Andreas A Schuppert

List of Publications by Year
in descending order

54 papers	1,747 citations	361045 20 h-index	315357 38 g-index
68 all docs	68 docs citations	68 times ranked	2846 citing authors

#	Article	IF	Citations
1	Swarm learning for decentralized artificial intelligence in cancer histopathology. Nature Medicine, 2022, 28, 1232-1239.	15.2	77
2	Future Medical Artificial Intelligence Application Requirements and Expectations of Physicians in German University Hospitals: Web-Based Survey. Journal of Medical Internet Research, 2021, 23, e26646.	2.1	46
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.	0.8	9
4	Plant PhysioSpace: a robust tool to compare stress response across plant species. Plant Physiology, 2021, 187, 1795-1811.	2.3	3
5	Different spreading dynamics throughout Germany during the second wave of the COVID-19 pandemic: a time series study based on national surveillance data. Lancet Regional Health - Europe, The, 2021, 6, 100151.	3.0	37
6	6-month mortality and readmissions of hospitalized COVID-19 patients: A nationwide cohort study of 8,679 patients in Germany. PLoS ONE, 2021, 16, e0255427.	1.1	65
7	Global hierarchy vs local structure: Spurious self-feedback in scale-free networks. Physical Review Research, 2021, 3, .	1.3	1
8	Big Data und künstliche Intelligenz in der Medizin. , 2021, , 423-436.		0
9	Effectiveness of extended shutdown measures during the ´Bundesnotbremse´ introduced in the third SARS-CoV-2 wave in Germany. Infection, 2021, 49, 1331-1335.	2.3	2
10	Effectiveness of extended shutdown measures during the ´Bundesnotbremse´ introduced in the third SARS-CoV-2 wave in Germany. Infection, 2021, 49, 1331-1335.	2.3	11
11	Quality-targeting dynamic optimization of monoclonal antibody production. Computers and Chemical Engineering, 2020, 142, 107004.	2.0	7
12	A modified Ising model of Barabási–Albert network with gene-type spins. Journal of Mathematical Biology, 2020, 81, 769-798.	0.8	8
13	Methodological challenges in translational drug response modeling in cancer: A systematic analysis with FORESEE. PLoS Computational Biology, 2020, 16, e1007803.	1.5	9
14	A neural network assisted Metropolis adjusted Langevin algorithm. Monte Carlo Methods and Applications, 2020, 26, 93-111.	0.3	3
15	Two-step multi-omics modelling of drug sensitivity in cancer cell lines to identify driving mechanisms. PLoS ONE, 2020, 15, e0238961.	1.1	5
16	Towards Model-Based Optimization for Quality by Design in Biotherapeutics Production. Computer Aided Chemical Engineering, 2019, , 25-30.	0.3	6
17	FORESEE: a tool for the systematic comparison of translational drug response modeling pipelines. Bioinformatics, 2019, 35, 3846-3848.	1.8	6
18	Whither systems medicine?. Experimental and Molecular Medicine, 2018, 50, e453-e453.	3.2	49

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19	Inflammatory processes during acute respiratory distress syndrome: a complex system. Current Opinion in Critical Care, 2018, 24, 1-9.	1.6	52
20	Smart Medical Information Technology for Healthcare (SMITH). Methods of Information in Medicine, 2018, 57, e92-e105.	0.7	89
21	Markov-Chain Monte-Carlo methods and non-identifiabilities. Monte Carlo Methods and Applications, 2018, 24, 203-214.	0.3	1
22	From hype to reality: data science enabling personalized medicine. BMC Medicine, 2018, 16, 150.	2.3	278
23	A systematic atlas of chaperome deregulation topologies across the human cancer landscape. PLoS Computational Biology, 2018, 14, e1005890.	1.5	46
24	Stem Cell Differentiation as a Non-Markov Stochastic Process. Cell Systems, 2017, 5, 268-282.e7.	2.9	178
25	Translational learning from clinical studies predicts drug pharmacokinetics across patient populations. Npj Systems Biology and Applications, 2017, 3, 11.	1.4	14
26	Physiologically-based modelling in mice suggests an aggravated loss of clearance capacity after toxic liver damage. Scientific Reports, 2017, 7, 6224.	1.6	57
27	How to Use Mechanistic Metabolic Modeling to Ensure High Quality Glycoprotein Production. Computer Aided Chemical Engineering, 2017, , 2839-2844.	0.3	5
28	â€œBig Data and Dynamicsâ€â€"The Mathematical Toolkit Towards Personalized Medicine. Springer Proceedings in Mathematics and Statistics, 2017, , 338-369.	0.1	0
29	Principal components analysis and the reported low intrinsic dimensionality of gene expression microarray data. Scientific Reports, 2016, 6, 25696.	1.6	72
30	Combined Population Dynamics and Entropy Modelling Supports Patient Stratification in Chronic Myeloid Leukemia. Scientific Reports, 2016, 6, 24057.	1.6	8
31	Assessing interindividual variability by Bayesian-PBPK modeling. Drug Discovery Today: Disease Models, 2016, 22, 15-19.	1.2	5
32	Robust PBPK/PD-Based Model Predictive Control of Blood Glucose. IEEE Transactions on Biomedical Engineering, 2016, 63, 1492-1504.	2.5	26
33	Systems Medicine in Pharmaceutical Research and Development. Methods in Molecular Biology, 2016, 1386, 87-104.	0.4	6
34	Bayesian Population Physiologically-Based Pharmacokinetic (PBPK) Approach for a Physiologically Realistic Characterization of Interindividual Variability in Clinically Relevant Populations. PLoS ONE, 2015, 10, e0139423.	1.1	37
35	Epigenetic Biomarker to Support Classification into Pluripotent and Non-Pluripotent Cells. Scientific Reports, 2015, 5, 8973.	1.6	49
36	Enabling multiscale modeling in systems medicine. Genome Medicine, 2014, 6, 21.	3.6	76

#	ARTICLE	IF	CITATIONS
37	Using Bayesian-PBPK modeling for assessment of inter-individual variability and subgroup stratification. In Silico Pharmacology, 2013, 1, 6.	1.8	41
38	Power-Laws and the Use of Pluripotent Stem Cell Lines. PLoS ONE, 2013, 8, e52068.	1.1	6
39	Combination of a Proteomics Approach and Reengineering of Meso Scale Network Models for Prediction of Mode-of-Action for Tyrosine Kinase Inhibitors. PLoS ONE, 2013, 8, e53668.	1.1	7
40	PhysioSpace: Relating Gene Expression Experiments from Heterogeneous Sources Using Shared Physiological Processes. PLoS ONE, 2013, 8, e77627.	1.1	17
41	A new Perspective on Closed-Loop Glucose Control using a Physiology-Based Pharmacokinetic / Pharmacodynamic Model Kernel. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2012, 45, 420-425.	0.4	1
42	Nanog-dependent feedback loops regulate murine embryonic stem cell heterogeneity. Nature Cell Biology, 2012, 14, 1139-1147.	4.6	141
43	What Can Networks Do for You?. , 2012, , 173-194.		0
44	Quantifying stability in gene list ranking across microarray derived clinical biomarkers. BMC Medical Genomics, 2011, 4, 73.	0.7	13
45	Efficient reengineering of meso-scale topologies for functional networks in biomedical applications. Journal of Mathematics in Industry, 2011, 1, 6.	0.7	6
46	Few inputs can reprogram biological networks. Nature, 2011, 478, E4-E4.	13.7	96
47	An elastic network model to identify characteristic stress response genes. Computational Biology and Chemistry, 2010, 34, 193-202.	1.1	1
48	Local identification of scalar hybrid models with tree structure. IMA Journal of Applied Mathematics, 2008, 73, 449-476.	0.8	36
49	Application of Data Mining and Evolutionary Optimization in Catalyst Discovery and High-Throughput Experimentation: Techniques, Strategies, and Software. ChemInform, 2005, 36, no.	0.1	0
50	Application of Data Mining and Evolutionary Optimization in Catalyst Discovery and High-Throughput Experimentation - Techniques, Strategies, and Software. QSAR and Combinatorial Science, 2005, 24, 29-37.	1.5	16
51	Data Mining mit Prozessdaten (Data Mining with Process Data). Automatisierungstechnik, 2005, 53, 342-349.	0.4	1
52	Extrapolability of structured hybrid models: a key to optimization of complex processes. , 2000, , 1135-1151.		11
53	Modelling the influence of monomer properties on hydrogen bond density in oriented, rigid copolymer systems. Journal of the Chemical Society, Faraday Transactions, 1995, 91, 2629.	1.7	0
54	Different Spreading Dynamics Throughout Germany During the Second Wave of the COVID-19 Pandemic: Link to Public Health Interventions. SSRN Electronic Journal, 0, , .	0.4	1