

Habtom W Resson

List of Publications by Year in descending order

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107
papers

4,623
citations

126907

33
h-index

106344

65
g-index

114
all docs

114
docs citations

114
times ranked

7751
citing authors

#	ARTICLE	IF	CITATIONS
1	The properties of high-dimensional data spaces: implications for exploring gene and protein expression data. <i>Nature Reviews Cancer</i> , 2008, 8, 37-49.	28.4	483
2	LC-MS-based metabolomics. <i>Molecular BioSystems</i> , 2012, 8, 470-481.	2.9	440
3	Metabolite identification and quantitation in LC-MS/MS-based metabolomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2012, 32, 1-14.	11.4	424
4	Progenitor/stem cells give rise to liver cancer due to aberrant TGF- β 2 and IL-6 signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2445-2450.	7.1	313
5	Activation of p53-Dependent Growth Suppression in Human Cells by Mutations in PTEN or PIK3CA. <i>Molecular and Cellular Biology</i> , 2007, 27, 662-677.	2.3	147
6	Utilization of metabolomics to identify serum biomarkers for hepatocellular carcinoma in patients with liver cirrhosis. <i>Analytica Chimica Acta</i> , 2012, 743, 90-100.	5.4	146
7	Enrichment of low molecular weight fraction of serum for MS analysis of peptides associated with hepatocellular carcinoma. <i>Proteomics</i> , 2006, 6, 2895-2902.	2.2	134
8	Detection of Hepatocellular Carcinoma Using Glycomic Analysis. <i>Clinical Cancer Research</i> , 2009, 15, 1808-1813.	7.0	133
9	LC-MS Based Serum Metabolomics for Identification of Hepatocellular Carcinoma Biomarkers in Egyptian Cohort. <i>Journal of Proteome Research</i> , 2012, 11, 5914-5923.	3.7	116
10	Mutational Inactivation of PTPRD in Glioblastoma Multiforme and Malignant Melanoma. <i>Cancer Research</i> , 2008, 68, 10300-10306.	0.9	114
11	Analysis of mass spectral serum profiles for biomarker selection. <i>Bioinformatics</i> , 2005, 21, 4039-4045.	4.1	92
12	The mitochondrial citrate carrier, SLC25A1, drives stemness and therapy resistance in non-small cell lung cancer. <i>Cell Death and Differentiation</i> , 2018, 25, 1239-1258.	11.2	81
13	YAP/TAZ Inhibition Induces Metabolic and Signaling Rewiring Resulting in Targetable Vulnerabilities in NF2-Deficient Tumor Cells. <i>Developmental Cell</i> , 2019, 49, 425-443.e9.	7.0	78
14	Maternal Early Pregnancy Serum Metabolites and Risk of Gestational Diabetes Mellitus. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2015, 100, 4348-4356.	3.6	76
15	MetaboSearch: Tool for Mass-Based Metabolite Identification Using Multiple Databases. <i>PLoS ONE</i> , 2012, 7, e40096.	2.5	71
16	LC-MS Based Detection of Differential Protein Expression. <i>Journal of Proteomics and Bioinformatics</i> , 2009, 02, 416-438.	0.4	70
17	iTRAQ-Based Quantitative Protein Expression Profiling and MRM Verification of Markers in Type 2 Diabetes. <i>Journal of Proteome Research</i> , 2012, 11, 5527-5539.	3.7	68
18	LC-MS/MS-based serum proteomics for identification of candidate biomarkers for hepatocellular carcinoma. <i>Proteomics</i> , 2015, 15, 2369-2381.	2.2	66

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19	Identification of N-Glycan Serum Markers Associated with Hepatocellular Carcinoma from Mass Spectrometry Data. <i>Journal of Proteome Research</i> , 2010, 9, 104-112.	3.7	63
20	GC-MS Based Plasma Metabolomics for Identification of Candidate Biomarkers for Hepatocellular Carcinoma in Egyptian Cohort. <i>PLoS ONE</i> , 2015, 10, e0127299.	2.5	60
21	Analysis of MALDI-TOF Mass Spectrometry Data for Discovery of Peptide and Glycan Biomarkers of Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2008, 7, 603-610.	3.7	58
22	Gamma-tocotrienol induced apoptosis is associated with unfolded protein response in human breast cancer cells. <i>Journal of Nutritional Biochemistry</i> , 2012, 23, 93-100.	4.2	57
23	Metabolomic Analysis of Liver Tissues for Characterization of Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2019, 18, 3067-3076.	3.7	56
24	Increasing the efficiency of fuzzy logic-based gene expression data analysis. <i>Physiological Genomics</i> , 2003, 13, 107-117.	2.3	54
25	Classification algorithms for phenotype prediction in genomics and proteomics. <i>Frontiers in Bioscience - Landmark</i> , 2008, 13, 691.	3.0	53
26	Identification of p18INK4c as a Tumor Suppressor Gene in Glioblastoma Multiforme. <i>Cancer Research</i> , 2008, 68, 2564-2569.	0.9	48
27	Candidate markers for the detection of hepatocellular carcinoma in low-molecular weight fraction of serum. <i>Carcinogenesis</i> , 2007, 28, 2149-2153.	2.8	47
28	LC-MS Profiling of N-Glycans Derived from Human Serum Samples for Biomarker Discovery in Hepatocellular Carcinoma. <i>Journal of Proteome Research</i> , 2014, 13, 4859-4868.	3.7	46
29	Pathway and Network Approaches for Identification of Cancer Signature Markers from Omics Data. <i>Journal of Cancer</i> , 2015, 6, 54-65.	2.5	44
30	Incorporating prior biological knowledge for network-based differential gene expression analysis using differentially weighted graphical LASSO. <i>BMC Bioinformatics</i> , 2017, 18, 99.	2.6	40
31	Metabolomic Characterization of Hepatocellular Carcinoma in Patients with Liver Cirrhosis for Biomarker Discovery. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2017, 26, 675-683.	2.5	40
32	Metabolomic profiles of current cigarette smokers. <i>Molecular Carcinogenesis</i> , 2017, 56, 594-606.	2.7	38
33	Analysis of LC-MS Data for Characterizing the Metabolic Changes in Response to Radiation. <i>Journal of Proteome Research</i> , 2010, 9, 2786-2793.	3.7	37
34	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. <i>BMC Bioinformatics</i> , 2008, 9, 203.	2.6	35
35	Biological network inference using low order partial correlation. <i>Methods</i> , 2014, 69, 266-273.	3.8	35
36	Transcriptome and Proteome Analyses of TNFAIP8 Knockdown Cancer Cells Reveal New Insights into Molecular Determinants of Cell Survival and Tumor Progression. <i>Methods in Molecular Biology</i> , 2017, 1513, 83-100.	0.9	35

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37	Feasibility of Identifying the Tobacco-related Global Metabolome in Blood by UPLC-QTOF-MS. <i>Journal of Proteome Research</i> , 2013, 12, 679-691.	3.7	34
38	Serotonin induced hepatic steatosis is associated with modulation of autophagy and notch signaling pathway. <i>Cell Communication and Signaling</i> , 2018, 16, 78.	6.5	30
39	MetFID: artificial neural network-based compound fingerprint prediction for metabolite annotation. <i>Metabolomics</i> , 2020, 16, 104.	3.0	30
40	Sample Type Bias in the Analysis of Cancer Genomes. <i>Cancer Research</i> , 2009, 69, 5630-5633.	0.9	29
41	INDEED: Integrated differential expression and differential network analysis of omic data for biomarker discovery. <i>Methods</i> , 2016, 111, 12-20.	3.8	28
42	Discoïdin Domain Receptor 1 is a therapeutic target for neurodegenerative diseases. <i>Human Molecular Genetics</i> , 2020, 29, 2882-2898.	2.9	28
43	Integrated Analysis of ATM Mediated Gene and Protein Expression Impacting Cellular Metabolism. <i>Journal of Proteome Research</i> , 2011, 10, 2651-2657.	3.7	27
44	Clustering gene expression data using adaptive double self-organizing map. <i>Physiological Genomics</i> , 2003, 14, 35-46.	2.3	24
45	Genomics and Bioinformatics of Parkinson's Disease. <i>Cold Spring Harbor Perspectives in Medicine</i> , 2012, 2, a009449-a009449.	6.2	24
46	Preprocessing and Analysis of LC-MS-Based Proteomic Data. <i>Methods in Molecular Biology</i> , 2016, 1362, 63-76.	0.9	24
47	Identification of aberrant pathways and network activities from high-throughput data. <i>Briefings in Bioinformatics</i> , 2012, 13, 406-419.	6.5	23
48	Metabolomic profiling of breast tumors using ductal fluid. <i>International Journal of Oncology</i> , 2016, 49, 2245-2254.	3.3	23
49	Type 3 innate lymphoid cells are associated with a successful intestinal transplant. <i>American Journal of Transplantation</i> , 2021, 21, 787-797.	4.7	22
50	Long-term culture and characterization of patient-derived primary hepatocytes using conditional reprogramming. <i>Experimental Biology and Medicine</i> , 2019, 244, 857-864.	2.4	20
51	Identification of race-associated metabolite biomarkers for hepatocellular carcinoma in patients with liver cirrhosis and hepatitis C virus infection. <i>PLoS ONE</i> , 2018, 13, e0192748.	2.5	19
52	Retinoic Acid Mediates Regulation of Network Formation by COUP-TFII and VE-Cadherin Expression by TGF β 2 Receptor Kinase in Breast Cancer Cells. <i>PLoS ONE</i> , 2010, 5, e10023.	2.5	19
53	Metabolomic profiling for biomarker discovery in pancreatic cancer. <i>International Journal of Mass Spectrometry</i> , 2012, 310, 44-51.	1.5	18
54	Using a spike-in experiment to evaluate analysis of LC-MS data. <i>Proteome Science</i> , 2012, 10, 13.	1.7	17

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55	Module-based breast cancer classification. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 284.	0.1	16
56	Integrative Analysis of Proteomic, Glycomic, and Metabolomic Data for Biomarker Discovery. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2016, 20, 1225-1231.	6.3	15
57	Ant Colony Optimization for Biomarker Identification from MALDI-TOF Mass Spectra. , 2006, 2006, 4560-3.		13
58	DNA Methylation Activates TP73 Expression in Hepatocellular Carcinoma and Gastrointestinal Cancer. <i>Scientific Reports</i> , 2019, 9, 19367.	3.3	13
59	Reconstruction of Gene Regulatory Modules in Cancer Cell Cycle by Multi-Source Data Integration. <i>PLoS ONE</i> , 2010, 5, e10268.	2.5	13
60	Functional Proteomics Analysis to Study ATM Dependent Signaling in Response to Ionizing Radiation. <i>Radiation Research</i> , 2013, 179, 674.	1.5	12
61	CSF MicroRNAs Reveal Impairment of Angiogenesis and Autophagy in Parkinson Disease. <i>Neurology: Genetics</i> , 2021, 7, e633.	1.9	12
62	Ion annotation-assisted analysis of LC-MS based metabolomic experiment. <i>Proteome Science</i> , 2012, 10, S8.	1.7	11
63	Apo E4 Alleles and Impaired Olfaction as Predictors of Alzheimer's Disease. <i>Clinical and Experimental Psychology</i> , 2017, 03, .	0.1	10
64	MOTA: Network-Based Multi-Omic Data Integration for Biomarker Discovery. <i>Metabolites</i> , 2020, 10, 144.	2.9	10
65	Evaluation of Metabolite Biomarkers for Hepatocellular Carcinoma through Stratified Analysis by Gender, Race, and Alcoholic Cirrhosis. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2014, 23, 64-72.	2.5	9
66	Prioritization of putative metabolite identifications in LC-MS/MS experiments using a computational pipeline. <i>Proteomics</i> , 2013, 13, 248-260.	2.2	8
67	SIMAT: GC-SIM-MS data analysis tool. <i>BMC Bioinformatics</i> , 2015, 16, 259.	2.6	8
68	Role of microRNAs in the development of hepatocellular carcinoma and drug resistance. <i>Frontiers in Bioscience - Landmark</i> , 2019, 24, 382-391.	3.0	8
69	A new method for alignment of LC-MALDI-TOF data. <i>Proteome Science</i> , 2011, 9, S10.	1.7	7
70	Evaluation of normalization methods for analysis of LC-MS data. , 2012, , .		7
71	Hepatitis C virus Genotype 1a core gene nucleotide patterns associated with hepatocellular carcinoma risk. <i>Journal of General Virology</i> , 2015, 96, 2928-2937.	2.9	7
72	Inferring Network Interactions Using Recurrent Neural Networks and Swarm Intelligence. , 2006, 2006, 4241-4.		6

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73	Metabolite Identification Using Artificial Neural Network. , 2019, , .		6
74	Multi-omic Pathway and Network Analysis to Identify Biomarkers for Hepatocellular Carcinoma. , 2019, 2019, 1350-1354.		6
75	Identification of miRNA-mRNA associations in hepatocellular carcinoma using hierarchical integrative model. BMC Medical Genomics, 2020, 13, 56.	1.5	6
76	Probabilistic Mixture Regression Models for Alignment of LC-MS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 1417-1424.	3.0	5
77	Integrating prior biological knowledge and graphical LASSO for network inference. , 2015, , .		5
78	Bayesian Normalization Model for Label-Free Quantitative Analysis by LC-MS. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 914-927.	3.0	5
79	Protein network construction using reverse phase protein array data. Methods, 2017, 124, 89-99.	3.8	5
80	Discovery of potential urine-accessible metabolite biomarkers associated with muscle disease and corticosteroid response in the mdx mouse model for Duchenne. PLoS ONE, 2019, 14, e0219507.	2.5	5
81	Establishment of ornithine transcarbamylase deficiency-derived primary human hepatocyte with hepatic functions. Experimental Cell Research, 2019, 384, 111621.	2.6	5
82	Integrative Analysis of DNA Methylation and microRNA Expression Reveals Mechanisms of Racial Heterogeneity in Hepatocellular Carcinoma. Frontiers in Genetics, 2021, 12, 708326.	2.3	5
83	¹³ C based proteinogenic amino acid (PAA) and metabolic flux ratio analysis of <i>Lactococcus lactis</i> reveals changes in pentose phosphate (PP) pathway in response to agitation and temperature related stresses. PeerJ, 2017, 5, e3451.	2.0	5
84	Integrated peptide and glycan biomarker discovery using MALDI-TOF mass spectrometry. , 2008, 2008, 3791-4.		4
85	SVM-based spectral matching for metabolite identification. , 2010, 2010, 756-9.		4
86	GPA: An algorithm for LC/MS based glycan profile annotation. , 2013, , .		4
87	A new approach for multi-omic data integration. , 2014, , .		4
88	INDEED: R package for network based differential expression analysis. , 2018, 2018, 2709-2712.		4
89	Analysis of MALDI-TOF mass spectrometry data for detection of glycan biomarkers. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2008, , 216-27.	0.7	4
90	A Computational Pipeline for LC-MS/MS Based Metabolite Identification. , 2011, , .		3

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91	Normalization of LC-MS data using Gaussian process. , 2012, , .		3
92	Convolutional Neural Network-Based Compound Fingerprint Prediction for Metabolite Annotation. Metabolites, 2022, 12, 605.	2.9	3
93	Iminodiacetic acid (IDA)-generated mesoporous nanopolymer: a template to relate surface area, hydrophilicity, and glycopeptides enrichment. Mikrochimica Acta, 2021, 188, 417.	5.0	2
94	Metabolomic Analysis of Plasma from Breast Cancer Patients Using Ultra-High-Performance Liquid Chromatography Coupled with Mass Spectrometry: An Untargeted Study. Metabolites, 2022, 12, 447.	2.9	2
95	Metabolomic profiling for biomarker discovery in pancreatic cancer. , 2010, , .		1
96	Purification of LC/GC-MS based biomolecular expression profiles using a topic model. , 2015, , .		1
97	Integrative analysis of LC-MS based glycomic and proteomic data. , 2015, 2015, 8185-8.		1
98	Metabolomic data deconvolution using probabilistic purification models. , 2016, , .		1
99	Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. BMC Genomics, 2016, 17, 545.	2.8	1
100	MOTA: Multi-omic integrative analysis for biomarker discovery. , 2019, 2019, 243-247.		1
101	Analysis of mass spectrometry data for serum biomarker discovery. , 2007, , .		0
102	Meta-analysis of LC-MS based metabolomic experiments. , 2011, , .		0
103	Variability assessment of LC-MS experiments and its application to experimental design and difference detection. , 2012, , .		0
104	Assessment of GC-MS in Detecting Changes in the Levels of Metabolites Using a Spike-in Experiment in Human Plasma. Metabolomics: Open Access, 2016, 6, .	0.1	0
105	Network-based analysis of reverse phase protein array data. , 2016, , .		0
106	Variability Assessment of Label-Free LC-MS Experiments for Difference Detection. , 2017, , 157-176.		0
107	Ant Colony Optimization for Biomarker Identification from MALDI-TOF Mass Spectra. Annual International Conference of the IEEE Engineering in Medicine and Biology Society, 2006, , .	0.5	0