

Peter Bowden

List of Publications by Year in descending order

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Version: 2024-02-01

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	Mass spectrometry of peptides and proteins from human blood. <i>Mass Spectrometry Reviews</i> , 2011, 30, 685-732.	5.4	57
2	Human Serum Proteins Fractionated by Preparative Partition Chromatography Prior to LC-ESI-MS/MS. <i>Journal of Proteome Research</i> , 2009, 8, 1143-1155.	3.7	40
3	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. <i>Analytical and Bioanalytical Chemistry</i> , 2010, 396, 1223-1247.	3.7	34
4	AMP-Activated Protein Kinase Regulates the Cell Surface Proteome and Integrin Membrane Traffic. <i>PLoS ONE</i> , 2015, 10, e0128013.	2.5	31
5	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. <i>Journal of Proteomics</i> , 2009, 73, 103-111.	2.4	28
6	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. <i>Journal of Proteomics</i> , 2012, 75, 1303-1317.	2.4	27
7	Quantitative Statistical Analysis of Standard and Human Blood Proteins from Liquid Chromatography, Electrospray Ionization, and Tandem Mass Spectrometry. <i>Journal of Proteome Research</i> , 2012, 11, 2032-2047.	3.7	26
8	Meta sequence analysis of human blood peptides and their parent proteins. <i>Journal of Proteomics</i> , 2010, 73, 1163-1175.	2.4	25
9	Chi-square comparison of tryptic peptide-to-protein distributions of tandem mass spectrometry from blood with those of random expectation. <i>Analytical Biochemistry</i> , 2011, 409, 189-194.	2.4	24
10	The Fc receptor-cytoskeleton complex from human neutrophils. <i>Journal of Proteomics</i> , 2011, 75, 450-468.	2.4	23
11	Peptide-to-protein distribution versus a competition for significance to estimate error rate in blood protein identification. <i>Analytical Biochemistry</i> , 2011, 411, 241-253.	2.4	22
12	Creation of a federated database of blood proteins: a powerful new tool for finding and characterizing biomarkers in serum. <i>Clinical Proteomics</i> , 2014, 11, 3.	2.1	19
13	The plasma peptides of Alzheimer's disease. <i>Clinical Proteomics</i> , 2021, 18, 17.	2.1	18
14	Comparison of protein expression lists from mass spectrometry of human blood fluids using exact peptide sequences versus BLAST. <i>Clinical Proteomics</i> , 2006, 2, 185-203.	2.1	17
15	Freeze-dried plasma proteins are stable at room temperature for at least 1 year. <i>Clinical Proteomics</i> , 2017, 14, 35.	2.1	17
16	Random and independent sampling of endogenous tryptic peptides from normal human EDTA plasma by liquid chromatography micro electrospray ionization and tandem mass spectrometry. <i>Clinical Proteomics</i> , 2017, 14, 41.	2.1	14
17	OxLDL receptor chromatography from live human U937 cells identifies SYK(L) that regulates phagocytosis of oxLDL. <i>Analytical Biochemistry</i> , 2016, 513, 7-20.	2.4	12
18	Comparison of methods to examine the endogenous peptides of fetal calf serum. <i>Clinical Proteomics</i> , 2006, 2, 67-89.	2.1	9

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19	Re-evaluation of the rabbit myosin protein standard used to create the empirical statistical model for decoy library searching. <i>Analytical Biochemistry</i> , 2018, 560, 39-49.	2.4	9
20	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. <i>Clinical Proteomics</i> , 2017, 14, 39.	2.1	8
21	Re-evaluation of the 18 non-human protein standards used to create the empirical statistical model for decoy library searching. <i>Analytical Biochemistry</i> , 2020, 599, 113680.	2.4	5
22	Capture and Qualitative Analysis of the Activated Fc Receptor Complex from Live Cells. <i>Current Protocols in Protein Science</i> , 2012, 67, Unit 19.22.	2.8	3