

Thomas P Quinn

List of Publications by Year in descending order

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29
papers

1,611
citations

706676

14
h-index

536525

29
g-index

48
all docs

48
docs citations

48
times ranked

2031
citing authors

#	ARTICLE	IF	CITATIONS
1	GraphDTA: predicting drug-target binding affinity with graph neural networks. <i>Bioinformatics</i> , 2021, 37, 1140-1147.	1.8	343
2	Understanding sequencing data as compositions: an outlook and review. <i>Bioinformatics</i> , 2018, 34, 2870-2878.	1.8	224
3	A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019, 8, .	3.3	187
4	propr: An R-package for Identifying Proportionally Abundant Features Using Compositional Data Analysis. <i>Scientific Reports</i> , 2017, 7, 16252.	1.6	158
5	The three ghosts of medical AI: Can the black-box present deliver?. <i>Artificial Intelligence in Medicine</i> , 2022, 124, 102158.	3.8	73
6	Aza-Crown Macrocycles as Chiral Solvating Agents for Mandelic Acid Derivatives. <i>Journal of Organic Chemistry</i> , 2011, 76, 10020-10030.	1.7	60
7	The maternal gut microbiome during pregnancy and offspring allergy and asthma. <i>Journal of Allergy and Clinical Immunology</i> , 2021, 148, 669-678.	1.5	55
8	Blood transcriptomic comparison of individuals with and without autism spectrum disorder: A combined-samples mega-analysis. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2017, 174, 181-201.	1.1	54
9	Trust and medical AI: the challenges we face and the expertise needed to overcome them. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021, 28, 890-894.	2.2	53
10	Benchmarking differential expression analysis tools for RNA-Seq: normalization-based vs. log-ratio transformation-based methods. <i>BMC Bioinformatics</i> , 2018, 19, 274.	1.2	48
11	Deep in the Bowel: Highly Interpretable Neural Encoder-Decoder Networks Predict Gut Metabolites from Gut Microbiome. <i>BMC Genomics</i> , 2020, 21, 256.	1.2	34
12	Machine-learning classification of 22q11.2 deletion syndrome: A diffusion tensor imaging study. <i>NeuroImage: Clinical</i> , 2017, 15, 832-842.	1.4	22
13	Bioinformatic analyses and conceptual synthesis of evidence linking <i>ZNF804A</i> to risk for schizophrenia and bipolar disorder. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2015, 168, 14-35.	1.1	19
14	Amalgams: data-driven amalgamation for the dimensionality reduction of compositional data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, 1-7.	1.5	19
15	DeepTRIAGE: interpretable and individualised biomarker scores using attention mechanism for the classification of breast cancer sub-types. <i>BMC Medical Genomics</i> , 2020, 13, 20.	0.7	17
16	Interpretable Log Contrasts for the Classification of Health Biomarkers: a New Approach to Balance Selection. <i>MSystems</i> , 2020, 5, .	1.7	16
17	Learning sparse log-ratios for high-throughput sequencing data. <i>Bioinformatics</i> , 2021, 38, 157-163.	1.8	16
18	Examining microbial metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 37-39.	9.0	15

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19	Visualizing balances of compositional data: A new alternative to balance dendrograms. <i>F1000Research</i> , 2018, 7, 1278.	0.8	15
20	Cancer as a Tissue Anomaly: Classifying Tumor Transcriptomes Based Only on Healthy Data. <i>Frontiers in Genetics</i> , 2019, 10, 599.	1.1	12
21	Editorial: Compositional data analysis and related methods applied to genomics—a first special issue from <i>NAR Genomics and Bioinformatics</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, 103.	1.5	10
22	exprso: an R-package for the rapid implementation of machine learning algorithms. <i>F1000Research</i> , 2016, 5, 2588.	0.8	9
23	Solving for X: Evidence for sex-specific autism biomarkers across multiple transcriptomic studies. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 377-389.	1.1	8
24	A cross-cancer metastasis signature in the microRNA-mRNA axis of paired tissue samples. <i>Molecular Biology Reports</i> , 2019, 46, 5919-5930.	1.0	7
25	Gut Microbiome Diversity and Composition Are Associated with Habitual Dairy Intakes: A Cross-Sectional Study in Men. <i>Journal of Nutrition</i> , 2021, 151, 3400-3412.	1.3	6
26	Improving the classification of neuropsychiatric conditions using gene ontology terms as features. <i>American Journal of Medical Genetics Part B: Neuropsychiatric Genetics</i> , 2019, 180, 508-518.	1.1	4
27	Test set verification is an essential step in model building. <i>Methods in Ecology and Evolution</i> , 2021, 12, 127-129.	2.2	4
28	Explaining Black Box Drug Target Prediction Through Model Agnostic Counterfactual Samples. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2023, 20, 1020-1029.	1.9	3
29	Personalized single-cell networks: a framework to predict the response of any gene to any drug for any patient. <i>BioData Mining</i> , 2021, 14, 37.	2.2	2