

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

586496

16
h-index

488211

31
g-index

37
all docs

37
docs citations

37
times ranked

2029
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.	1.8	54
2	Federated Random Forests can improve local performance of predictive models for various healthcare applications. <i>Bioinformatics</i> , 2022, 38, 2278-2286.	1.8	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.	3.9	6
4	Fractal construction of constrained code words for DNA storage systems. <i>Nucleic Acids Research</i> , 2022, 50, e30-e30.	6.5	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.	3.2	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.	2.4	22
7	A large-scale comparative study on peptide encodings for biomedical classification. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab039.	1.5	15
8	Integrative Analysis of Next-Generation Sequencing for Next-Generation Cancer Research toward Artificial Intelligence. <i>Cancers</i> , 2021, 13, 3148.	1.7	15
9	Fostering reproducibility, reusability, and technology transfer in health informatics. <i>IScience</i> , 2021, 24, 102803.	1.9	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.	1.5	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.	1.7	28
12	Urinary proteomics links keratan sulfate degradation and lysosomal enzymes to early type 1 diabetes. <i>PLoS ONE</i> , 2020, 15, e0233639.	1.1	6
13	CORDITE: The Curated CORona Drug INTERactions Database for SARS-CoV-2. <i>IScience</i> , 2020, 23, 101297.	1.9	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.	0.7	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.	0.3	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.	1.5	60
18	mirDIP 4.1—integrative database of human microRNA target predictions. <i>Nucleic Acids Research</i> , 2018, 46, D360-D370.	6.5	430

#	ARTICLE	IF	CITATIONS
19	LifeStyle-Specific-Islands (LISSI): Integrated Bioinformatics Platform for Genomic Island Analysis. <i>Journal of Integrative Bioinformatics</i> , 2017, 14, .	1.0	1
20	Machine Learning for In Silico Modeling of Tumor Growth. <i>Lecture Notes in Computer Science</i> , 2016, , 415-434.	1.0	7
21	Volatile Organic Compounds during Inflammation and Sepsis in Rats. <i>Anesthesiology</i> , 2015, 122, 117-126.	1.3	32
22	Carotta: Revealing Hidden Confounder Markers in Metabolic Breath Profiles. <i>Metabolites</i> , 2015, 5, 344-363.	1.3	18
23	Signals of neutropenia in human breath?. <i>International Journal for Ion Mobility Spectrometry</i> , 2014, 17, 19-23.	1.4	5
24	On the limits of computational functional genomics for bacterial lifestyle prediction. <i>Briefings in Functional Genomics</i> , 2014, 13, 398-408.	1.3	11
25	MIMA—a software for analyte identification in MCC/IMS chromatograms by mapping accompanying GC/MS measurements. <i>International Journal for Ion Mobility Spectrometry</i> , 2014, 17, 95-101.	1.4	12
26	On the importance of statistics in breath analysis—hope or curse?. <i>Journal of Breath Research</i> , 2014, 8, 012001.	1.5	17
27	Classification of Breast Cancer Subtypes by combining Gene Expression and DNA Methylation Data. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 1-14.	1.0	52
28	Classification of breast cancer subtypes by combining gene expression and DNA methylation data. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 236.	1.0	23
29	An Integrative Clinical Database and Diagnostics Platform for Biomarker Identification and Analysis in Ion Mobility Spectra of Human Exhaled Air. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 35-47.	1.0	10
30	Peak Detection Method Evaluation for Ion Mobility Spectrometry by Using Machine Learning Approaches. <i>Metabolites</i> , 2013, 3, 277-293.	1.3	24
31	An integrative clinical database and diagnostics platform for biomarker identification and analysis in ion mobility spectra of human exhaled air. <i>Journal of Integrative Bioinformatics</i> , 2013, 10, 218.	1.0	5
32	Computational Methods for Metabolomic Data Analysis of Ion Mobility Spectrometry Data—Reviewing the State of the Art. <i>Metabolites</i> , 2012, 2, 733-755.	1.3	29
33	Integrated statistical learning of metabolic ion mobility spectrometry profiles for pulmonary disease identification. <i>Genetics and Molecular Research</i> , 2012, 11, 2733-2744.	0.3	42
34	Robust modelling, measurement and analysis of human and animal metabolic systems. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2009, 367, 1971-1992.	1.6	5