## Tim O F Conrad

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/5072169/publications.pdf

Version: 2024-02-01

623574 526166 36 800 14 27 citations g-index h-index papers 40 40 40 1266 docs citations times ranked citing authors all docs

#	Article	IF	Citations
1	Serum amino acid profiles and their alterations in colorectal cancer. Metabolomics, 2012, 8, 643-653.	1.4	117
2	Serum Peptidome Profiling Revealed Platelet Factor 4 as a Potential Discriminating Peptide Associated with Pancreatic Cancer. Clinical Cancer Research, 2009, 15, 3812-3819.	3.2	101
3	Transfer learning for ECG classification. Scientific Reports, 2021, 11, 5251.	1.6	95
4	Acfs: accurate circRNA identification and quantification from RNA-Seq data. Scientific Reports, 2016, 6, 38820.	1.6	70
5	elF5A hypusination, boosted by dietary spermidine, protects from premature brain aging and mitochondrial dysfunction. Cell Reports, 2021, 35, 108941.	2.9	56
6	Pancreatic carcinoma, pancreatitis, and healthy controls: metabolite models in a three-class diagnostic dilemma. Metabolomics, 2013, 9, 677-687.	1.4	39
7	Can we distinguish respiratory viral infections based on clinical features? A prospective pediatric cohort compared to systematic literature review. Reviews in Medical Virology, 2018, 28, e1997.	3.9	38
8	Educating parents about the vaccination status of their children: A user-centered mobile application. Preventive Medicine Reports, 2017, 5, 241-250.	0.8	32
9	Human Parechovirus Infections Associated with Seizures and Rash in Infants and Toddlers. Pediatric Infectious Disease Journal, 2015, 34, 1049-1055.	1.1	29
10	Enabling Precision Medicine With Digital Case Classification at the Point-of-Care. EBioMedicine, 2016, 4, 191-196.	2.7	26
11	Influenza and other respiratory viruses: standardizing disease severity in surveillance and clinical trials. Expert Review of Anti-Infective Therapy, 2017, 15, 545-568.	2.0	26
12	Sparse Proteomics Analysis – a compressed sensing-based approach for feature selection and classification of high-dimensional proteomics mass spectrometry data. BMC Bioinformatics, 2017, 18, 160.	1.2	21
13	Combining Phage Display and Next-Generation Sequencing for Materials Sciences: A Case Study on Probing Polypropylene Surfaces. Journal of the American Chemical Society, 2020, 142, 10624-10628.	6.6	21
14	An Inception Cohort Study Assessing the Role of Pneumococcal and other Bacterial Pathogens in Children with Influenza and ILI and a Clinical Decision Model for Stringent Antibiotic Use. Antiviral Therapy, 2016, 21, 413-424.	0.6	15
15	Accuracy of the unified approach in maternally influenced traits - illustrated by a simulation study in the honey bee (Apis mellifera). BMC Genetics, 2013, 14, 36.	2.7	14
16	Modularity revisited: A novel dynamics-based concept for decomposing complex networks. Journal of Computational Dynamics, 2014, 1, 191-212.	0.4	14
17	Prediction of Covid-19 spreading and optimal coordination of counter-measures: From microscopic to macroscopic models to Pareto fronts. PLoS ONE, 2021, 16, e0249676.	1.1	13
18	Towards a Personalised Approach to Managing Influenza Infections in Infants and Children – Food for Thought and a Note on Oseltamivir. Infectious Disorders - Drug Targets, 2013, 13, 25-33.	0.4	8

#	Article	IF	CITATIONS
19	Innovative Digital Tools and Surveillance Systems for the Timely Detection of Adverse Events at the Point of Care: A Proof-of-Concept Study. Drug Safety, 2016, 39, 977-988.	1.4	8
20	Finding metastable states in real-world time series with recurrence networks. Physica A: Statistical Mechanics and Its Applications, 2016, 445, 1-17.	1.2	7
21	Beating the Noise: New Statistical Methods for Detecting Signals in MALDI-TOF Spectra Below Noise Level. Lecture Notes in Computer Science, 2006, , 119-128.	1.0	7
22	Simulating a base population in honey bee for molecular genetic studies. Genetics Selection Evolution, 2012, 44, 14.	1.2	6
23	Reusable building blocks in biological systems. Journal of the Royal Society Interface, 2018, 15, 20180595.	1.5	6
24	EMT network-based feature selection improves prognosis prediction in lung adenocarcinoma. PLoS ONE, 2019, 14, e0204186.	1.1	6
25	Surface-enhanced laser desorption/ionization time-of-flight mass spectrometry: serum protein profiling in seminoma patients. World Journal of Urology, 2010, 28, 193-197.	1.2	4
26	Epithelial-Mesenchymal Transition Regulatory Network-Based Feature Selection in Lung Cancer Prognosis Prediction. Lecture Notes in Computer Science, 2016, , 135-146.	1.0	4
27	Learning Chemical Reaction Networks from Trajectory Data. SIAM Journal on Applied Dynamical Systems, 2019, 18, 2000-2046.	0.7	3
28	GraphKKE: graph Kernel Koopman embedding for human microbiome analysis. Applied Network Science, 2020, 5, .	0.8	3
29	Epithelial Mesenchymal Transition Network-Based Feature Engineering in Lung Adenocarcinoma Prognosis Prediction Using Multiple Omic Data. Genomics and Computational Biology, 2017, 3, 57.	0.7	3
30	Inferring Proteolytic Processes from Mass Spectrometry Time Series Data Using Degradation Graphs. PLoS ONE, 2012, 7, e40656.	1.1	2
31	Deep Learning for Proteomics Data for Feature Selection and Classification. Lecture Notes in Computer Science, 2019, , 301-316.	1.0	2
32	Minimum-overlap Clusterings and the Sparsity of Overcomplete Decompositions of Binary Matrices. Procedia Computer Science, 2015, 51, 2967-2971.	1.2	1
33	Linking digital surveillance and in-depth virology to study clinical patterns of viral respiratory infections in vulnerable patient populations. IScience, 2022, 25, 104276.	1.9	1
34	A Convergent Discretization Method for Transition Path Theory for Diffusion Processes. Multiscale Modeling and Simulation, 2021, 19, 242-266.	0.6	0
35	Finding Modules in Networks with Non-modular Regions. Lecture Notes in Computer Science, 2013, , 188-199.	1.0	0
36	Dictionary learning for transcriptomics data reveals type-specific gene modules in a multi-class setting. IT - Information Technology, 2020, 62, 119-134.	0.6	0