

A Perera

List of Publications by Year in descending order

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Version: 2024-02-01

99
papers

2,019
citations

257450

24
h-index

265206

42
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104
all docs

104
docs citations

104
times ranked

3341
citing authors

#	ARTICLE	IF	CITATIONS
1	Mapping layperson medical terminology into the Human Phenotype Ontology using neural machine translation models. <i>Expert Systems With Applications</i> , 2022, 204, 117446.	7.6	3
2	Eye Vergence Responses During an Attention Task in Adults With ADHD and Clinical Controls. <i>Journal of Attention Disorders</i> , 2021, 25, 1302-1310.	2.6	8
3	The effect of statistical normalization on network propagation scores. <i>Bioinformatics</i> , 2021, 37, 845-852.	4.1	2
4	Global Collaborative Social Network (Share4Rare) to Promote Citizen Science in Rare Disease Research: Platform Development Study. <i>JMIR Formative Research</i> , 2021, 5, e22695.	1.4	6
5	Balancing Data on Deep Learning-Based Proteochemometric Activity Classification. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 1657-1669.	5.4	5
6	MMP1 drives tumor progression in large cell carcinoma of the lung through fibroblast senescence. <i>Cancer Letters</i> , 2021, 507, 1-12.	7.2	33
7	mWISE: An Algorithm for Context-Based Annotation of Liquid Chromatography-Mass Spectrometry Features through Diffusion in Graphs. <i>Analytical Chemistry</i> , 2021, 93, 10772-10778.	6.5	5
8	Game learning analytics of instant messaging and online discussion forums in higher education. <i>Education and Training</i> , 2021, 63, 1288-1308.	3.1	5
9	MultiPaths: a Python framework for analyzing multi-layer biological networks using diffusion algorithms. <i>Bioinformatics</i> , 2021, 37, 137-139.	4.1	3
10	Benchmarking network propagation methods for disease gene identification. <i>PLoS Computational Biology</i> , 2019, 15, e1007276.	3.2	30
11	Heart Failure With Preserved Ejection Fraction Infrequently Evolves Toward a Reduced Phenotype in Long-Term Survivors. <i>Circulation: Heart Failure</i> , 2019, 12, e005652.	3.9	53
12	Evaluation of Cross-Validation Strategies in Sequence-Based Binding Prediction Using Deep Learning. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 1645-1657.	5.4	26
13	Multiview: a software package for multiview pattern recognition methods. <i>Bioinformatics</i> , 2019, 35, 2877-2879.	4.1	3
14	Clinical Validation of Eye Vergence as an Objective Marker for Diagnosis of ADHD in Children. <i>Journal of Attention Disorders</i> , 2019, 23, 599-614.	2.6	25
15	Applying learning analytics to students' interaction in business simulation games. The usefulness of learning analytics to know what students really learn. <i>Computers in Human Behavior</i> , 2019, 92, 600-612.	8.5	53
16	Validity of the Polar V800 monitor for measuring heart rate variability in mountain running route conditions. <i>European Journal of Applied Physiology</i> , 2018, 118, 669-677.	2.5	84
17	diffuStats: an R package to compute diffusion-based scores on biological networks. <i>Bioinformatics</i> , 2018, 34, 533-534.	4.1	23
18	Multiview and multifeature spectral clustering using common eigenvectors. <i>Pattern Recognition Letters</i> , 2018, 102, 30-36.	4.2	34

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19	FELLA: an R package to enrich metabolomics data. BMC Bioinformatics, 2018, 19, 538.	2.6	61
20	Dynamic Trajectories of Left Ventricular Ejection Fraction in Heart Failure. Journal of the American College of Cardiology, 2018, 72, 591-601.	2.8	132
21	Non-targeted metabolomics reveals alterations in liver and plasma of gilt-head bream exposed to oxybenzone. Chemosphere, 2018, 211, 624-631.	8.2	39
22	Baitmet, a computational approach for GC-MS library-driven metabolite profiling. Metabolomics, 2017, 13, 1.	3.0	7
23	Machine-Learning QSAR Model for Predicting Activity against Malaria Parasite's Ion Pump PfATP4 and In Silico Binding Assay Validation. Proceedings (mdpi), 2017, 1, 652.	0.2	1
24	Assessment of Heart Rate Variability during an Endurance Mountain Trail Race by Multi-Scale Entropy Analysis. Entropy, 2017, 19, 658.	2.2	7
25	Early Prediction of Alzheimer's Disease Using Null Longitudinal Model-Based Classifiers. PLoS ONE, 2017, 12, e0168011.	2.5	28
26	Null diffusion-based enrichment for metabolomics data. PLoS ONE, 2017, 12, e0189012.	2.5	29
27	Affected pathways and transcriptional regulators in gene expression response to an ultra-marathon trail: Global and independent activity approaches. PLoS ONE, 2017, 12, e0180322.	2.5	7
28	Applicability of semi-supervised learning assumptions for gene ontology terms prediction. Revista Facultad De Ingenieria, 2016, , .	0.5	1
29	eRah: A Computational Tool Integrating Spectral Deconvolution and Alignment with Quantification and Identification of Metabolites in GC/MS-Based Metabolomics. Analytical Chemistry, 2016, 88, 9821-9829.	6.5	101
30	Avoiding hard chromatographic segmentation: A moving window approach for the automated resolution of gas chromatography-mass spectrometry-based metabolomics signals by multivariate methods. Journal of Chromatography A, 2016, 1474, 145-151.	3.7	6
31	Clinical phenotype clustering in cardiovascular risk patients for the identification of responsive metabolotypes after red wine polyphenol intake. Journal of Nutritional Biochemistry, 2016, 28, 114-120.	4.2	53
32	solarius: an R interface to SOLAR for variance component analysis in pedigrees. Bioinformatics, 2016, 32, 1901-1902.	4.1	24
33	Automated resolution of chromatographic signals by independent component analysis-orthogonal signal deconvolution in comprehensive gas chromatography/mass spectrometry-based metabolomics. Computer Methods and Programs in Biomedicine, 2016, 130, 135-141.	4.7	9
34	The Central Role of KNG1 Gene as a Genetic Determinant of Coagulation Pathway-Related Traits: Exploring Metaphenotypes. PLoS ONE, 2016, 11, e0167187.	2.5	8
35	Sequence information gain based motif analysis. BMC Bioinformatics, 2015, 16, 377.	2.6	1
36	Data set from gas sensor array under flow modulation. Data in Brief, 2015, 3, 131-136.	1.0	2

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37	Training-induced gene expression plasticity in cardiac function and neural regulation for ultra-trail runners. , 2015, , .		0
38	Compound identification in gas chromatography/mass spectrometry-based metabolomics by blind source separation. Journal of Chromatography A, 2015, 1409, 226-233.	3.7	26
39	Aberrant DNA methylation in non-small cell lung cancer-associated fibroblasts. Carcinogenesis, 2015, 36, bgv146.	2.8	84
40	Synthetic benchmarks for machine olfaction: Classification, segmentation and sensor damage. Data in Brief, 2015, 3, 126-130.	1.0	0
41	Bioinspired early detection through gas flow modulation in chemo-sensory systems. Sensors and Actuators B: Chemical, 2015, 206, 538-547.	7.8	33
42	Compound Identification in Comprehensive Gas Chromatographyâ€”Mass Spectrometry-Based Metabolomics by Blind Source Separation. Advances in Intelligent Systems and Computing, 2015, , 49-57.	0.6	0
43	Data Simulation in Machine Olfaction with the R Package Chemosensors. PLoS ONE, 2014, 9, e88839.	2.5	9
44	An R package to analyse LC/MS metabolomic data: MAIT (Metabolite Automatic Identification Toolkit). Bioinformatics, 2014, 30, 1937-1939.	4.1	62
45	Peak Aggregation as an Innovative Strategy for Improving the Predictive Power of LC-MS Metabolomic Profiles. Analytical Chemistry, 2014, 86, 2320-2325.	6.5	9
46	A biomimetic approach to machine olfaction, featuring a very large-scale chemical sensor array and embedded neuro-bio-inspired computation. Microsystem Technologies, 2014, 20, 729-742.	2.0	36
47	Intensity drift removal in LC/MS metabolomics by common variance compensation. Bioinformatics, 2014, 30, 2899-2905.	4.1	56
48	Automatic capacitor bank identification in power distribution systems. Electric Power Systems Research, 2014, 111, 96-102.	3.6	7
49	Predictability of gene ontology slim-terms from primary structure information in Embryophyta plant proteins. BMC Bioinformatics, 2013, 14, 68.	2.6	14
50	Effect of genetic regions on the correlation between single point mutation variability and morbidity. Computers in Biology and Medicine, 2013, 43, 594-599.	7.0	0
51	A software tool for large-scale synthetic experiments based on polymeric sensor arrays. Sensors and Actuators B: Chemical, 2013, 177, 596-604.	7.8	8
52	Biologically inspired large scale chemical sensor arrays and embedded data processing. Proceedings of SPIE, 2013, , .	0.8	1
53	Title is missing!. Journal of Medical and Biological Engineering, 2013, 33, 504.	1.8	1
54	A subspace method for the detection of transcription factor binding sites. Bioinformatics, 2012, 28, 1328-1335.	4.1	6

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55	Multiview approach to spectral clustering. , 2012, 2012, 1254-7.		0
56	Network-based enrichment analysis of gene expression through protein-protein interaction data. , 2012, 2012, 6317-20.		0
57	Biologically Inspired Computation for Chemical Sensing. Procedia Computer Science, 2011, 7, 226-227.	2.0	7
58	Analysis of incomplete gene expression dataset through protein-protein interaction information. , 2011, 2011, 6845-8.		0
59	MEET: Motif elements estimation toolkit. , 2011, 2011, 6483-6.		1
60	A Large Scale Virtual Gas Sensor Array. , 2011, , .		1
61	Odour Mapping Under Strong Backgrounds With a Metal Oxide Sensor Array. , 2011, , .		0
62	Drift compensation of gas sensor array data by common principal component analysis. Sensors and Actuators B: Chemical, 2010, 146, 460-465.	7.8	167
63	Computational Detection of Transcription Factor Binding Sites Through Differential Rényi Entropy. IEEE Transactions on Information Theory, 2010, 56, 734-741.	2.4	6
64	Evaluation of fish spoilage by means of a single metal oxide sensor under temperature modulation. Sensors and Actuators B: Chemical, 2010, 146, 477-482.	7.8	23
65	Drift compensation of gas sensor array data by Orthogonal Signal Correction. Chemometrics and Intelligent Laboratory Systems, 2010, 100, 28-35.	3.5	189
66	Exons and introns characterization in nucleic acid sequences by time-frequency analysis. , 2010, 2010, 1783-6.		0
67	Predictability of protein subcellular locations by pattern recognition techniques. , 2010, 2010, 5512-5.		6
68	An information theory-based tool for characterizing the interaction environment of a protein. , 2010, 2010, 5529-32.		1
69	MISS: a non-linear methodology based on mutual information for genetic association studies in both population and sib-pairs analysis. Bioinformatics, 2010, 26, 1811-1818.	4.1	36
70	Fault detection, identification, and reconstruction of faulty chemical gas sensors under drift conditions, using Principal Component Analysis and Multiscale-PCA. , 2010, , .		10
71	Graph theory-based measures as predictors of gene morbidity. , 2010, 2010, 803-6.		3
72	Transcription factor binding site detection through position cross-mutual information variability analysis. , 2009, 2009, 7087-90.		1

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73	Search of phenotype related candidate genes using gene ontology-based semantic similarity and protein interaction information: Application to Brugada syndrome. , 2009, 2009, 7079-82.		3
74	A new gene-based association test for genome-wide association studies. BMC Proceedings, 2009, 3, S130.	1.6	19
75	Improving Drift Correction by Double Projection Preprocessing in Gas Sensor Arrays. , 2009, , .		1
76	Common Principal Component Analysis For Drift Compensation Of Gas Sensor Array Data. , 2009, , .		9
77	Total solvent amount and human panel test predictions using gas sensor fast chromatography and multivariate linear and non-linear processing. , 2009, , .		0
78	Dimensionality Reduction Oriented Toward the Feature Visualization for Ischemia Detection. IEEE Transactions on Information Technology in Biomedicine, 2009, 13, 590-598.	3.2	13
79	Use of Gene Ontology semantic information in protein interaction data visualization. , 2008, , .		0
80	DNA Binding Site Characterization by Means of R_{nyi} Entropy Measures on Nucleotide Transitions. IEEE Transactions on Nanobioscience, 2008, 7, 133-141.	3.3	4
81	Detection of transcription factor binding sites using R_{nyi} entropy. , 2008, , .		1
82	Floating Feature Selection for multiloci association of quantitative traits in sib-pairs analysis. , 2008, , .		0
83	SNP sets selection under mutual information criterion, application to F7/FVII dataset. , 2008, 2008, 3783-6.		3
84	Clustering of individuals given SNPs similarity based on normalized mutual information: F7 SNPs in the GAIT sample. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2007, 2007, 123-6.	0.5	2
85	On-line novelty detection by recursive dynamic principal component analysis and gas sensor arrays under drift conditions. IEEE Sensors Journal, 2006, 6, 770-783.	4.7	46
86	A dimensionality-reduction technique inspired by receptor convergence in the olfactory system. Sensors and Actuators B: Chemical, 2006, 116, 17-22.	7.8	23
87	Feature extraction on three way nose signals. Sensors and Actuators B: Chemical, 2006, 116, 145-150.	7.8	21
88	Gas measurement systems based on IEEE1451.2 standard. Sensors and Actuators B: Chemical, 2006, 116, 11-16.	7.8	21
89	DNA Binding Sites Characterization by Means of R_{nyi} Entropy Measures on Nucleotide Transitions. , 2006, 2006, 5783-6.		0
90	DNA Binding Sites Characterization by Means of R_{nyi} Entropy Measures on Nucleotide Transitions. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0

#	ARTICLE	IF	CITATIONS
91	A portable electronic nose based on embedded PC technology and GNU/Linux: hardware, software and applications. IEEE Sensors Journal, 2002, 2, 235-246.	4.7	39
92	Fuzzy inference system for sensor array calibration: prediction of CO and CH4 levels in variable humidity conditions. Chemometrics and Intelligent Laboratory Systems, 2002, 64, 103-122.	3.5	20
93	An intelligent detector based on temperature modulation of a gas sensor with a digital signal processor. Sensors and Actuators B: Chemical, 2001, 78, 32-39.	7.8	52
94	A bio-inspired nonlinear algorithm to integrate carbon monoxide concentration aiming to fulfil international standards. Sensors and Actuators B: Chemical, 2000, 69, 308-313.	7.8	2
95	Potato creams recognition from electronic nose and tongue signals: feature extraction/selection and RBF neural networks classifiers. , 0, , .		0
96	Machine olfaction: pattern recognition for the identification of aromas. , 0, , .		2
97	On-line event detection by recursive Dynamic Principal Component Analysis and gas sensor arrays under drift conditions. , 0, , .		5
98	Finding the best calibration points for a gas sensor array with support vector regression. , 0, , .		4
99	Principal discriminants analysis for small-sample-size problems: application to chemical sensing. , 0, , .		8