

# Lars Kuepfer

## List of Publications by Year in Descending Order

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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.

58  
papers

2,532  
citations

26  
h-index

50  
g-index

64  
ext. papers

3,075  
ext. citations

5.9  
avg, IF

4.9  
L-index

#	Paper	IF	Citations
58	Early prediction of decompensation (EPOD) Score - non-invasive determination of liver cirrhosis decompensation risk.. <i>Liver International</i> , <b>2022</b> ,	7.9	1
57	Computational Models for Clinical Applications in Personalized Medicine-Guidelines and Recommendations for Data Integration and Model Validation.. <i>Journal of Personalized Medicine</i> , <b>2022</b> , 12,	3.6	2
56	PK-Sim $\square$ for Modeling Oral Drug Delivery of Modified-Release Formulations <b>2022</b> , 375-389		1
55	Algorithmic surveillance of ICU patients with acute respiratory distress syndrome (ASIC): protocol for a multicentre stepped-wedge cluster randomised quality improvement strategy. <i>BMJ Open</i> , <b>2021</b> , 11, e045589	3	0
54	Subcellular spatio-temporal intravital kinetics of aflatoxin B and ochratoxin A in liver and kidney. <i>Archives of Toxicology</i> , <b>2021</b> , 95, 2163-2177	5.8	3
53	Data-driven personalization of a physiologically based pharmacokinetic model for caffeine: A systematic assessment. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2021</b> , 10, 782-793	4.5	2
52	A Model-Based Workflow to Benchmark the Clinical Cholestasis Risk of Drugs. <i>Clinical Pharmacology and Therapeutics</i> , <b>2021</b> , 110, 1293-1301	6.1	0
51	Network integration and modelling of dynamic drug responses at multi-omics levels. <i>Communications Biology</i> , <b>2020</b> , 3, 573	6.7	7
50	A workflow to build PBTK models for novel species. <i>Archives of Toxicology</i> , <b>2020</b> , 94, 3847-3860	5.8	4
49	A Physiology-Based Model of Human Bile Acid Metabolism for Predicting Bile Acid Tissue Levels After Drug Administration in Healthy Subjects and BRIC Type 2 Patients. <i>Frontiers in Physiology</i> , <b>2019</b> , 10, 1192	4.6	4
48	Quantitative systems pharmacology of interferon alpha administration: A multi-scale approach. <i>PLoS ONE</i> , <b>2019</b> , 14, e0209587	3.7	6
47	Bile Microinfarcts in Cholestasis Are Initiated by Rupture of the Apical Hepatocyte Membrane and Cause Shunting of Bile to Sinusoidal Blood. <i>Hepatology</i> , <b>2019</b> , 69, 666-683	11.2	46
46	Prediction of human drug-induced liver injury (DILI) in relation to oral doses and blood concentrations. <i>Archives of Toxicology</i> , <b>2019</b> , 93, 1609-1637	5.8	53
45	Integration of genome-scale metabolic networks into whole-body PBPK models shows phenotype-specific cases of drug-induced metabolic perturbation. <i>Npj Systems Biology and Applications</i> , <b>2018</b> , 4, 10	5	17
44	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , <b>2018</b> , 50, e453	12.8	37
43	Using quantitative systems pharmacology to evaluate the drug efficacy of COX-2 and 5-LOX inhibitors in therapeutic situations. <i>Npj Systems Biology and Applications</i> , <b>2018</b> , 4, 28	5	11
42	Spatio-temporal visualization of the distribution of acetaminophen as well as its metabolites and adducts in mouse livers by MALDI MSI. <i>Archives of Toxicology</i> , <b>2018</b> , 92, 2963-2977	5.8	28

41	A model-based assay design to reproduce in vivo patterns of acute drug-induced toxicity. <i>Archives of Toxicology</i> , <b>2018</b> , 92, 553-555	5.8	17
40	A generic whole body physiologically based pharmacokinetic model for therapeutic proteins in PK-Sim. <i>Journal of Pharmacokinetics and Pharmacodynamics</i> , <b>2018</b> , 45, 235-257	2.7	39
39	Bringing in vitro analysis closer to in vivo: Studying doxorubicin toxicity and associated mechanisms in 3D human microtissues with PBPK-based dose modelling. <i>Toxicology Letters</i> , <b>2018</b> , 294, 184-192	4.4	20
38	Model-based contextualization of in vitro toxicity data quantitatively predicts in vivo drug response in patients. <i>Archives of Toxicology</i> , <b>2017</b> , 91, 865-883	5.8	14
37	Multiscale modeling reveals inhibitory and stimulatory effects of caffeine on acetaminophen-induced toxicity in humans. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2017</b> , 6, 136-146	4.5	5
36	In vivo imaging of systemic transport and elimination of xenobiotics and endogenous molecules in mice. <i>Archives of Toxicology</i> , <b>2017</b> , 91, 1335-1352	5.8	24
35	Translational learning from clinical studies predicts drug pharmacokinetics across patient populations. <i>Npj Systems Biology and Applications</i> , <b>2017</b> , 3, 11	5	8
34	Physiologically-based modelling in mice suggests an aggravated loss of clearance capacity after toxic liver damage. <i>Scientific Reports</i> , <b>2017</b> , 7, 6224	4.9	23
33	A Comparative Analysis of Drug-Induced Hepatotoxicity in Clinically Relevant Situations. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005280	5	8
32	Modeling and Simulation of In Vivo Drug Effects. <i>Handbook of Experimental Pharmacology</i> , <b>2016</b> , 232, 313-29	3.2	4
31	Modeling approaches for hepatic spatial heterogeneity in pharmacokinetic simulations. <i>Drug Discovery Today: Disease Models</i> , <b>2016</b> , 22, 35-43	1.3	3
30	Zonated quantification of steatosis in an entire mouse liver. <i>Computers in Biology and Medicine</i> , <b>2016</b> , 73, 108-18	7	26
29	Model-guided identification of a therapeutic strategy to reduce hyperammonemia in liver diseases. <i>Journal of Hepatology</i> , <b>2016</b> , 64, 860-71	13.4	58
28	Systems Medicine in Pharmaceutical Research and Development. <i>Methods in Molecular Biology</i> , <b>2016</b> , 1386, 87-104	1.4	5
27	PBPK Modelling of Intracellular Drug Delivery Through Active and Passive Transport Processes. <i>Fundamental Biomedical Technologies</i> , <b>2016</b> , 363-374		
26	Towards knowledge-driven cross-species extrapolation. <i>Drug Discovery Today: Disease Models</i> , <b>2016</b> , 22, 21-26	1.3	2
25	A multiscale, model-based analysis of the multi-tissue interplay underlying blood glucose regulation in type I diabetes. <i>Annual International Conference of the IEEE Engineering in Medicine and Biology Society IEEE Engineering in Medicine and Biology Society Annual International Conference</i> , <b>2016</b> , 2016, 1417-1421	0.9	6
24	A Physiologically Based Pharmacokinetic Model of Isoniazid and Its Application in Individualizing Tuberculosis Chemotherapy. <i>Antimicrobial Agents and Chemotherapy</i> , <b>2016</b> , 60, 6134-45	5.9	31

23	Applied Concepts in PBPK Modeling: How to Build a PBPK/PD Model. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2016</b> , 5, 516-531	4.5	139
22	A systematic evaluation of the use of physiologically based pharmacokinetic modeling for cross-species extrapolation. <i>Journal of Pharmaceutical Sciences</i> , <b>2015</b> , 104, 191-206	3.9	63
21	Representative Sinusoids for Hepatic Four-Scale Pharmacokinetics Simulations. <i>PLoS ONE</i> , <b>2015</b> , 10, e0133653	3.6	31
20	Bayesian Population Physiologically-Based Pharmacokinetic (PBPK) Approach for a Physiologically Realistic Characterization of Interindividual Variability in Clinically Relevant Populations. <i>PLoS ONE</i> , <b>2015</b> , 10, e0139423	3.7	30
19	Modellierung metabolischer Netzwerke im menschlichen Körper. <i>BioSpektrum</i> , <b>2014</b> , 20, 39-41	0.1	
18	Enabling multiscale modeling in systems medicine. <i>Genome Medicine</i> , <b>2014</b> , 6, 21	14.4	61
17	Clinical translation in the virtual liver network. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2014</b> , 3, e127	4.5	10
16	Spatio-temporal simulation of first pass drug perfusion in the liver. <i>PLoS Computational Biology</i> , <b>2014</b> , 10, e1003499	5	35
15	Stoichiometric modelling of microbial metabolism. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1191, 3-18	1.4	1
14	Using Bayesian-PBPK modeling for assessment of inter-individual variability and subgroup stratification. <i>In Silico Pharmacology</i> , <b>2013</b> , 1, 6	4.3	33
13	Development of a physiologically based computational kidney model to describe the renal excretion of hydrophilic agents in rats. <i>Frontiers in Physiology</i> , <b>2012</b> , 3, 494	4.6	10
12	Integrating cellular metabolism into a multiscale whole-body model. <i>PLoS Computational Biology</i> , <b>2012</b> , 8, e1002750	5	88
11	Multiscale mechanistic modeling in pharmaceutical research and development. <i>Advances in Experimental Medicine and Biology</i> , <b>2012</b> , 736, 543-61	3.6	14
10	Using expression data for quantification of active processes in physiologically based pharmacokinetic modeling. <i>Drug Metabolism and Disposition</i> , <b>2012</b> , 40, 892-901	4	63
9	A mechanistic, model-based approach to safety assessment in clinical development. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , <b>2012</b> , 1, e13	4.5	32
8	Evaluation of the efficacy and safety of rivaroxaban using a computer model for blood coagulation. <i>PLoS ONE</i> , <b>2011</b> , 6, e17626	3.7	29
7	A computational systems biology software platform for multiscale modeling and simulation: integrating whole-body physiology, disease biology, and molecular reaction networks. <i>Frontiers in Physiology</i> , <b>2011</b> , 2, 4	4.6	136
6	Metabolic flux distributions: genetic information, computational predictions, and experimental validation. <i>Applied Microbiology and Biotechnology</i> , <b>2010</b> , 86, 1243-55	5.7	27

5	Ensemble modeling for analysis of cell signaling dynamics. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 1001-6	44.5	171
4	Efficient classification of complete parameter regions based on semidefinite programming. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 12	3.6	36
3	Systematic evaluation of objective functions for predicting intracellular fluxes in Escherichia coli. <i>Molecular Systems Biology</i> , <b>2007</b> , 3, 119	12.2	526
2	Large-scale <sup>13</sup> C-flux analysis reveals mechanistic principles of metabolic network robustness to null mutations in yeast. <i>Genome Biology</i> , <b>2005</b> , 6, R49	18.3	249
1	Metabolic functions of duplicate genes in <i>Saccharomyces cerevisiae</i> . <i>Genome Research</i> , <b>2005</b> , 15, 1421-30.7	30.7	184