Jenny M Forshed

List of Publications by Year
in descending order

28 papers	1,282 citations	393982 19 h-index	580395 25 g-index
28 all docs	28 docs citations	28 times ranked	2792 citing authors

#	Article	IF	Citations
1	Early symptoms and sensations as predictors of lung cancer: a machine learning multivariate model. Scientific Reports, 2019, 9, 16504.	1.6	12
2	Discrimination of pancreatic cancer and pancreatitis by LC-MS metabolomics. Metabolomics, 2017, 13, 61.	1.4	42
3	Experimental Design in Clinical â€˜Omics Biomarker Discovery. Journal of Proteome Research, 2017, 16, 3954-3960.	1.8	32
4	Overlap in serum metabolic profiles between non-related diseases: Implications for LC-MS metabolomics biomarker discovery. Biochemical and Biophysical Research Communications, 2016, 478, 1472-1477.	1.0	27
5	Proteomics profiling identify CAPS as a potential predictive marker of tamoxifen resistance in estrogen receptor positive breast cancer. Clinical Proteomics, 2015, 12, 8.	1.1	31
6	SpliceVista, a Tool for Splice Variant Identification and Visualization in Shotgun Proteomics Data. Molecular and Cellular Proteomics, 2014, 13, 1552-1562.	2.5	28
7	Proteome Screening of Pleural Effusions Identifies Galectin 1 as a Diagnostic Biomarker and Highlights Several Prognostic Biomarkers for Malignant Mesothelioma. Molecular and Cellular Proteomics, 2014, 13, 701-715.	2.5	42
8	Quantitative accuracy in mass spectrometry based proteomics of complex samples: The impact of labeling and precursor interference. Journal of Proteomics, 2014, 96, 133-144.	1.2	82
9	HiRIEF LC-MS enables deep proteome coverage and unbiased proteogenomics. Nature Methods, 2014, 11, 59-62.	9.0	222
10	Retinoic acid receptor alpha is associated with tamoxifen resistance in breast cancer. Nature Communications, 2013, 4, 2175.	5.8	53
11	Protein Quantification by Peptide Quality Control (PQPQ) of Shotgun Proteomics Data. Methods in Molecular Biology, 2013, 1023, 149-158.	0.4	4
12	Defining, Comparing, and Improving iTRAQ Quantification in Mass Spectrometry Proteomics Data. Molecular and Cellular Proteomics, 2013, 12, 2021-2031.	2.5	53
13	A10.23â€¦Stratification of SLE Patients for Improved Diagnosis and Treatment. Annals of the Rheumatic Diseases, 2013, 72, A80.2-A80.	0.5	0
14	Tumor Proteomics by Multivariate Analysis on Individual Pathway Data for Characterization of Vulvar Cancer Phenotypes. Molecular and Cellular Proteomics, 2012, 11, M112.016998-1-M112.016998-14.	2.5	83
15	Systems biology of SLE: biochemical characterisation of subgroups within sle for improved diagnosis and treatment. Annals of the Rheumatic Diseases, 2012, 71, A12.2-A12.	0.5	1
16	Enhanced Information Output From Shotgun Proteomics Data by Protein Quantification and Peptide Quality Control (PQPQ). Molecular and Cellular Proteomics, 2011, 10, M111.010264.	2.5	28
17	Multivariate meta-analysis of proteomics data from human prostate and colon tumours. BMC Bioinformatics, 2010, 11, 468.	1.2	15
18	Herman Wold medal winners 2007-2009. Journal of Chemometrics, 2010, 24, 635-635.	0.7	0

#	Article	IF	Citations
19	Intra- and inter-metabolite correlation spectroscopy of tomato metabolomics data obtained by liquid chromatography-mass spectrometry and nuclear magnetic resonance. Metabolomics, 2008, 4, 202-215.	1.4	74
20	Proteomic Data Analysis Workflow for Discovery of Candidate Biomarker Peaks Predictive of Clinical Outcome for Patients with Acute Myeloid Leukemia. Journal of Proteome Research, 2008, 7, 2332-2341.	1.8	22
21	Effects of Pyridine Exposure upon Structural Lipid Metabolism in Swiss Webster Mice. Chemical Research in Toxicology, 2008, 21, 583-590.	1.7	7
22	B7-06: Mass Spectrometry Profiling of Low Molecular Weight Platelet Proteome for the Detection of Lung Cancer Specific Biomarkers. Journal of Thoracic Oncology, 2007, 2, S356-S357.	0.5	0
23	Evaluation of different techniques for data fusion of LC/MS and 1H-NMR. Chemometrics and Intelligent Laboratory Systems, 2007, 85, 102-109.	1.8	65
24	Enhanced multivariate analysis by correlation scaling and fusion of LC/MS and 1H NMR data. Chemometrics and Intelligent Laboratory Systems, 2007, 85, 179-185.	1.8	13
25	A comparison of methods for alignment of NMR peaks in the context of cluster analysis. Journal of Pharmaceutical and Biomedical Analysis, 2005, 38, 824-832.	1.4	83
26	Quantification of aldehyde impurities in poloxamer by 1H NMR spectrometry. Analytica Chimica Acta, 2005, 552, 160-165.	2.6	19
27	Peak alignment of NMR signals by means of a genetic algorithm. Analytica Chimica Acta, 2003, 487, 189-199.	2.6	189
28	NMR and Bayesian regularized neural network regression for impurity determination of 4-aminophenol. Journal of Pharmaceutical and Biomedical Analysis, 2002, 29, 495-505.	1.4	55