

Thomas Burger

List of Publications by Year in descending order

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47
papers

1,361
citations

623734

14
h-index

395702

33
g-index

53
all docs

53
docs citations

53
times ranked

2141
citing authors

#	ARTICLE	IF	CITATIONS
1	Accounting for the Multiple Natures of Missing Values in Label-Free Quantitative Proteomics Data Sets to Compare Imputation Strategies. <i>Journal of Proteome Research</i> , 2016, 15, 1116-1125.	3.7	345
2	DAPAR & ProStaR: software to perform statistical analyses in quantitative discovery proteomics. <i>Bioinformatics</i> , 2017, 33, 135-136.	4.1	245
3	Deciphering Thylakoid Sub-compartments using a Mass Spectrometry-based Approach. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2147-2167.	3.8	96
4	Mass-spectrometry-based spatial proteomics data analysis using <tt>pRoloc</tt> and <tt>pRolocdata</tt>. <i>Bioinformatics</i> , 2014, 30, 1322-1324.	4.1	85
5	Calibration plot for proteomics: A graphical tool to visually check the assumptions underlying FDR control in quantitative experiments. <i>Proteomics</i> , 2016, 16, 29-32.	2.2	66
6	Gentle Introduction to the Statistical Foundations of False Discovery Rate in Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 12-22.	3.7	65
7	Toward an Axiomatic Definition of Conflict Between Belief Functions. <i>IEEE Transactions on Cybernetics</i> , 2013, 43, 585-596.	9.5	63
8	A Foundation for Reliable Spatial Proteomics Data Analysis. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1937-1952.	3.8	49
9	A belief-based sequential fusion approach for fusing manual signs and non-manual signals. <i>Pattern Recognition</i> , 2009, 42, 812-822.	8.1	40
10	Beyond Targetâ€Decoy Competition: Stable Validation of Peptide and Protein Identifications in Mass Spectrometry-Based Discovery Proteomics. <i>Analytical Chemistry</i> , 2020, 92, 14898-14906.	6.5	39
11	A Dempsterâ€Shafer Theory based combination of handwriting recognition systems with multiple rejection strategies. <i>Pattern Recognition</i> , 2015, 48, 534-544.	8.1	33
12	A Consistency-Specificity Trade-Off to Select Source Behavior in Information Fusion. <i>IEEE Transactions on Cybernetics</i> , 2015, 45, 598-609.	9.5	31
13	Uses and misuses of the fudge factor in quantitative discovery proteomics. <i>Proteomics</i> , 2016, 16, 1955-1960.	2.2	20
14	Geometric views on conflicting mass functions: From distances to angles. <i>International Journal of Approximate Reasoning</i> , 2016, 70, 36-50.	3.3	18
15	HOW TO RANDOMLY GENERATE MASS FUNCTIONS. <i>International Journal of Uncertainty, Fuzziness and Knowledge-Based Systems</i> , 2013, 21, 645-673.	1.9	14
16	PerTurbo Manifold Learning Algorithm for Weakly Labeled Hyperspectral Image Classification. <i>IEEE Journal of Selected Topics in Applied Earth Observations and Remote Sensing</i> , 2014, 7, 1070-1078.	4.9	13
17	Protein-Level Statistical Analysis of Quantitative Label-Free Proteomics Data with ProStaR. <i>Methods in Molecular Biology</i> , 2019, 1959, 225-246.	0.9	11
18	An analysis of proteogenomics and how and when transcriptome-informed reduction of protein databases can enhance eukaryotic proteomics. <i>Genome Biology</i> , 2022, 23, .	8.8	11

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19	Dempster-Shafer Based Rejection Strategy for Handwritten Word Recognition. , 2011, , .		9
20	Evidential Combination of Multiple HMM Classifiers for Multi-script Handwriting Recognition. Lecture Notes in Computer Science, 2010, , 445-454.	1.3	7
21	Five simple yet essential steps to correctly estimate the rate of false differentially abundant proteins in mass spectrometry analyses. Journal of Proteomics, 2019, 207, 103441.	2.4	7
22	A Low-Cost Natural User Interaction Based on a Camera Hand-Gestures Recognizer. Lecture Notes in Computer Science, 2011, , 214-221.	1.3	7
23	ProMetIS, deep phenotyping of mouse models by combined proteomics and metabolomics analysis. Scientific Data, 2021, 8, 311.	5.3	6
24	Modeling Hesitation and Conflict: A Belief-Based Approach for Multi-class Problems. , 2006, , .		5
25	Random Generation of Mass Functions: A Short Howto. Advances in Intelligent and Soft Computing, 2012, , 145-152.	0.2	5
26	A non-intrusive context-aware system for ambient assisted living in smart home. Health and Technology, 2013, 3, 129-138.	3.6	5
27	Comprehensive and comparative exploration of the <i>Atp7b</i> mouse plasma proteome. Metallomics, 2020, 12, 249-258.	2.4	5
28	A Dempster-Shafer Theory Based Combination of Classifiers for Hand Gesture Recognition. Communications in Computer and Information Science, 2008, , 137-150.	0.5	5
29	Sequential Belief-Based Fusion of Manual and Non-manual Information for Recognizing Isolated Signs. Lecture Notes in Computer Science, 2009, , 134-144.	1.3	5
30	Geodesic Analysis on the Gaussian RKHS Hypersphere. Lecture Notes in Computer Science, 2012, , 299-313.	1.3	5
31	A Non-intrusive Monitoring System for Ambient Assisted Living Service Delivery. Lecture Notes in Computer Science, 2012, , 148-156.	1.3	4
32	Image and Video for Hearing Impaired People. Eurasip Journal on Image and Video Processing, 2007, 2007, 1-14.	2.6	3
33	Distinguishing between Spectral Clustering and Cluster Analysis of Mass Spectra. Journal of Proteome Research, 2018, 18, 571-573.	3.7	3
34	Constructing Dynamic Frames of Discernment in Cases of Large Number of Classes. Lecture Notes in Computer Science, 2011, , 275-286.	1.3	3
35	SAGA: sparse and geometry-aware non-negative matrix factorization through non-linear local embedding. Machine Learning, 2014, 97, 205-226.	5.4	2
36	CHICKN: extraction of peptide chromatographic elution profiles from large scale mass spectrometry data by means of Wasserstein compressive hierarchical cluster analysis. BMC Bioinformatics, 2021, 22, 68.	2.6	2

#	ARTICLE	IF	CITATIONS
37	Sketched Stochastic Dictionary Learning for large-scale data and application to high-throughput mass spectrometry. <i>Statistical Analysis and Data Mining</i> , 0, , .	2.8	2
38	A Generalization of the Pignistic Transform for Partial Bet. <i>Lecture Notes in Computer Science</i> , 2009, , 252-263.	1.3	2
39	Cued Speech Gesture Recognition: A First Prototype Based on Early Reduction. <i>Eurasip Journal on Image and Video Processing</i> , 2007, 2007, 1-19.	2.6	1
40	A Kernel View on Manifold Sub-sampling Based on Karcher Variance Optimization. <i>Lecture Notes in Computer Science</i> , 2013, , 751-758.	1.3	1
41	Selecting Source Behavior in Information Fusion on the Basis of Consistency and Specificity. <i>Lecture Notes in Computer Science</i> , 2013, , 473-484.	1.3	1
42	PEPA test: fast and powerful differential analysis from relative quantitative proteomics data using shared peptides. <i>Biostatistics</i> , 2019, 20, 632-647.	1.5	1
43	Gestural Interfaces for Hearing-Impaired Communication. , 2008, , 219-250.		1
44	Can Omics Biology Go Subjective because of Artificial Intelligence? A Comment on "Challenges and Opportunities for Bayesian Statistics in Proteomics" by Crook et al.. <i>Journal of Proteome Research</i> , 2022, 21, 1783-1786.	3.7	1
45	Extracting Static Hand Gestures in Dynamic Context. , 2006, , .		0
46	Dealing with Precise and Imprecise Decisions with a Dempster-Shafer Theory Based Algorithm in the Context of Handwritten Word Recognition. , 2010, , .		0
47	Geometric Interpretations of Conflict: A Viewpoint. <i>Lecture Notes in Computer Science</i> , 2014, , 412-421.	1.3	0