

# David Page

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7456702/publications.pdf>

Version: 2024-02-01

18  
papers

382  
citations

840776

11  
h-index

888059

17  
g-index

21  
all docs

21  
docs citations

21  
times ranked

708  
citing authors

#	ARTICLE	IF	CITATIONS
1	Artificial intelligence-assisted phenotype discovery of fragile X syndrome in a population-based sample. <i>Genetics in Medicine</i> , 2021, 23, 1273-1280.	2.4	16
2	Machine learning approach to measurement of criticism: The core dimension of expressed emotion.. <i>Journal of Family Psychology</i> , 2021, 35, 1007-1015.	1.3	2
3	KinderMiner Web: a simple web tool for ranking pairwise associations in biomedical applications. <i>F1000Research</i> , 2020, 9, 832.	1.6	1
4	Data-driven phenotype discovery of <i>FMR1</i> premutation carriers in a population-based sample. <i>Science Advances</i> , 2019, 5, eaaw7195.	10.3	33
5	Applying family analyses to electronic health records to facilitate genetic research. <i>Bioinformatics</i> , 2018, 34, 635-642.	4.1	8
6	Health Profiles of Mosaic Versus Non-mosaic <i>FMR1</i> Premutation Carrier Mothers of Children With Fragile X Syndrome. <i>Frontiers in Genetics</i> , 2018, 9, 173.	2.3	18
7	Drug-Drug Interaction Discovery: Kernel Learning from Heterogeneous Similarities. <i>Smart Health</i> , 2018, 9-10, 88-100.	3.2	14
8	Using machine learning to identify patterns of lifetime health problems in decedents with autism spectrum disorder. <i>Autism Research</i> , 2018, 11, 1120-1128.	3.8	47
9	Comparative Evaluation of MS-based Metabolomics Software and Its Application to Preclinical Alzheimer's Disease. <i>Scientific Reports</i> , 2018, 8, 9291.	3.3	45
10	Markov logic networks for adverse drug event extraction from text. <i>Knowledge and Information Systems</i> , 2017, 51, 435-457.	3.2	10
11	Adverse Drug Event Discovery Using Biomedical Literature: A Big Data Neural Network Adventure. <i>JMIR Medical Informatics</i> , 2017, 5, e51.	2.6	46
12	A Simple Text Mining Approach for Ranking Pairwise Associations in Biomedical Applications. <i>AMIA Summits on Translational Science Proceedings</i> , 2017, 2017, 166-174.	0.4	15
13	In-Depth Characterization and Validation of Human Urine Metabolomes Reveal Novel Metabolic Signatures of Lower Urinary Tract Symptoms. <i>Scientific Reports</i> , 2016, 6, 30869.	3.3	31
14	Structure-Leveraged Methods in Breast Cancer Risk Prediction. <i>Journal of Machine Learning Research</i> , 2016, 17, .	62.4	5
15	Phenome-wide association studies (PheWASs) for functional variants. <i>European Journal of Human Genetics</i> , 2015, 23, 523-529.	2.8	38
16	Relational machine learning for electronic health record-driven phenotyping. <i>Journal of Biomedical Informatics</i> , 2014, 52, 260-270.	4.3	47
17	Multiple Testing under Dependence via Semiparametric Graphical Models. <i>JMLR Workshop and Conference Proceedings</i> , 2014, 32, 955-963.	1.4	1
18	KinderMiner Web: a simple web tool for ranking pairwise associations in biomedical applications. <i>F1000Research</i> , 0, 9, 832.	1.6	3