

Anne-Christin Hauschild

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5984115/publications.pdf>

Version: 2024-02-01

34
papers

1,137
citations

516710

16
h-index

434195

31
g-index

37
all docs

37
docs citations

37
times ranked

1872
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of antimicrobial resistance based on whole-genome sequencing and machine learning. <i>Bioinformatics</i> , 2022, 38, 325-334.	4.1	54
2	Federated Random Forests can improve local performance of predictive models for various healthcare applications. <i>Bioinformatics</i> , 2022, 38, 2278-2286.	4.1	23
3	Evaluation of machine learning strategies for imaging confirmed prostate cancer recurrence prediction on electronic health records. <i>Computers in Biology and Medicine</i> , 2022, 143, 105263.	7.0	6
4	Fractal construction of constrained code words for DNA storage systems. <i>Nucleic Acids Research</i> , 2022, 50, e30-e30.	14.5	14
5	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	6.5	110
6	Genome-wide analysis suggests the importance of vascular processes and neuroinflammation in late-life antidepressant response. <i>Translational Psychiatry</i> , 2021, 11, 127.	4.8	22
7	A large-scale comparative study on peptide encodings for biomedical classification. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab039.	3.2	15
8	Integrative Analysis of Next-Generation Sequencing for Next-Generation Cancer Research toward Artificial Intelligence. <i>Cancers</i> , 2021, 13, 3148.	3.7	15
9	Fostering reproducibility, reusability, and technology transfer in health informatics. <i>IScience</i> , 2021, 24, 102803.	4.1	3
10	Transfer learning compensates limited data, batch effects and technological heterogeneity in single-cell sequencing. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab104.	3.2	8
11	Interleukin-6 Gene Expression Changes after a 4-Week Intake of a Multispecies Probiotic in Major Depressive Disorder—Preliminary Results of the PROVIT Study. <i>Nutrients</i> , 2020, 12, 2575.	4.1	28
12	Urinary proteomics links keratan sulfate degradation and lysosomal enzymes to early type 1 diabetes. <i>PLoS ONE</i> , 2020, 15, e0233639.	2.5	6
13	CORDITE: The Curated CORona Drug INTERactions Database for SARS-CoV-2. <i>IScience</i> , 2020, 23, 101297.	4.1	30
14	Visualization of Biomedical Networks. , 2019, , 1016-1035.		2
15	S79. Predicting Venlafaxine Remission in Late-Life Depression Using Genome-Wide and Clinical Data. <i>Biological Psychiatry</i> , 2019, 85, S327-S328.	1.3	0
16	F24SYSTEMS BIOLOGY APPROACH TO EVALUATE GENETIC FACTORS OF ANTIPSYCHOTIC INDUCED WEIGHT GAIN IN PATIENTS WITH SCHIZOPHRENIA. <i>European Neuropsychopharmacology</i> , 2019, 29, S1122.	0.7	0
17	CWAS-based machine learning approach to predict duloxetine response in major depressive disorder. <i>Journal of Psychiatric Research</i> , 2018, 99, 62-68.	3.1	60
18	mirDIP 4.1—integrative database of human microRNA target predictions. <i>Nucleic Acids Research</i> , 2018, 46, D360-D370.	14.5	430

#	ARTICLE	IF	CITATIONS
19	LifeStyle-Specific-Islands (LISSI): Integrated Bioinformatics Platform for Genomic Island Analysis. Journal of Integrative Bioinformatics, 2017, 14, .	1.5	1
20	Machine Learning for In Silico Modeling of Tumor Growth. Lecture Notes in Computer Science, 2016, , 415-434.	1.3	7
21	Volatile Organic Compounds during Inflammation and Sepsis in Rats. Anesthesiology, 2015, 122, 117-126.	2.5	32
22	Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles. Metabolites, 2015, 5, 344-363.	2.9	18
23	Signals of neutropenia in human breath?. International Journal for Ion Mobility Spectrometry, 2014, 17, 19-23.	1.4	5
24	On the limits of computational functional genomics for bacterial lifestyle prediction. Briefings in Functional Genomics, 2014, 13, 398-408.	2.7	11
25	MIMAâ€”a software for analyte identification in MCC/IMS chromatograms by mapping accompanying GC/MS measurements. International Journal for Ion Mobility Spectrometry, 2014, 17, 95-101.	1.4	12
26	On the importance of statistics in breath analysisâ€”hope or curse?. Journal of Breath Research, 2014, 8, 012001.	3.0	17
27	Classification of Breast Cancer Subtypes by combining Gene Expression and DNA Methylation Data. Journal of Integrative Bioinformatics, 2014, 11, 1-14.	1.5	52
28	Classification of breast cancer subtypes by combining gene expression and DNA methylation data. Journal of Integrative Bioinformatics, 2014, 11, 236.	1.5	23
29	An Integrative Clinical Database and Diagnostics Platform for Biomarker Identification and Analysis in Ion Mobility Spectra of Human Exhaled Air. Journal of Integrative Bioinformatics, 2013, 10, 35-47.	1.5	10
30	Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches. Metabolites, 2013, 3, 277-293.	2.9	24
31	An integrative clinical database and diagnostics platform for biomarker identification and analysis in ion mobility spectra of human exhaled air. Journal of Integrative Bioinformatics, 2013, 10, 218.	1.5	5
32	Computational Methods for Metabolomic Data Analysis of Ion Mobility Spectrometry Data—Reviewing the State of the Art. Metabolites, 2012, 2, 733-755.	2.9	29
33	Integrated statistical learning of metabolic ion mobility spectrometry profiles for pulmonary disease identification. Genetics and Molecular Research, 2012, 11, 2733-2744.	0.2	42
34	Robust modelling, measurement and analysis of human and animal metabolic systems. Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences, 2009, 367, 1971-1992.	3.4	5