Lars Kuepfer

List of Publications by Year
in descending order

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59	3,464	186265	144013
papers	citations	28 h-index	57 g-index

64	64	64	4054
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Early prediction of decompensation (<scp>EPOD</scp>) score: Nonâ€invasive determination of cirrhosis decompensation risk. Liver International, 2022, 42, 640-650.	3.9	6
2	Computational Models for Clinical Applications in Personalized Medicineâ€”Guidelines and Recommendations for Data Integration and Model Validation. Journal of Personalized Medicine, 2022, 12, 166.	2.5	24
3	Algorithmic surveillance of ICU patients with acute respiratory distress syndrome (ASIC): protocol for a multicentre stepped-wedge cluster randomised quality improvement strategy. BMJ Open, 2021, 11, e045589.	1.9	9
4	Subcellular spatio-temporal intravital kinetics of aflatoxin B1 and ochratoxin A in liver and kidney. Archives of Toxicology, 2021, 95, 2163-2177.	4.2	15
5	Dataâ€driven personalization of a physiologically based pharmacokinetic model for caffeine: A systematic assessment. CPT: Pharmacometrics and Systems Pharmacology, 2021, 10, 782-793.	2.5	13
6	A Modelâ€Based Workflow to Benchmark the Clinical Cholestasis Risk of Drugs. Clinical Pharmacology and Therapeutics, 2021, 110, 1293-1301.	4.7	3
7	Network integration and modelling of dynamic drug responses at multi-omics levels. Communications Biology, 2020, 3, 573.	4.4	28
8	A workflow to build PBTK models for novel species. Archives of Toxicology, 2020, 94, 3847-3860.	4.2	15
9	Bile Microinfarcts in Cholestasis Are Initiated by Rupture of the Apical Hepatocyte Membrane and Cause Shunting of Bile to Sinusoidal Blood. Hepatology, 2019, 69, 666-683.	7.3	89
10	Prediction of human drug-induced liver injury (DILI) in relation to oral doses and blood concentrations. Archives of Toxicology, 2019, 93, 1609-1637.	4.2	86
11	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. Frontiers in Physiology, 2019, 10, 1192.	2.8	10
12	Quantitative systems pharmacology of interferon alpha administration: A multi-scale approach. PLoS ONE, 2019, 14, e0209587.	2.5	7
13	Integration of genome-scale metabolic networks into whole-body PBPK models shows phenotype-specific cases of drug-induced metabolic perturbation. Npj Systems Biology and Applications, 2018, 4, 10.	3.0	28
14	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	7.7	49
15	A model-based assay design to reproduce in vivo patterns of acute drug-induced toxicity. Archives of Toxicology, 2018, 92, 553-555.	4.2	23
16	A generic whole body physiologically based pharmacokinetic model for therapeutic proteins in PK-Sim. Journal of Pharmacokinetics and Pharmacodynamics, 2018, 45, 235-257.	1.8	60
17	Bringing in vitro analysis closer to in vivo: Studying doxorubicin toxicity and associated mechanisms in 3D human microtissues with PBPK-based dose modelling. Toxicology Letters, 2018, 294, 184-192.	0.8	28
18	Using quantitative systems pharmacology to evaluate the drug efficacy of COX-2 and 5-LOX inhibitors in therapeutic situations. Npj Systems Biology and Applications, 2018, 4, 28.	3.0	15

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19	Spatio-temporal visualization of the distribution of acetaminophen as well as its metabolites and adducts in mouse livers by MALDI MSI. Archives of Toxicology, 2018, 92, 2963-2977.	4.2	51
20	Model-based contextualization of in vitro toxicity data quantitatively predicts in vivo drug response in patients. Archives of Toxicology, 2017, 91, 865-883.	4.2	16
21	Multiscale modeling reveals inhibitory and stimulatory effects of caffeine on acetaminophenâ€induced toxicity in humans. CPT: Pharmacometrics and Systems Pharmacology, 2017, 6, 136-146.	2.5	8
22	In vivo imaging of systemic transport and elimination of xenobiotics and endogenous molecules in mice. Archives of Toxicology, 2017, 91, 1335-1352.	4.2	64
23	Editorial overview: Systems biology approaches in pharmacology and drug discovery. Current Opinion in Systems Biology, 2017, 4, vii-ix.	2.6	0
24	Translational learning from clinical studies predicts drug pharmacokinetics across patient populations. Npj Systems Biology and Applications, 2017, 3, 11.	3.0	14
25	Physiologically-based modelling in mice suggests an aggravated loss of clearance capacity after toxic liver damage. Scientific Reports, 2017, 7, 6224.	3.3	57
26	A Comparative Analysis of Drug-Induced Hepatotoxicity in Clinically Relevant Situations. PLoS Computational Biology, 2017, 13, e1005280.	3.2	10
27	Towards knowledge-driven cross-species extrapolation. Drug Discovery Today: Disease Models, 2016, 22, 21-26.	1.2	3
28	A multiscale, model-based analysis of the multi-tissue interplay underlying blood glucose regulation in type I diabetes. , 2016, 2016, 1417-1421.		8
29	A Physiologically Based Pharmacokinetic Model of Isoniazid and Its Application in Individualizing Tuberculosis Chemotherapy. Antimicrobial Agents and Chemotherapy, 2016, 60, 6134-6145.	3.2	40
30	Applied Concepts in PBPK Modeling: How to Build a PBPK/PD Model. CPT: Pharmacometrics and Systems Pharmacology, 2016, 5, 516-531.	2.5	232
31	Modeling approaches for hepatic spatial heterogeneity in pharmacokinetic simulations. Drug Discovery Today: Disease Models, 2016, 22, 35-43.	1.2	6
32	Zonated quantification of steatosis in an entire mouse liver. Computers in Biology and Medicine, 2016, 73, 108-118.	7.0	39
33	Model-guided identification of a therapeutic strategy to reduce hyperammonemia in liver diseases. Journal of Hepatology, 2016, 64, 860-871.	3.7	110
34	Systems Medicine in Pharmaceutical Research and Development. Methods in Molecular Biology, 2016, 1386, 87-104.	0.9	6
35	PBPK Modelling of Intracellular Drug Delivery Through Active and Passive Transport Processes. Fundamental Biomedical Technologies, 2016, , 363-374.	0.2	0
36	Representative Sinusoids for Hepatic Four-Scale Pharmacokinetics Simulations. PLoS ONE, 2015, 10, e0133653.	2.5	47

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37	Bayesian Population Physiologically-Based Pharmacokinetic (PBPK) Approach for a Physiologically Realistic Characterization of Interindividual Variability in Clinically Relevant Populations. PLoS ONE, 2015, 10, e0139423.	2.5	37
38	Modeling and Simulation of In Vivo Drug Effects. Handbook of Experimental Pharmacology, 2015, 232, 313-329.	1.8	5
39	A Systematic Evaluation of the Use of Physiologically Based Pharmacokinetic Modeling for Cross-Species Extrapolation. Journal of Pharmaceutical Sciences, 2015, 104, 191-206.	3.3	99
40	Spatio-Temporal Simulation of First Pass Drug Perfusion in the Liver. PLoS Computational Biology, 2014, 10, e1003499.	3.2	41
41	The virtual liver: state of the art and future perspectives. Archives of Toxicology, 2014, 88, 2071-2075.	4.2	41
42	Enabling multiscale modeling in systems medicine. Genome Medicine, 2014, 6, 21.	8.2	76
43	Clinical Translation in the Virtual Liver Network. CPT: Pharmacometrics and Systems Pharmacology, 2014, 3, 1-4.	2.5	18
44	Stoichiometric Modelling of Microbial Metabolism. Methods in Molecular Biology, 2014, 1191, 3-18.	0.9	3
45	Using Bayesian-PBPK modeling for assessment of inter-individual variability and subgroup stratification. In Silico Pharmacology, 2013, 1, 6.	3.3	41
46	Integrating Cellular Metabolism into a Multiscale Whole-Body Model. PLoS Computational Biology, 2012, 8, e1002750.	3.2	112
47	Multiscale Mechanistic Modeling in Pharmaceutical Research and Development. Advances in Experimental Medicine and Biology, 2012, 736, 543-561.	1.6	20
48	Using Expression Data for Quantification of Active Processes in Physiologically Based Pharmacokinetic Modeling. Drug Metabolism and Disposition, 2012, 40, 892-901.	3.3	81
49	A Mechanistic, Modelâ€Based Approach to Safety Assessment in Clinical Development. CPT: Pharmacometrics and Systems Pharmacology, 2012, 1, 1-8.	2.5	36
50	Development of a Physiologically Based Computational Kidney Model to Describe the Renal Excretion of Hydrophilic Agents in Rats. Frontiers in Physiology, 2012, 3, 494.	2.8	11
51	Evaluation of the Efficacy and Safety of Rivaroxaban Using a Computer Model for Blood Coagulation. PLoS ONE, 2011, 6, e17626.	2.5	32
52	A Computational Systems Biology Software Platform for Multiscale Modeling and Simulation: Integrating Whole-Body Physiology, Disease Biology, and Molecular Reaction Networks. Frontiers in Physiology, 2011, 2, 4.	2.8	167
53	Towards wholeâ€body systems physiology. Molecular Systems Biology, 2010, 6, 409.	7.2	26
54	Metabolic flux distributions: genetic information, computational predictions, and experimental validation. Applied Microbiology and Biotechnology, 2010, 86, 1243-1255.	3.6	29

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55	Systematic evaluation of objective functions for predicting intracellular fluxes in Escherichia coli. Molecular Systems Biology, 2007, 3, 119.	7.2	623
56	Ensemble modeling for analysis of cell signaling dynamics. Nature Biotechnology, 2007, 25, 1001-1006.	17.5	214
57	Efficient classification of complete parameter regions based on semidefinite programming. BMC Bioinformatics, 2007, 8, 12.	2.6	47
58	Metabolic functions of duplicate genes in Saccharomyces cerevisiae. Genome Research, 2005, 15, 1421-1430.	5.5	208
59	Large-scale 13C-flux analysis reveals mechanistic principles of metabolic network robustness to null mutations in yeast. Genome Biology, 2005, 6, R49.	9.6	274