Peter Bowden

List of Publications by Year
in descending order

22 papers	**468** citations	623734 **14** h-index	677142 **22** g-index
22 all docs	**22** docs citations	**22** times ranked	**412** citing authors

#	Article	IF	Citations
1	The plasma peptides of Alzheimer's disease. Clinical Proteomics, 2021, 18, 17.	2.1	18
2	Re-evaluation of the 18 non-human protein standards used to create the empirical statistical model for decoy library searching. Analytical Biochemistry, 2020, 599, 113680.	2.4	5
3	Re-evaluation of the rabbit myosin protein standard used to create the empirical statistical model for decoy library searching. Analytical Biochemistry, 2018, 560, 39-49.	2.4	9
4	Freeze-dried plasma proteins are stable at room temperature for at least 1 year. Clinical Proteomics, 2017, 14, 35.	2.1	17
5	Random and independent sampling of endogenous tryptic peptides from normal human EDTA plasma by liquid chromatography micro electrospray ionization and tandem mass spectrometry. Clinical Proteomics, 2017, 14, 41.	2.1	14
6	The proteins cleaved by endogenous tryptic proteases in normal EDTA plasma by C18 collection of peptides for liquid chromatography micro electrospray ionization and tandem mass spectrometry. Clinical Proteomics, 2017, 14, 39.	2.1	8
7	OxLDL receptor chromatography from live human U937 cells identifies SYK(L) that regulates phagocytosis of oxLDL. Analytical Biochemistry, 2016, 513, 7-20.	2.4	12
8	AMP-Activated Protein Kinase Regulates the Cell Surface Proteome and Integrin Membrane Traffic. PLoS ONE, 2015, 10, e0128013.	2.5	31
9	Creation of a federated database of blood proteins: a powerful new tool for finding and characterizing biomarkers in serum. Clinical Proteomics, 2014, 11, 3.	2.1	19
10	Capture and Qualitative Analysis of the Activated Fc Receptor Complex from Live Cells. Current Protocols in Protein Science, 2012, 67, Unit 19.22.	2.8	3
11	Quantitative Statistical Analysis of Standard and Human Blood Proteins from Liquid Chromatography, Electrospray Ionization, and Tandem Mass Spectrometry. Journal of Proteome Research, 2012, 11, 2032-2047.	3.7	26
12	Identification and quantification of peptides and proteins secreted from prostate epithelial cells by unbiased liquid chromatography tandem mass spectrometry using goodness of fit and analysis of variance. Journal of Proteomics, 2012, 75, 1303-1317.	2.4	27
13	The Fc receptor-cytoskeleton complex from human neutrophils. Journal of Proteomics, 2011, 75, 450-468.	2.4	23
14	Mass spectrometry of peptides and proteins from human blood. Mass Spectrometry Reviews, 2011, 30, 685-732.	5.4	57
15	Chi-square comparison of tryptic peptide-to-protein distributions of tandem mass spectrometry from blood with those of random expectation. Analytical Biochemistry, 2011, 409, 189-194.	2.4	24
16	Peptide-to-protein distribution versus a competition for significance to estimate error rate in blood protein identification. Analytical Biochemistry, 2011, 411, 241-253.	2.4	22
17	Precipitation and selective extraction of human serum endogenous peptides with analysis by quadrupole time-of-flight mass spectrometry reveals posttranslational modifications and low-abundance peptides. Analytical and Bioanalytical Chemistry, 2010, 396, 1223-1247.	3.7	34
18	Meta sequence analysis of human blood peptides and their parent proteins. Journal of Proteomics, 2010, 73, 1163-1175.	2.4	25

#	Article	IF	Citations
19	Tandem mass spectrometry of human tryptic blood peptides calculated by a statistical algorithm and captured by a relational database with exploration by a general statistical analysis system. Journal of Proteomics, 2009, 73, 103-111.	2.4	28
20	Human Serum Proteins Fractionated by Preparative Partition Chromatography Prior to LC-ESI-MS/MS. Journal of Proteome Research, 2009, 8, 1143-1155.	3.7	40
21	Comparison of methods to examine the endogenous peptides of fetal calf serum. Clinical Proteomics, 2006, 2, 67-89.	2.1	9
22	Comparison of protein expression lists from mass spectrometry of human blood fluids using exact peptide sequences versus BLAST. Clinical Proteomics, 2006, 2, 185-203.	2.1	17