

# Christiane Fuchs

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8887954/christiane-fuchs-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

44  
papers

609  
citations

14  
h-index

24  
g-index

48  
ext. papers

820  
ext. citations

5.4  
avg. IF

3.82  
L-index

#	Paper	IF	Citations
44	Prediction of overall survival for patients with metastatic castration-resistant prostate cancer: development of a prognostic model through a crowdsourced challenge with open clinical trial data. <i>Lancet Oncology, The</i> , <b>2017</b> , 18, 132-142	21.7	90
43	Atrx promotes heterochromatin formation at retrotransposons. <i>EMBO Reports</i> , <b>2015</b> , 16, 836-50	6.5	79
42	Inference for Diffusion Processes <b>2013</b> ,		49
41	Dissection of cell cycle-dependent dynamics of Dnmt1 by FRAP and diffusion-coupled modeling. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, 4860-76	20.1	46
40	Metabolite profiling reveals new insights into the regulation of serum urate in humans. <i>Metabolomics</i> , <b>2014</b> , 10, 141-151	4.7	36
39	Parameterizing cell-to-cell regulatory heterogeneities via stochastic transcriptional profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E626-35	11.5	29
38	Protocol of a population-based prospective COVID-19 cohort study Munich, Germany (KoCo19). <i>BMC Public Health</i> , <b>2020</b> , 20, 1036	4.1	26
37	Inter-chromosomal contact networks provide insights into Mammalian chromatin organization. <i>PLoS ONE</i> , <b>2015</b> , 10, e0126125	3.7	23
36	In Search of the SARS-CoV-2 Protection Correlate: Head-to-Head Comparison of Two Quantitative S1 Assays in Pre-characterized Oligo-/Asymptomatic Patients. <i>Infectious Diseases and Therapy</i> , <b>2021</b> , 10, 1505-1518	6.2	23
35	Model selection using limiting distributions of second-order blind source separation algorithms. <i>Signal Processing</i> , <b>2015</b> , 113, 95-103	4.4	22
34	High risk of recurrent venous thromboembolism in BCR-ABL-negative myeloproliferative neoplasms after termination of anticoagulation. <i>Annals of Hematology</i> , <b>2019</b> , 98, 93-100	3	20
33	Prevalence and Risk Factors of Infection in the Representative COVID-19 Cohort Munich. <i>International Journal of Environmental Research and Public Health</i> , <b>2021</b> , 18,	4.6	19
32	Metabolomics reveals determinants of weight loss during lifestyle intervention in obese children. <i>Metabolomics</i> , <b>2013</b> , 9, 1157-1167	4.7	17
31	A strategy for high-dimensional multivariable analysis classifies childhood asthma phenotypes from genetic, immunological, and environmental factors. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , <b>2019</b> , 74, 1364-1373	9.3	16
30	A mechanistic model for the negative binomial distribution of single-cell mRNA counts		11
29	Pheno-seq - linking visual features and gene expression in 3D cell culture systems. <i>Scientific Reports</i> , <b>2019</b> , 9, 12367	4.9	10
28	CORALINA: a universal method for the generation of gRNA libraries for CRISPR-based screening. <i>BMC Genomics</i> , <b>2016</b> , 17, 917	4.5	10

27	Asthma in farm children is more determined by genetic polymorphisms and in non-farm children by environmental factors. <i>Pediatric Allergy and Immunology</i> , <b>2021</b> , 32, 295-304	4.2	8
26	A DREAM Challenge to Build Prediction Models for Short-Term Discontinuation of Docetaxel in Metastatic Castration-Resistant Prostate Cancer. <i>JCO Clinical Cancer Informatics</i> , <b>2017</b> , 1, 1-15	5.2	7
25	Significant association of cutaneous adverse events with hydroxyurea: results from a prospective non-interventional study in BCR-ABL1-negative myeloproliferative neoplasms (MPN) - on behalf of the German Study Group-MPN. <i>Leukemia</i> , <b>2021</b> , 35, 628-631	10.7	7
24	Correcting Classifiers for Sample Selection Bias in Two-Phase Case-Control Studies. <i>Computational and Mathematical Methods in Medicine</i> , <b>2017</b> , 2017, 7847531	2.8	6
23	Broad T Cell Targeting of Structural Proteins After SARS-CoV-2 Infection: High Throughput Assessment of T Cell Reactivity Using an Automated Interferon Gamma Release Assay. <i>Frontiers in Immunology</i> , <b>2021</b> , 12, 688436	8.4	6
22	A Serology Strategy for Epidemiological Studies Based on the Comparison of the Performance of Seven Different Test Systems - The Representative COVID-19 Cohort Munich		6
21	netReg: network-regularized linear models for biological association studies. <i>Bioinformatics</i> , <b>2018</b> , 34, 896-898	7.2	5
20	Ruxolitinib-treated polycythemia vera patients and their risk of secondary malignancies. <i>Annals of Hematology</i> , <b>2021</b> , 100, 2707-2716	3	5
19	Non parametric estimation for fractional diffusion processes with random effects. <i>Statistics</i> , <b>2019</b> , 53, 753-769	0.5	4
18	Identifying latent dynamic components in biological systems. <i>IET Systems Biology</i> , <b>2015</b> , 9, 193-203	1.4	4
17	Head-to-head evaluation of seven different seroassays including direct viral neutralisation in a representative cohort for SARS-CoV-2. <i>Journal of General Virology</i> , <b>2021</b> , 102,	4.9	4
16	Bayesian blind source separation for data with network structure. <i>Journal of Computational Biology</i> , <b>2014</b> , 21, 855-65	1.7	3
15	From first to second wave: follow-up of the prospective COVID-19 cohort (KoCo19) in Munich (Germany). <i>BMC Infectious Diseases</i> , <b>2021</b> , 21, 925	4	3
14	Integrative modelling of reported case numbers and seroprevalence reveals time-dependent test efficiency and infection rates		2
13	Three general concepts to improve risk prediction: good data, wisdom of the crowd, recalibration. <i>F1000Research</i> , <b>5</b> , 2671	3.6	2
12	Bayesian inference for diffusion processes: using higher-order approximations for transition densities. <i>Royal Society Open Science</i> , <b>2020</b> , 7, 200270	3.3	2
11	stochprofML: stochastic profiling using maximum likelihood estimation in R. <i>BMC Bioinformatics</i> , <b>2021</b> , 22, 123	3.6	2
10	From first to second wave: follow-up of the prospective Covid-19 cohort (KoCo19) in Munich (Germany)		2

9	CLUE: a bioinformatic and wet-lab pipeline for multiplexed cloning of custom sgRNA libraries. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, e78	20.1	1
8	Bleeding complications in bcr-abl-negative myeloproliferative neoplasms (MPN): A retrospective single-center study of 829 MPN patients. <i>European Journal of Haematology</i> , <b>2021</b> , 108, 154	3.8	1
7	Inferring catalysis in biological systems. <i>IET Systems Biology</i> , <b>2016</b> , 10, 210-218	1.4	1
6	Impact of Brain Fatty Acid Signaling on Peripheral Insulin Action in Mice. <i>Experimental and Clinical Endocrinology and Diabetes</i> , <b>2020</b> , 128, 20-29	2.3	1
5	The interplay of viral loads, clinical presentation, and serological responses in SARS-CoV-2 - Results from a prospective cohort of outpatient COVID-19 cases.. <i>Virology</i> , <b>2022</b> , 569, 37-43	3.6	1
4	Adapted single-cell consensus clustering (adaSC3). <i>Advances in Data Analysis and Classification</i> , <b>2020</b> , 14, 885-896	1.8	0
3	An MCMC computational approach for a continuous time state-dependent regime switching diffusion process. <i>Journal of Applied Statistics</i> , <b>2020</b> , 47, 1354-1374	1	0
2	Identifiability analysis for models of the translation kinetics after mRNA transfection.. <i>Journal of Mathematical Biology</i> , <b>2022</b> , 84, 56	2	0
1	Application II: Analysis of Molecular Binding <b>2013</b> , 305-369		