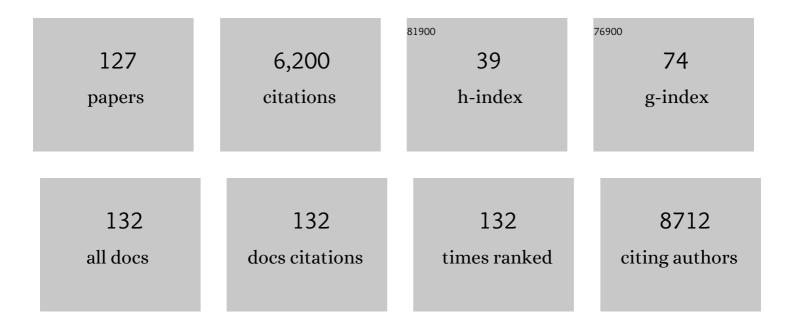
Hermann-Georg Holzhütter

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	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
2	Identifying MHC Class I Epitopes by Predicting the TAP Transport Efficiency of Epitope Precursors. Journal of Immunology, 2003, 171, 1741-1749.	0.8	290
3	The principle of flux minimization and its application to estimate stationary fluxes in metabolic networks. FEBS Journal, 2004, 271, 2905-2922.	0.2	265
4	Finding one's way in proteomics: a protein species nomenclature. Chemistry Central Journal, 2009, 3, 11.	2.6	229
5	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
6	How an Inhibitor of the HIV-I Protease Modulates Proteasome Activity. Journal of Biological Chemistry, 1999, 274, 35734-35740.	3.4	138
7	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
8	Mathematical analysis of enzymic reaction systems using optimization principles. FEBS Journal, 1991, 201, 1-21.	0.2	128
9	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
10	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
11	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
12	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
13	A kinetic model for lipoxygenases based on experimental data with the lipoxygenase of reticulocytes. FEBS Journal, 1987, 168, 325-337.	0.2	103
14	Antimalarial drug targets in Plasmodium falciparum predicted by stage-specific metabolic network analysis. BMC Systems Biology, 2010, 4, 120.	3.0	101
15	Prediction of temporal gene expression. FEBS Journal, 2002, 269, 5406-5413.	0.2	98
16	The stability and robustness of metabolic states: identifying stabilizing sites in metabolic networks. Molecular Systems Biology, 2007, 3, 146.	7.2	97
17	The virtual liver: a multidisciplinary, multilevel challenge for systems biology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2012, 4, 221-235.	6.6	93
18	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

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19	Rapid Flip-Flop of Phospholipids in Endoplasmic Reticulum Membranes Studied by a Stopped-Flow Approach. Biophysical Journal, 2000, 78, 2628-2640.	0.5	85
20	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
21	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
22	Kinetic evidences for facilitation of peptide channelling by the proteasome activator PA28. FEBS Journal, 2000, 267, 6221-6230.	0.2	67
23	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
24	Polyubiquitin substrates allosterically activate their own degradation by the 26S proteasome. Nature Structural and Molecular Biology, 2009, 16, 219-225.	8.2	64
25	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
26	Characterization of Lipid and Lipid Droplet Metabolism in Human HCC. Cells, 2019, 8, 512.	4.1	60
27	CardioNet: A human metabolic network suited for the study of cardiomyocyte metabolism. BMC Systems Biology, 2012, 6, 114.	3.0	58
28	Enzymatic features of the glucose metabolism in tumor cells. FEBS Journal, 2011, 278, 2436-2459.	4.7	56
29	FASIMU: flexible software for flux-balance computation series in large metabolic networks. BMC Bioinformatics, 2011, 12, 28.	2.6	55
30	Genetic determinants of steatosis and fibrosis progression in paediatric nonâ€ e lcoholic fatty liver disease. Liver International, 2019, 39, 540-556.	3.9	54
31	Pathobiochemical signatures of cholestatic liver disease in bile duct ligated mice. BMC Systems Biology, 2015, 9, 83.	3.0	51
32	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
33	CySBML: a Cytoscape plugin for SBML. Bioinformatics, 2012, 28, 2402-2403.	4.1	49
34	Regulation of Liver Metabolism by the Endosomal GTPase Rab5. Cell Reports, 2015, 11, 884-892.	6.4	47
35	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
36	<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

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37	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
38	HEPATOKIN1 is a biochemistry-based model of liver metabolism for applications in medicine and pharmacology. Nature Communications, 2018, 9, 2386.	12.8	44
39	Assessment of Proteasomal Cleavage Probabilities from Kinetic Analysis of Time-dependent Product Formation. Journal of Molecular Biology, 2002, 318, 847-862.	4.2	43
40	Targeting pathogen metabolism without collateral damage to the host. Scientific Reports, 2017, 7, 40406.	3.3	42
41	The virtual liver: state of the art and future perspectives. Archives of Toxicology, 2014, 88, 2071-2075.	4.2	41
42	A Kinetic Model for the Interaction of Nitric Oxide with a Mammalian Lipoxygenase. FEBS Journal, 1997, 245, 608-616.	0.2	40
43	Characterizing the N-Terminal Processing Motif of MHC Class I Ligands. Journal of Immunology, 2008, 180, 3210-3217.	0.8	39
44	Quantitative time-resolved analysis reveals intricate, differential regulation of standard- and immuno-proteasomes. ELife, 2015, 4, e07545.	6.0	39
45	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
46	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
47	Nitric oxide oxidises a ferrous mammalian lipoxygenase to a pre-activated ferric species. FEBS Letters, 1996, 389, 229-232.	2.8	36
48	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
49	Functional Consequences of Metabolic Zonation in Murine Livers: Insights for an Old Story. Hepatology, 2021, 73, 795-810.	7.3	35
50	The relative importance of kinetic mechanisms and variable enzyme abundances for the regulation of hepatic glucose metabolism – insights from mathematical modeling. BMC Biology, 2016, 14, 15.	3.8	34
51	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
52	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
53	Dual role of oxygen during lipoxygenase reactions. FEBS Journal, 2005, 272, 2523-2535.	4.7	31
54	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

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55	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
56	Hepatitis B Virus HBx Peptide 116–138 and Proteasome Activator PA28 Compete for Binding to the Proteasome α4/MC6 Subunit. Biological Chemistry, 2003, 384, 39-49.	2.5	29
57	Modeling the in Vitro 20S Proteasome Activity: The Effect of PA28–αβ and of the Sequence and Length of Polypeptides on the Degradation Kinetics. Journal of Molecular Biology, 2008, 377, 1607-1617.	4.2	28
58	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>α</mml:mi>-Ketoglutarate Dehydrogenase Activities on ATP Production and Generation of Reactive Oxygen Species. International</mml:math 	2.5	28
59	Journal of Cell Biology, 2012, 2012, 1-11. 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
60	Tomoelastography for the Evaluation of Pediatric Nonalcoholic Fatty Liver Disease. Investigative Radiology, 2019, 54, 198-203.	6.2	28
61	The generalized flux-minimization method and its application to metabolic networks affected by enzyme deficiencies. BioSystems, 2006, 83, 98-107.	2.0	27
62	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
63	Computational Lipidology: Predicting Lipoprotein Density Profiles in Human Blood Plasma. PLoS Computational Biology, 2008, 4, e1000079.	3.2	27
64	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
65	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
66	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
67	A Conceptual Mathematical Model of the Dynamic Self-Organisation of Distinct Cellular Organelles. PLoS ONE, 2009, 4, e8295.	2.5	25
68	The Axonal Membrane Protein PRG2 Inhibits PTEN and Directs Growth to Branches. Cell Reports, 2019, 29, 2028-2040.e8.	6.4	25
69	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
70	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
71	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
72	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

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73	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
74	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
75	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
76	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
77	Kinetic modelling of quantitative proteome data predicts metabolic reprogramming of liver cancer. British Journal of Cancer, 2020, 122, 233-244.	6.4	16
78	Fluxviz - Cytoscape plug-in for visualization of flux distributions in networks. Genome Informatics, 2010, 24, 96-103.	0.4	16
79	Computational Design of Reduced Metabolic Networks. ChemBioChem, 2004, 5, 1401-1422.	2.6	15
80	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
81	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
82	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
83	MATHEMATICAL MODELLING OF CELLULAR RESPONSES TO EXTERNAL SIGNALS. Journal of Biological Systems, 1995, 03, 127-138.	1.4	14
84	Mathematical modelling of the purine metabolism of the rat liver. Biochimica Et Biophysica Acta - General Subjects, 1990, 1035, 331-339.	2.4	13
85	METANNOGEN: compiling features of biochemical reactions needed for the reconstruction of metabolic networks. BMC Systems Biology, 2007, 1, 5.	3.0	13
86	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
87	How histopathologic changes in pediatric nonalcoholic fatty liver disease influence in vivo liver stiffness. Acta Biomaterialia, 2021, 123, 178-186.	8.3	13
88	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
89	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
90	Metabolic heterogeneity of human hepatocellular carcinoma: implications for personalized pharmacological treatment. FEBS Journal, 2021, 288, 2332-2346.	4.7	12

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91	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
92	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
93	CARDIOKIN1: Computational Assessment of Myocardial Metabolic Capability in Healthy Controls and Patients With Valve Diseases. Circulation, 2021, 144, 1926-1939.	1.6	11
94	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
95	Modelling Proteasome and Proteasome Regulator Activities. Biomolecules, 2014, 4, 585-599.	4.0	10
96	In vitro proteasome processing of neo-splicetopes does not predict their presentation in vivo. ELife, 2021, 10, .	6.0	10
97	Composition of metabolic flux distributions by functionally interpretable minimal flux modes (MinModes). Genome Informatics, 2006, 17, 195-207.	0.4	10
98	Uncovering Metabolic Objectives Pursued by Changes of Enzyme Levels. Annals of the New York Academy of Sciences, 2009, 1158, 57-70.	3.8	9
99	A Hypothetical Model of Cargo-Selective Rab Recruitment During Organelle Maturation. Cell Biochemistry and Biophysics, 2012, 63, 59-71.	1.8	9
100	Assessment of Hepatic Detoxification Activity: Proposal of an Improved Variant of the 13C-Methacetin Breath Test. PLoS ONE, 2013, 8, e70780.	2.5	8
101	Stochastic Simulation of Hemagglutinin-Mediated Fusion Pore Formation. Biophysical Journal, 2001, 81, 1360-1372.	0.5	7
102	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
103	FLUXVIZ — CYTOSCAPE PLUG-IN FOR VISUALIZATION OF FLUX DISTRIBUTIONS IN NETWORKS. , 2010, , .		7
104	Computer Simulations Suggest a Key Role of Membranous Nanodomains in Biliary Lipid Secretion. PLoS Computational Biology, 2015, 11, e1004033.	3.2	6
105	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
106	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
107	SEE: structured representation of scientific evidence in the biomedical domain using Semantic Web techniques. Journal of Biomedical Semantics, 2014, 5, S1.	1.6	5
108	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

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109	Mathematical Modeling of Cellular Metabolism. Recent Results in Cancer Research, 2016, 207, 221-232.	1.8	5
110	Pruning genome-scale metabolic models to consistent ad functionem networks. Genome Informatics, 2007, 18, 308-19.	0.4	5
111	The importance of membrane microdomains for bile salt-dependent biliary lipid secretion. Journal of Cell Science, 2018, 131, .	2.0	4
112	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
113	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
114	Metannogen: annotation of biological reaction networks. Bioinformatics, 2011, 27, 2763-2764.	4.1	3
115	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
116	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
117	Metabolic Consequences of TGFb Stimulation in CulturedPrimary Mouse Hepatocytes Screened from Transcript Data with ModeScore. Metabolites, 2012, 2, 983-1003.	2.9	2
118	Metabolic modelling of kidney diseases: Lessons learned from the liver. Acta Physiologica, 2019, 227, e13350.	3.8	2
119	Functional consequences of metabolic zonation in murine livers: new insights for an old story. Journal of Hepatology, 2020, 73, S293-S294.	3.7	2
120	Sequential Metabolic Phases as a Means to Optimize Cellular Output in a Constant Environment. PLoS ONE, 2015, 10, e0118347.	2.5	2
121	PRUNING GENOME-SCALE METABOLIC MODELS TO CONSISTENT <i>AD FUNCTIONEM</i> NETWORKS. , 2007, , .		1
122	On the Influence of Growth in Perfusion Dependent Biological Systems – at the Example of the Human Liver. Proceedings in Applied Mathematics and Mechanics, 2015, 15, 119-120.	0.2	1
123	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
124	Stochastic Model of Influenza Virus Fusion. , 2004, , 411-420.		0
125	Rapid degradation of solidâ€phase bound peptides by the 20S proteasome. Journal of Peptide Science, 2013, 19, 588-597.	1.4	0
126	On growth effects in the human liver. Proceedings in Applied Mathematics and Mechanics, 2014, 14, 105-106.	0.2	0

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127	COMPUTER AIDED OPTIMIZATION OF CARBON ATOM LABELING FOR TRACER EXPERIMENTS. , 2008, , .		0