## Angela M Jackson

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Process and Workflow for Preparation of Disparate Mouse Tissues for Proteomic Analysis. Journal of Proteome Research, 2021, 20, 305-316.	1.8	3
2	Proteomic Portraits Reveal Evolutionarily Conserved and Divergent Responses to Spinal Cord Injury. Molecular and Cellular Proteomics, 2021, 20, 100096.	2.5	14
3	Verification of a proteomic biomarker panel to diagnose minor stroke and transient ischaemic attack: phase 1 of SpecTRA, a large scale translational study. Biomarkers, 2018, 23, 392-405.	0.9	21
4	Validation of a proteomic biomarker panel to diagnose minor-stroke and transient ischaemic attack: phase 2 of SpecTRA, a large scale translational study. Biomarkers, 2018, 23, 793-803.	0.9	23
5	PeptideTracker: A knowledge base for collecting and storing information on protein concentrations in biological tissues. Proteomics, 2017, 17, 1600210.	1.3	20
6	Identification and Validation of Potential New Biomarkers for Prostate Cancer Diagnosis and Prognosis Using 2D-DIGE and MS. BioMed Research International, 2015, 2015, 1-23.	0.9	44
7	Large-Scale Interlaboratory Study to Develop, Analytically Validate and Apply Highly Multiplexed, Quantitative Peptide Assays to Measure Cancer-Relevant Proteins in Plasma. Molecular and Cellular Proteomics, 2015, 14, 2357-2374.	2.5	153
8	The application of multiple reaction monitoring to assess ApoA-I methionine oxidations in diabetes and cardiovascular disease. Translational Proteomics, 2014, 4-5, 18-24.	1.2	26
9	The application of multiple reaction monitoring and multi-analyte profiling to HDL proteins. Lipids in Health and Disease, 2014, 13, 8.	1.2	19
10	PeptidePicker: A scientific workflow with web interface for selecting appropriate peptides for targeted proteomics experiments. Journal of Proteomics, 2014, 106, 151-161.	1.2	117
11	Method and platform standardization in MRM-based quantitative plasma proteomics. Journal of Proteomics, 2013, 95, 66-76.	1.2	55
12	Design, Implementation and Multisite Evaluation of a System Suitability Protocol for the Quantitative Assessment of Instrument Performance in Liquid Chromatography-Multiple Reaction Monitoring-MS (LC-MRM-MS). Molecular and Cellular Proteomics, 2013, 12, 2623-2639.	2.5	100
13	Interlaboratory Evaluation of Automated, Multiplexed Peptide Immunoaffinity Enrichment Coupled to Multiple Reaction Monitoring Mass Spectrometry for Quantifying Proteins in Plasma. Molecular and Cellular Proteomics, 2012, 11, M111.013854.	2.5	176
14	High-Flow Multiplexed MRM-Based Analysis of Proteins in Human Plasma Without Depletion or Enrichment. Clinics in Laboratory Medicine, 2011, 31, 371-384.	0.7	14
15	Quantification of Proteins Using Peptide Immunoaffinity Enrichment Coupled with Mass Spectrometry. Journal of Visualized Experiments, 2011, , .	0.2	22
16	MALDI Immunoscreening (MiSCREEN): A method for selection of anti-peptide monoclonal antibodies for use in immunoproteomics. Journal of Immunological Methods, 2011, 364, 50-64.	0.6	26
17	A Quantitative Study of the Effects of Chaotropic Agents, Surfactants, and Solvents on the Digestion Efficiency of Human Plasma Proteins by Trypsin. Journal of Proteome Research, 2010, 9, 5422-5437. 	1.8	301
18	Killing of Trypanosomatid Parasites by a Modified Bovine Host Defense Peptide, BMAP-18. PLoS Neglected Tropical Diseases, 2009, 3, e373.	1.3	52

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19	Multiple Reaction Monitoring-based, Multiplexed, Absolute Quantitation of 45 Proteins in Human Plasma. Molecular and Cellular Proteomics, 2009, 8, 1860-1877.	2.5	468
20	SISCAPA Peptide Enrichment on Magnetic Beads Using an In-line Bead Trap Device. Molecular and Cellular Proteomics, 2009, 8, 995-1005.	2.5	134
21	Multi-site assessment of the precision and reproducibility of multiple reaction monitoring–based measurements of proteins in plasma. Nature Biotechnology, 2009, 27, 633-641.	9.4	958
22	On the Mechanism of Mitochondrial Uncoupling Protein 1 Function. Journal of Biological Chemistry, 2006, 281, 2114-2119.	1.6	35