by R. Huber. Journal of Molecular Biology, 1999, 286, 1251-1265.	4.2	128
114	A General Measure of <i>In Vitro</i> Phototoxicity Derived from Pairs of Dose-Response Curves and its Use for Predicting the <i>In Vivo</i> Phototoxicity of Chemicals. ATLA Alternatives To Laboratory Animals, 1997, 25, 445-462.	1.0	36
115	A Kinetic Model for the Interaction of Nitric Oxide with a Mammalian Lipoxygenase. FEBS Journal, 1997, 245, 608-616.	0.2	40
116	Nitric oxide oxidises a ferrous mammalian lipoxygenase to a pre-activated ferric species. FEBS Letters, 1996, 389, 229-232.	2.8	36
117	Recommendations for the Application of Biostatistical Methods during the Development and Validation of Alternative Toxicological Methods. ATLA Alternatives To Laboratory Animals, 1996, 24, 511-530.	1.0	46
118	Use of Mathematical Models for Predicting the Metabolic Effect of Large-Scale Enzyme Activity Alterations. Application to Enzyme Deficiencies of Red Blood Cells. FEBS Journal, 1995, 229, 403-418.	0.2	86
119	MATHEMATICAL MODELLING OF CELLULAR RESPONSES TO EXTERNAL SIGNALS. Journal of Biological Systems, 1995, 03, 127-138.	1.4	14
120	THE POSSIBLE CONSEQUENCES OF LARGE-SCALE ENZYME ALTERATIONS ON THE METABOLIC EFFICIENCY OF RED BLOOD CELLS AS STUDIED ON THE BASIS OF A MATHEMATICAL MODEL. Journal of Biological Systems, 1995, 03, 207-215.	1.4	2
121	Estimation of metabolic flux rates in liver purine catabolism of tumour-bearing mice by computer simulation of radioactive tracer experiments. Cell Biochemistry and Function, 1994, 12, 1-9.	2.9	0
122	Mathematical analysis of enzymic reaction systems using optimization principles. FEBS Journal, 1991, 201, 1-21.	0.2	128
123	Mathematical modelling of the purine metabolism of the rat liver. Biochimica Et Biophysica Acta - General Subjects, 1990, 1035, 331-339.	2.4	13
124	Mathematical modelling of metabolic pathways affected by an enzyme deficiency. Energy and redox metabolism of glucose-6-phosphate-dehydrogenase-deficient erythrocytes. FEBS Journal, 1989, 182, 605-612.	0.2	25
125	Interrelations between glycolysis and the hexose monophosphate shunt in erythrocytes as studied on the basis of a mathematical model. BioSystems, 1988, 22, 19-36.	2.0	50
126	A kinetic model for lipoxygenases based on experimental data with the lipoxygenase of reticulocytes. FEBS Journal, 1987, 168, 325-337.	0.2	103

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127	Mathematical modelling of metabolic pathways affected by an enzyme deficiency. A mathematical model of glycolysis in normal and pyruvate-kinase-deficient red blood cells. FEBS Journal, 1985, 149, 101-111.	0.2	65