

Thomas P Quinn

List of Publications by Year in descending order

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Version: 2024-02-01

29
papers

1,611
citations

623734

14
h-index

477307

29
g-index

48
all docs

48
docs citations

48
times ranked

1831
citing authors

#	ARTICLE	IF	CITATIONS
1	GraphDTA: predicting drug–target binding affinity with graph neural networks. <i>Bioinformatics</i> , 2021, 37, 1140-1147.	4.1	343
2	Understanding sequencing data as compositions: an outlook and review. <i>Bioinformatics</i> , 2018, 34, 2870-2878.	4.1	224
3	A field guide for the compositional analysis of any-omics data. <i>GigaScience</i> , 2019, 8, .	6.4	187
4	propr: An R-package for Identifying Proportionally Abundant Features Using Compositional Data Analysis. <i>Scientific Reports</i> , 2017, 7, 16252.	3.3	158
5	The three ghosts of medical AI: Can the black-box present deliver?. <i>Artificial Intelligence in Medicine</i> , 2022, 124, 102158.	6.5	73
6	Aza-Crown Macrocycles as Chiral Solvating Agents for Mandelic Acid Derivatives. <i>Journal of Organic Chemistry</i> , 2011, 76, 10020-10030.	3.2	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.	2.9	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.	1.7	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.	4.4	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.	2.6	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.	2.8	34
12	Machine-learning classification of 22q11.2 deletion syndrome: A diffusion tensor imaging study. <i>NeuroImage: Clinical</i> , 2017, 15, 832-842.	2.7	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.	1.7	19
14	Amalgams: data-driven amalgamation for the dimensionality reduction of compositional data. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, 1-7.	3.2	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.	1.5	17
16	Interpretable Log Contrasts for the Classification of Health Biomarkers: a New Approach to Balance Selection. <i>MSystems</i> , 2020, 5, .	3.8	16
17	Learning sparse log-ratios for high-throughput sequencing data. <i>Bioinformatics</i> , 2021, 38, 157-163.	4.1	16
18	Examining microbe–metabolite correlations by linear methods. <i>Nature Methods</i> , 2021, 18, 37-39.	19.0	15

#	ARTICLE	IF	CITATIONS
19	Visualizing balances of compositional data: A new alternative to balance dendrograms. F1000Research, 2018, 7, 1278.	1.6	15
20	Cancer as a Tissue Anomaly: Classifying Tumor Transcriptomes Based Only on Healthy Data. Frontiers in Genetics, 2019, 10, 599.	2.3	12
21	Editorial:ÂCompositional data analysis and related methods applied to genomicsâ€”a first special issue from <i>NAR Genomics and Bioinformatics</i>. NAR Genomics and Bioinformatics, 2020, 2, lqaa103.	3.2	10
22	exprso: an R-package for the rapid implementation of machine learning algorithms. F1000Research, 2016, 5, 2588.	1.6	9
23	Solving for X: Evidence for sexâ€™specific autism biomarkers across multiple transcriptomic studies. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 377-389.	1.7	8
24	A cross-cancer metastasis signature in the microRNAâ€™mRNA axis of paired tissue samples. Molecular Biology Reports, 2019, 46, 5919-5930.	2.3	7
25	Gut Microbiome Diversity and Composition Are Associated with Habitual Dairy Intakes: A Cross-Sectional Study in Men. Journal of Nutrition, 2021, 151, 3400-3412.	2.9	6
26	Improving the classification of neuropsychiatric conditions using gene ontology terms as features. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2019, 180, 508-518.	1.7	4
27	Test set verification is an essential step in model building. Methods in Ecology and Evolution, 2021, 12, 127-129.	5.2	4
28	Explaining Black Box Drug Target Prediction Through Model Agnostic Counterfactual Samples. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 1020-1029.	3.0	3
29	Personalized single-cell networks: a framework to predict the response of any gene to any drug for any patient. BioData Mining, 2021, 14, 37.	4.0	2