

ChloÃ©-Agathe Azencott

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7661485/publications.pdf>

Version: 2024-02-01

30
papers

972
citations

933447

10
h-index

713466

21
g-index

49
all docs

49
docs citations

49
times ranked

2239
citing authors

#	ARTICLE	IF	CITATIONS
1	The Evaluation of Tools Used to Predict the Impact of Missense Variants Is Hindered by Two Types of Circularity. <i>Human Mutation</i> , 2015, 36, 513-523.	2.5	283
2	Learning to Predict Chemical Reactions. <i>Journal of Chemical Information and Modeling</i> , 2011, 51, 2209-2222.	5.4	148
3	A CROC stronger than ROC: measuring, visualizing and optimizing early retrieval. <i>Bioinformatics</i> , 2010, 26, 1348-1356.	4.1	88
4	Crowdsourced assessment of common genetic contribution to predicting anti-TNF treatment response in rheumatoid arthritis. <i>Nature Communications</i> , 2016, 7, 12460.	12.8	73
5	One- to Four-Dimensional Kernels for Virtual Screening and the Prediction of Physical, Chemical, and Biological Properties. <i>Journal of Chemical Information and Modeling</i> , 2007, 47, 965-974.	5.4	56
6	Efficient network-guided multi-locus association mapping with graph cuts. <i>Bioinformatics</i> , 2013, 29, i171-i179.	4.1	52
7	Influence Relevance Voting: An Accurate And Interpretable Virtual High Throughput Screening Method. <i>Journal of Chemical Information and Modeling</i> , 2009, 49, 756-766.	5.4	49
8	Machine learning and genomics: precision medicine versus patient privacy. <i>Philosophical Transactions Series A, Mathematical, Physical, and Engineering Sciences</i> , 2018, 376, 20170350.	3.4	46
9	Block HSIC Lasso: model-free biomarker detection for ultra-high dimensional data. <i>Bioinformatics</i> , 2019, 35, i427-i435.	4.1	44
10	GLIDE: GPU-Based Linear Regression for Detection of Epistasis. <i>Human Heredity</i> , 2012, 73, 220-236.	0.8	32
11	Efficient multi-task chemogenomics for drug specificity prediction. <i>PLoS ONE</i> , 2018, 13, e0204999.	2.5	10
12	The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.	19.0	9
13	Novel methods for epistasis detection in genome-wide association studies. <i>PLoS ONE</i> , 2020, 15, e0242927.	2.5	9
14	Multi-Task Feature Selection on Multiple Networks via Maximum Flows. , 2014, , .		7
15	Drug Target Identification with Machine Learning: How to Choose Negative Examples. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5118.	4.1	6
16	Interpretable network-guided epistasis detection. <i>GigaScience</i> , 2022, 11, .	6.4	5
17	The French Early Breast Cancer Cohort (FRESH): A Resource for Breast Cancer Research and Evaluations of Oncology Practices Based on the French National Healthcare System Database (SNDS). <i>Cancers</i> , 2022, 14, 2671.	3.7	5
18	Network-Guided Biomarker Discovery. <i>Lecture Notes in Computer Science</i> , 2016, , 319-336.	1.3	4

#	ARTICLE	IF	CITATIONS
19	Boosting GWAS using biological networks: A study on susceptibility to familial breast cancer. PLoS Computational Biology, 2021, 17, e1008819.	3.2	4
20	A new hybrid record linkage process to make epidemiological databases interoperable: application to the GEMO and GENEPSO studies involving BRCA1 and BRCA2 mutation carriers. BMC Medical Research Methodology, 2021, 21, 155.	3.1	3
21	A systematic analysis of gene-gene interaction in multiple sclerosis. BMC Medical Genomics, 2022, 15, 100.	1.5	3
22	Where Do We Stand in Regularization for Life Science Studies?. Journal of Computational Biology, 2022, 29, 213-232.	1.6	1
23	MULTITASK FEATURE SELECTION WITH TASK DESCRIPTORS. , 2016, , .		1
24	Multitask group Lasso for Genome Wide association Studies in diverse populations. , 2021, , .		0
25	Multitask group Lasso for Genome Wide association Studies in diverse populations. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 163-174.	0.7	0
26	Novel methods for epistasis detection in genome-wide association studies. , 2020, 15, e0242927.		0
27	Novel methods for epistasis detection in genome-wide association studies. , 2020, 15, e0242927.		0
28	Novel methods for epistasis detection in genome-wide association studies. , 2020, 15, e0242927.		0
29	Novel methods for epistasis detection in genome-wide association studies. , 2020, 15, e0242927.		0
30	Novel methods for epistasis detection in genome-wide association studies. , 2020, 15, e0242927.		0