Habtom W Ressom

List of Publications by Year
in descending order

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	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
2	Convolutional Neural Network-Based Compound Fingerprint Prediction for Metabolite Annotation. Metabolites, 2022, 12, 605.	2.9	3
3	Type 3 innate lymphoid cells are associated with a successful intestinal transplant. American Journal of Transplantation, 2021, 21, 787-797.	4.7	22
4	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
5	CSF MicroRNAs Reveal Impairment of Angiogenesis and Autophagy in Parkinson Disease. Neurology: Genetics, 2021, 7, e633.	1.9	12
6	Iminodiacetic acid (IDA)-generated mesoporous nanopolymer: a template to relate surface area, hydrophilicity, and glycopeptides enrichment. Mikrochimica Acta, 2021, 188, 417.	5.0	2
7	MetFID: artificial neural network-based compound fingerprint prediction for metabolite annotation. Metabolomics, 2020, 16, 104.	3.0	30
8	Discoidin Domain Receptor 1 is a therapeutic target for neurodegenerative diseases. Human Molecular Genetics, 2020, 29, 2882-2898.	2.9	28
9	MOTA: Network-Based Multi-Omic Data Integration for Biomarker Discovery. Metabolites, 2020, 10, 144.	2.9	10
10	Identification of miRNA-mRNA associations in hepatocellular carcinoma using hierarchical integrative model. BMC Medical Genomics, 2020, 13, 56.	1.5	6
11	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
12	Establishment of ornithine transcarbamylase deficiency-derived primary human hepatocyte with hepatic functions. Experimental Cell Research, 2019, 384, 111621.	2.6	5
13	Metabolomic Analysis of Liver Tissues for Characterization of Hepatocellular Carcinoma. Journal of Proteome Research, 2019, 18, 3067-3076.	3.7	56
14	Long-term culture and characterization of patient-derived primary hepatocytes using conditional reprogramming. Experimental Biology and Medicine, 2019, 244, 857-864.	2.4	20
15	YAP/TAZ Inhibition Induces Metabolic and Signaling Rewiring Resulting in Targetable Vulnerabilities in NF2-Deficient Tumor Cells. Developmental Cell, 2019, 49, 425-443.e9.	7.0	78
16	Metabolite Identification Using Artificial Neural Network. , 2019, , .		6
17	DNA Methylation Activates TP73 Expression in Hepatocellular Carcinoma and Gastrointestinal Cancer. Scientific Reports, 2019, 9, 19367.	3.3	13
18	Multi-omic Pathway and Network Analysis to Identify Biomarkers for Hepatocellular Carcinoma. , 2019, 2019, 1350-1354.		6

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19	MOTA: Multi-omic integrative analysis for biomarker discovery. , 2019, 2019, 243-247.		1
20	Role of microRNAs in the development of hepatocellular carcinoma and drug resistance. Frontiers in Bioscience - Landmark, 2019, 24, 382-391.	3.0	8
21	The mitochondrial citrate carrier, SLC25A1, drives stemness and therapy resistance in non-small cell lung cancer. Cell Death and Differentiation, 2018, 25, 1239-1258.	11.2	81
22	INDEED: R package for network based differential expression analysis. , 2018, 2018, 2709-2712.		4
23	Serotonin induced hepatic steatosis is associated with modulation of autophagy and notch signaling pathway. Cell Communication and Signaling, 2018, 16, 78.	6.5	30
24	Identification of race-associated metabolite biomarkers for hepatocellular carcinoma in patients with liver cirrhosis and hepatitis C virus infection. PLoS ONE, 2018, 13, e0192748.	2.5	19
25	Metabolomic profiles of current cigarette smokers. Molecular Carcinogenesis, 2017, 56, 594-606.	2.7	38
26	Incorporating prior biological knowledge for network-based differential gene expression analysis using differentially weighted graphical LASSO. BMC Bioinformatics, 2017, 18, 99.	2.6	40
27	Metabolomic Characterization of Hepatocellular Carcinoma in Patients with Liver Cirrhosis for Biomarker Discovery. Cancer Epidemiology Biomarkers and Prevention, 2017, 26, 675-683.	2.5	40
28	Protein network construction using reverse phase protein array data. Methods, 2017, 124, 89-99.	3.8	5
29	Transcriptome and Proteome Analyses of TNFAIP8 Knockdown Cancer Cells Reveal New Insights into Molecular Determinants of Cell Survival and Tumor Progression. Methods in Molecular Biology, 2017, 1513, 83-100.	0.9	35
30	Apo E4 Alleles and Impaired Olfaction as Predictors of Alzheimer's Disease. Clinical and Experimental Psychology, 2017, 03, .	0.1	10
31	^{13}C based proteinogenic amino acid (PAA) and metabolic flux ratio analysis of *Lactococcus lactis* reveals changes in pentose phosphate (PP) pathway in response to agitation and temperature related stresses. PeerJ, 2017, 5, e3451.	2.0	5
32	Variability Assessment of Label-Free LC-MS Experiments for Difference Detection. , 2017, , 157-176.		0
33	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
34	Metabolomic data deconvolution using probabilistic purification models. , 2016, , .		1
35	Network-based analysis of reverse phase protein array data. , 2016, , .		0
36	INDEED: Integrated differential expression and differential network analysis of omic data for biomarker discovery. Methods, 2016, 111, 12-20.	3.8	28

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37	Metabolomic profiling of breast tumors using ductal fluid. International Journal of Oncology, 2016, 49, 2245-2254.	3.3	23
38	Topic model-based mass spectrometric data analysis in cancer biomarker discovery studies. BMC Genomics, 2016, 17, 545.	2.8	1
39	Integrative Analysis of Proteomic, Glycomic, and Metabolomic Data for Biomarker Discovery. IEEE Journal of Biomedical and Health Informatics, 2016, 20, 1225-1231.	6.3	15
40	Preprocessing and Analysis of LC-MS-Based Proteomic Data. Methods in Molecular Biology, 2016, 1362, 63-76.	0.9	24
41	Pathway and Network Approaches for Identification of Cancer Signature Markers from Omics Data. Journal of Cancer, 2015, 6, 54-65.	2.5	44
42	GC-MS Based Plasma Metabolomics for Identification of Candidate Biomarkers for Hepatocellular Carcinoma in Egyptian Cohort. PLoS ONE, 2015, 10, e0127299.	2.5	60
43	LCâ€MS/MSâ€based serum proteomics for identification of candidate biomarkers for hepatocellular carcinoma. Proteomics, 2015, 15, 2369-2381.	2.2	66
44	Purification of LC/GC-MS based biomolecular expression profiles using a topic model. , 2015, , .		1
45	Integrating prior biological knowledge and graphical LASSO for network inference. , 2015, , .		5
46	Integrative analysis of LC-MS based glycomic and proteomic data. , 2015, 2015, 8185-8.		1
47	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
48	SIMAT: GC-SIM-MS data analysis tool. BMC Bioinformatics, 2015, 16, 259.	2.6	8
49	Maternal Early Pregnancy Serum Metabolites and Risk of Gestational Diabetes Mellitus. Journal of Clinical Endocrinology and Metabolism, 2015, 100, 4348-4356.	3.6	76
50	Hepatitis C virus Genotype 1a core gene nucleotide patterns associated with hepatocellular carcinoma risk. Journal of General Virology, 2015, 96, 2928-2937.	2.9	7
51	A new approach for multi-omic data integration. , 2014, , .		4
52	Evaluation of Metabolite Biomarkers for Hepatocellular Carcinoma through Stratified Analysis by Gender, Race, and Alcoholic Cirrhosis. Cancer Epidemiology Biomarkers and Prevention, 2014, 23, 64-72.	2.5	9
53	LCâ€"MS Profiling of N-Glycans Derived from Human Serum Samples for Biomarker Discovery in Hepatocellular Carcinoma. Journal of Proteome Research, 2014, 13, 4859-4868.	3.7	46
54	Biological network inference using low order partial correlation. Methods, 2014, 69, 266-273.	3.8	35

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55	Prioritization of putative metabolite identifications in <scp>LC</scp>â€‹<scp>MS</scp>/<scp>MS</scp> experiments using a computational pipeline. Proteomics, 2013, 13, 248-260.	2.2	8
56	Feasibility of Identifying the Tobacco-related Global Metabolome in Blood by UPLCâ€"QTOF-MS. Journal of Proteome Research, 2013, 12, 679-691.	3.7	34
57	Module-based breast cancer classification. International Journal of Data Mining and Bioinformatics, 2013, 7, 284.	0.1	16
58	GPA: An algorithm for LC/MS based glycan profile annotation. , 2013, , .		4
59	Functional Proteomics Analysis to Study ATM Dependent Signaling in Response to Ionizing Radiation. Radiation Research, 2013, 179, 674.	1.5	12
60	Genomics and Bioinformatics of Parkinson's Disease. Cold Spring Harbor Perspectives in Medicine, 2012, 2, a009449-a009449.	6.2	24
61	Evaluation of normalization methods for analysis of LC-MS data. , 2012, , .		7
62	Normalization of LC-MS data using Gaussian process. , 2012, , .		3
63	Variability assessment of LC-MS experiments and its application to experimental design and difference detection. , 2012, , .		0
64	LC-MS-based metabolomics. Molecular BioSystems, 2012, 8, 470-481.	2.9	440
65	Utilization of metabolomics to identify serum biomarkers for hepatocellular carcinoma in patients with liver cirrhosis. Analytica Chimica Acta, 2012, 743, 90-100.	5.4	146
66	LCâ€"MS Based Serum Metabolomics for Identification of Hepatocellular Carcinoma Biomarkers in Egyptian Cohort. Journal of Proteome Research, 2012, 11, 5914-5923.	3.7	116
67	iTRAQ-Based Quantitative Protein Expression Profiling and MRM Verification of Markers in Type 2 Diabetes. Journal of Proteome Research, 2012, 11, 5527-5539.	3.7	68
68	Identification of aberrant pathways and network activities from high-throughput data. Briefings in Bioinformatics, 2012, 13, 406-419.	6.5	23
69	Metabolomic profiling for biomarker discovery in pancreatic cancer. International Journal of Mass Spectrometry, 2012, 310, 44-51.	1.5	18
70	Gamma-tocotrienol induced apoptosis is associated with unfolded protein response in human breast cancer cells. Journal of Nutritional Biochemistry, 2012, 23, 93-100.	4.2	57
71	Metabolite identification and quantitation in LC-MS/MS-based metabolomics. TrAC - Trends in Analytical Chemistry, 2012, 32, 1-14.	11.4	424
72	Using a spike-in experiment to evaluate analysis of LC-MS data. Proteome Science, 2012, 10, 13.	1.7	17

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73	Ion annotation-assisted analysis of LC-MS based metabolomic experiment. Proteome Science, 2012, 10, S8.	1.7	11
74	MetaboSearch: Tool for Mass-Based Metabolite Identification Using Multiple Databases. PLoS ONE, 2012, 7, e40096.	2.5	71
75	A Computational Pipeline for LC-MS/MS Based Metabolite Identification. , 2011, , .		3
76	Meta-analysis of LC-MS based metabolomic experiments. , 2011, , .		0
77	Integrated Analysis of ATM Mediated Gene and Protein Expression Impacting Cellular Metabolism. Journal of Proteome Research, 2011, 10, 2651-2657.	3.7	27
78	A new method for alignment of LC-MALDI-TOF data. Proteome Science, 2011, 9, S10.	1.7	7
79	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
80	Analysis of LCâˆ'MS Data for Characterizing the Metabolic Changes in Response to Radiation. Journal of Proteome Research, 2010, 9, 2786-2793.	3.7	37
81	Identification of N-Glycan Serum Markers Associated with Hepatocellular Carcinoma from Mass Spectrometry Data. Journal of Proteome Research, 2010, 9, 104-112.	3.7	63
82	SVM-based spectral matching for metabolite identification. , 2010, 2010, 756-9.		4
83	Metabolomic profiling for biomarker discovery in pancreatic cancer. , 2010, , .		1
84	Retinoic Acid Mediates Regulation of Network Formation by COUP-TFII and VE-Cadherin Expression by TGFÎ²² Receptor Kinase in Breast Cancer Cells. PLoS ONE, 2010, 5, e10023.	2.5	19
85	Reconstruction of Gene Regulatory Modules in Cancer Cell Cycle by Multi-Source Data Integration. PLoS ONE, 2010, 5, e10268.	2.5	13
86	LCâ€"MS Based Detection of Differential Protein Expression. Journal of Proteomics and Bioinformatics, 2009, 02, 416-438.	0.4	70
87	Detection of Hepatocellular Carcinoma Using Glycomic Analysis. Clinical Cancer Research, 2009, 15, 1808-1813.	7.0	133
88	Sample Type Bias in the Analysis of Cancer Genomes. Cancer Research, 2009, 69, 5630-5633.	0.9	29
89	The properties of high-dimensional data spaces: implications for exploring gene and protein expression data. Nature Reviews Cancer, 2008, 8, 37-49.	28.4	483
90	Network motif-based identification of transcription factor-target gene relationships by integrating multi-source biological data. BMC Bioinformatics, 2008, 9, 203.	2.6	35

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91	Analysis of MALDI-TOF Mass Spectrometry Data for Discovery of Peptide and Glycan Biomarkers of Hepatocellular Carcinoma. Journal of Proteome Research, 2008, 7, 603-610.	3.7	58
92	Progenitor/stem cells give rise to liver cancer due to aberrant TGF-β and IL-6 signaling. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 2445-2450.	7.1	313
93	Identification of p18INK4c as a Tumor Suppressor Gene in Glioblastoma Multiforme. Cancer Research, 2008, 68, 2564-2569.	0.9	48
94	Mutational Inactivation of PTPRD in Glioblastoma Multiforme and Malignant Melanoma. Cancer Research, 2008, 68, 10300-10306.	0.9	114
95	Integrated peptide and glycan biomarker discovery using MALDI-TOF mass spectrometry. , 2008, 2008, 3791-4.		4
96	Classification algorithms for phenotype prediction in genomics and proteomics. Frontiers in Bioscience - Landmark, 2008, 13, 691.	3.0	53
97	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
98	Analysis of mass spectrometry data for serum biomarker discovery. , 2007, , .		0
99	Candidate markers for the detection of hepatocellular carcinoma in low-molecular weight fraction of serum. Carcinogenesis, 2007, 28, 2149-2153.	2.8	47
100	Activation of p53-Dependent Growth Suppression in Human Cells by Mutations in PTEN or PIK3CA. Molecular and Cellular Biology, 2007, 27, 662-677.	2.3	147
101	Enrichment of low molecular weight fraction of serum for MS analysis of peptides associated with hepatocellular carcinoma. Proteomics, 2006, 6, 2895-2902.	2.2	134
102	Inferring Network Interactions Using Recurrent Neural Networks and Swarm Intelligence. , 2006, 2006, 4241-4.		6
103	Ant Colony Optimization for Biomarker Identification from MALDI-TOF Mass Spectra. , 2006, 2006, 4560-3.		13
104	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
105	Analysis of mass spectral serum profiles for biomarker selection. Bioinformatics, 2005, 21, 4039-4045.	4.1	92
106	Increasing the efficiency of fuzzy logic-based gene expression data analysis. Physiological Genomics, 2003, 13, 107-117.	2.3	54
107	Clustering gene expression data using adaptive double self-organizing map. Physiological Genomics, 2003, 14, 35-46.	2.3	24