

Peter L Horvatovich

List of Publications by Year in descending order

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121
papers

3,578
citations

147786

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175241

52
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133
all docs

133
docs citations

133
times ranked

6034
citing authors

#	ARTICLE	IF	CITATIONS
1	TiO ₂ Photocatalysis Damages Lipids and Proteins in Escherichia coli. Applied and Environmental Microbiology, 2014, 80, 2573-2581.	3.1	195
2	Ustekinumab in hidradenitis suppurativa: clinical results and a search for potential biomarkers in serum. British Journal of Dermatology, 2016, 174, 839-846.	1.5	160
3	Comparative proteomic analysis of Lactobacillus plantarum for the identification of key proteins in bile tolerance. BMC Microbiology, 2011, 11, 63.	3.3	152
4	Multi-omic data analysis using Galaxy. Nature Biotechnology, 2015, 33, 137-139.	17.5	140
5	A Critical Assessment of Feature Selection Methods for Biomarker Discovery in Clinical Proteomics. Molecular and Cellular Proteomics, 2013, 12, 263-276.	3.8	120
6	Aflatoxin, fumonisin, ochratoxin, zearalenone and deoxynivalenol biomarkers in human biological fluids: A systematic literature review, 2001–2018. Food and Chemical Toxicology, 2019, 129, 211-228.	3.6	119
7	A systems study reveals concurrent activation of AMPK and mTOR by amino acids. Nature Communications, 2016, 7, 13254.	12.8	113
8	The Effect of Preanalytical Factors on Stability of the Proteome and Selected Metabolites in Cerebrospinal Fluid (CSF). Journal of Proteome Research, 2009, 8, 5511-5522.	3.7	102
9	2D-DE and MS analysis of key proteins in the adhesion of <i>Lactobacillus plantarum</i> , a first step toward early selection of probiotics based on bacterial biomarkers. Electrophoresis, 2009, 30, 949-956.	2.4	97
10	Multidimensional chromatography coupled to mass spectrometry in analysing complex proteomics samples. Journal of Separation Science, 2010, 33, 1421-1437.	2.5	86
11	Optimized Time Alignment Algorithm for LC-MS Data: Correlation Optimized Warping Using Component Detection Algorithm-Selected Mass Chromatograms. Analytical Chemistry, 2008, 80, 7012-7021.	6.5	79
12	A noise model for mass spectrometry based proteomics. Bioinformatics, 2008, 24, 1070-1077.	4.1	59
13	The Impact of Delayed Storage on the Measured Proteome and Metabolome of Human Cerebrospinal Fluid. Clinical Chemistry, 2011, 57, 1703-1711.	3.2	59
14	Investigation of Biomarkers of Bile Tolerance in <i>Lactobacillus casei</i> Using Comparative Proteomics. Journal of Proteome Research, 2012, 11, 109-118.	3.7	55
15	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2015, 14, 3415-3431.	3.7	53
16	Time Alignment Algorithms Based on Selected Mass Traces for Complex LC-MS Data. Journal of Proteome Research, 2010, 9, 1483-1495.	3.7	52
17	Profiling and Identification of Cerebrospinal Fluid Proteins in a Rat EAE Model of Multiple Sclerosis. Journal of Proteome Research, 2012, 11, 2048-2060.	3.7	51
18	Assessment of Sample Preparation Bias in Mass Spectrometry-Based Proteomics. Analytical Chemistry, 2018, 90, 5405-5413.	6.5	51

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19	One- vs two-phase extraction: re-evaluation of sample preparation procedures for untargeted lipidomics in plasma samples. <i>Analytical and Bioanalytical Chemistry</i> , 2018, 410, 5859-5870.	3.7	51
20	Supercritical fluid extraction of hydrocarbons and 2-alkylcyclobutanones for the detection of irradiated foodstuffs. <i>Journal of Chromatography A</i> , 2000, 897, 259-268.	3.7	49
21	Comparative Urine Analysis by Liquid Chromatography-Mass Spectrometry and Multivariate Statistics: Method Development, Evaluation, and Application to Proteinuria. <i>Journal of Proteome Research</i> , 2007, 6, 194-206.	3.7	48
22	High resolution full scan liquid chromatography mass spectrometry comprehensive screening in sports antidoping urine analysis. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 151, 10-24.	2.8	48
23	Two-Dimensional Method for Time Aligning Liquid Chromatography-Mass Spectrometry Data. <i>Analytical Chemistry</i> , 2008, 80, 3095-3104.	6.5	44
24	Tuning liposome composition to modulate corona formation in human serum and cellular uptake. <i>Acta Biomaterialia</i> , 2020, 106, 314-327.	8.3	43
25	Bioconjugation of Supramolecular Metallacages to Integrin Ligands for Targeted Delivery of Cisplatin. <i>Bioconjugate Chemistry</i> , 2018, 29, 3856-3865.	3.6	41
26	Translational Targeted Proteomics Profiling of Mitochondrial Energy Metabolic Pathways in Mouse and Human Samples. <i>Journal of Proteome Research</i> , 2016, 15, 3204-3213.	3.7	40
27	msCompare: A Framework for Quantitative Analysis of Label-free LC-MS Data for Comparative Candidate Biomarker Studies. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015974.	3.8	39
28	Investigation of potential markers of acid resistance in <i>Lactobacillus plantarum</i> by comparative proteomics. <i>Journal of Applied Microbiology</i> , 2014, 116, 134-144.	3.1	37
29	Imaging of protein distribution in tissues using mass spectrometry: An interdisciplinary challenge. <i>TrAC - Trends in Analytical Chemistry</i> , 2019, 112, 13-28.	11.4	37
30	Comparative Proteomic Analysis of Extracellular Vesicles Isolated by Acoustic Trapping or Differential Centrifugation. <i>Analytical Chemistry</i> , 2016, 88, 8577-8586.	6.5	36
31	Proteomic analysis of <i>Lactobacillus pentosus</i> for the identification of potential markers involved in acid resistance and their influence on other probiotic features. <i>Food Microbiology</i> , 2018, 72, 31-38.	4.2	36
32	Bioconjugation strategies to couple supramolecular exo-functionalized palladium cages to peptides for biomedical applications. <i>Chemical Communications</i> , 2017, 53, 1405-1408.	4.1	33
33	Clinical protein science in translational medicine targeting malignant melanoma. <i>Cell Biology and Toxicology</i> , 2019, 35, 293-332.	5.3	33
34	Susceptibility to COPD: Differential Proteomic Profiling after Acute Smoking. <i>PLoS ONE</i> , 2014, 9, e102037.	2.5	32
35	Gas chromatographic quadrupole time-of-flight full scan high resolution mass spectrometric screening of human urine in antidoping analysis. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1063, 74-83.	2.3	32
36	Biomarker discovery by proteomics: challenges not only for the analytical chemist. <i>Analyst</i> , The, 2006, 131, 1193.	3.5	31

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37	Chipâ€“MS for labelâ€“free profiling of human serum. <i>Electrophoresis</i> , 2007, 28, 4493-4505.	2.4	31
38	Data processing pipelines for comprehensive profiling of proteomics samples by label-free LCâ€“MS for biomarker discovery. <i>Talanta</i> , 2011, 83, 1209-1224.	5.5	30
39	Detection of 2-Alkylcyclobutanones, Markers for Irradiated Foods, in Adipose Tissues of Animals Fed with These Substances. <i>Journal of Food Protection</i> , 2002, 65, 1610-1613.	1.7	27
40	Association of chromosome 19 to lung cancer genotypes and phenotypes. <i>Cancer and Metastasis Reviews</i> , 2015, 34, 217-226.	5.9	26
41	Comparative proteomic analysis of a potentially probiotic <i>Lactobacillus pentosus</i> MP-10 for the identification of key proteins involved in antibiotic resistance and biocide tolerance. <i>International Journal of Food Microbiology</i> , 2016, 222, 8-15.	4.7	26
42	2-Alkylcyclobutanones as markers for irradiated foodstuffs. <i>Journal of Chromatography A</i> , 1999, 858, 109-115.	3.7	25
43	Investigation of the feeding effect on the ¹³ C/ ¹² C isotope ratio of the hormones in bovine urine using gas chromatography/combustion isotope ratio mass spectrometry. <i>Journal of Chromatography A</i> , 2005, 1067, 323-330.	3.7	25
44	Determination of Monounsaturated Alkyl Side Chain 2-Alkylcyclobutanones in Irradiated Foods. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 5836-5841.	5.2	25
45	A fully validated liquid chromatography-mass spectrometry method for the quantification of the soluble receptor of advanced glycation end-products (sRAGE) in serum using immunopurification in a 96-well plate format. <i>Talanta</i> , 2018, 182, 414-421.	5.5	25
46	Toxicological potential of 2-alkylcyclobutanones â€“ specific radiolytic products in irradiated fat-containing food â€“ in bacteria and human cell lines. <i>Food and Chemical Toxicology</i> , 2007, 45, 2581-2591.	3.6	24
47	Diclofenac toxicity in human intestine ex vivo is not related to the formation of intestinal metabolites. <i>Archives of Toxicology</i> , 2015, 89, 107-119.	4.2	24
48	Comparison of gas chromatography/quadrupole timeâ€“ofâ€“flight and quadrupole Orbitrap mass spectrometry in antiâ€“doping analysis: I. Detection of anabolicâ€“androgenic steroids. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 2055-2064.	1.5	22
49	Proteomic analysis of <i>Lactobacillus pentosus</i> for the identification of potential markers of adhesion and other probiotic features. <i>Food Research International</i> , 2018, 111, 58-66.	6.2	22
50	Dietary exposure of the Qatari population to food mycotoxins and reflections on the regulation limits. <i>Toxicology Reports</i> , 2019, 6, 975-982.	3.3	22
51	Lipid peroxidation is involved in calcium dependent upregulation of mitochondrial metabolism in skeletal muscle. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129487.	2.4	22
52	Influence of clotting time on the protein composition of serum samples based on LCâ€“MS dataâ€“†. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009, 877, 1281-1291.	2.3	21
53	Liquid Chromatographyâ€“Electrospray Ionization Tandem Mass Spectrometric Analysis of 2-Alkylcyclobutanones in Irradiated Chicken by Precolumn Derivatization with Hydroxylamine. <i>Journal of Agricultural and Food Chemistry</i> , 2013, 61, 5758-5763.	5.2	21
54	Current Technological Challenges in Biomarker Discovery and Validation. <i>European Journal of Mass Spectrometry</i> , 2010, 16, 101-121.	1.0	20

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55	Affimers as an Alternative to Antibodies in an Affinity LC-MS Assay for Quantification of the Soluble Receptor of Advanced Glycation End-Products (sRAGE) in Human Serum. <i>Journal of Proteome Research</i> , 2018, 17, 2892-2899.	3.7	20
56	Toward Spectral Library-Free Matrix-Assisted Laser Desorption/Ionization Time-of-Flight Mass Spectrometry Bacterial Identification. <i>Journal of Proteome Research</i> , 2018, 17, 2124-2130.	3.7	20
57	The Human Melanoma Proteome Atlas—Complementing the melanoma transcriptome. <i>Clinical and Translational Medicine</i> , 2021, 11, e451.	4.0	20
58	Proteomic alterations in early stage cervical cancer. <i>Oncotarget</i> , 2018, 9, 18128-18147.	1.8	20
59	Supercritical fluid extraction for the detection of 2-dodecylcyclobutanone in low dose irradiated plant foods. <i>Journal of Chromatography A</i> , 2002, 968, 251-255.	3.7	19
60	Cigarette Smoking Acutely Decreases Serum Levels of the Chronic Obstructive Pulmonary Disease Biomarker sRAGE. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2018, 198, 1456-1458.	5.6	19
61	Genotoxicity of 2-alkylcyclobutanones, markers for an irradiation treatment in fat-containing food—Part I: cyto- and genotoxic potential of 2-tetradecylcyclobutanone. <i>Radiation Physics and Chemistry</i> , 2002, 63, 431-435.	2.8	18
62	Threshold-Avoiding Proteomics Pipeline. <i>Analytical Chemistry</i> , 2011, 83, 7786-7794.	6.5	18
63	Whole Blood Storage in CPDA1 Blood Bags Alters Erythrocyte Membrane Proteome. <i>Oxidative Medicine and Cellular Longevity</i> , 2018, 2018, 1-12.	4.0	18
64	Detection of Irradiated Ingredients Included in Low Quantity in Non-irradiated Food Matrix. 1. Extraction and ESR Analysis of Bones from Mechanically Recovered Poultry Meat. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 3769-3773.	5.2	17
65	Proteogenomics: Key Driver for Clinical Discovery and Personalized Medicine. <i>Advances in Experimental Medicine and Biology</i> , 2016, 926, 21-47.	1.6	17
66	Application of Displacement Chromatography to Online Two-Dimensional Liquid Chromatography Coupled to Tandem Mass Spectrometry Improves Peptide Separation Efficiency and Detectability for the Analysis of Complex Proteomes. <i>Analytical Chemistry</i> , 2018, 90, 9951-9958.	6.5	17
67	Innovations in studying in vivo cell behavior and pharmacology in complex tissues — microvascular endothelial cells in the spotlight. <i>Cell and Tissue Research</i> , 2013, 354, 647-669.	2.9	16
68	The antifibrotic potential of a sustained release formulation of a PDGF β -receptor targeted rho kinase inhibitor. <i>Journal of Controlled Release</i> , 2019, 296, 250-257.	9.9	16
69	The Hidden Story of Heterogeneous B-raf V600E Mutation Quantitative Protein Expression in Metastatic Melanoma—Association with Clinical Outcome and Tumor Phenotypes. <i>Cancers</i> , 2019, 11, 1981.	3.7	16
70	Integrated proteogenomic approach identifying a protein signature of COPD and a new splice variant of SORBS1. <i>Thorax</i> , 2020, 75, 180-183.	5.6	16
71	Fragment Mass Spectrum Prediction Facilitates Site Localization of Phosphorylation. <i>Journal of Proteome Research</i> , 2021, 20, 634-644.	3.7	16
72	Detection of Irradiated Ingredients Included in Low Quantity in Non-irradiated Food Matrix. 2. ESR Analysis of Mechanically Recovered Poultry Meat and TL Analysis of Spices. <i>Journal of Agricultural and Food Chemistry</i> , 2005, 53, 3774-3778.	5.2	15

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73	Proteomic Studies Related to Genetic Determinants of Variability in Protein Concentrations. <i>Journal of Proteome Research</i> , 2014, 13, 5-14.	3.7	15
74	Determination of 2-Alkylcyclobutanones with Electronic Impact and Chemical Ionization Gas Chromatography/Mass Spectrometry (GC/MS) in Irradiated Foods. <i>Journal of Agricultural and Food Chemistry</i> , 2006, 54, 1990-1996.	5.2	14
75	Correlation Queries for Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2013, 85, 4398-4404.	6.5	14
76	Population reference ranges of urinary endogenous sulfate steroids concentrations and ratios as complement to the steroid profile in sports antidoping. <i>Steroids</i> , 2019, 152, 108477.	1.8	14
77	Gene network approach reveals co-expression patterns in nasal and bronchial epithelium. <i>Scientific Reports</i> , 2019, 9, 15835.	3.3	14
78	The human melanoma proteome atlas—Defining the molecular pathology. <i>Clinical and Translational Medicine</i> , 2021, 11, e473.	4.0	14
79	Detection of low amount of irradiated ingredients in non-irradiated precooked meals. <i>Radiation Physics and Chemistry</i> , 2002, 63, 447-450.	2.8	13
80	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017, 6, 875.	1.6	13
81	Assuring Consistent Performance of an Insulin-Like Growth Factor 1 MALDIImmunoassay by Monitoring Measurement Quality Indicators. <i>Analytical Chemistry</i> , 2017, 89, 6188-6195.	6.5	12
82	Tutorial: Correction of shifts in single-stage LC-MS(/MS) data. <i>Analytica Chimica Acta</i> , 2018, 999, 37-53.	5.4	12
83	Quantification of surfactant protein D (SPD) in human serum by liquid chromatography-mass spectrometry (LC-MS). <i>Talanta</i> , 2019, 202, 507-513.	5.5	12
84	Improved survival prognostication of node-positive malignant melanoma patients utilizing shotgun proteomics guided by histopathological characterization and genomic data. <i>Scientific Reports</i> , 2019, 9, 5154.	3.3	12
85	Targeted imaging of integrins in cancer tissues using photocleavable Ru(II) polypyridine complexes as mass-tags. <i>Chemical Communications</i> , 2020, 56, 5941-5944.	4.1	12
86	In Vitro Transcription/Translation System: A Versatile Tool in the Search for Missing Proteins. <i>Journal of Proteome Research</i> , 2015, 14, 3441-3451.	3.7	11
87	Queries of MALDI-imaging global datasets identifying ion mass signatures associated with tissue compartments. <i>Proteomics</i> , 2014, 14, 862-871.	2.2	10
88	Identification of Analytical Factors Affecting Complex Proteomics Profiles Acquired in a Factorial Design Study with Analysis of Variance: Simultaneous Component Analysis. <i>Analytical Chemistry</i> , 2016, 88, 4229-4238.	6.5	10
89	Genomic variability and protein species—Improving sequence coverage for proteogenomics. <i>Journal of Proteomics</i> , 2016, 134, 25-36.	2.4	10
90	Efficient reaction pathway for the synthesis of saturated and mono-unsaturated 2-alkylcyclobutanones. <i>Radiation Physics and Chemistry</i> , 2002, 65, 233-239.	2.8	9

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91	A high-throughput processing service for retention time alignment of complex proteomics and metabolomics LC-MS data. <i>Bioinformatics</i> , 2011, 27, 1176-1178.	4.1	9
92	Methyl jasmonate treatment increases podophyllotoxin production in <i>Podophyllum hexandrum</i> roots under glasshouse conditions. <i>Plant and Soil</i> , 2017, 417, 117-126.	3.7	9
93	Ultra-fast retroactive processing of liquid chromatography high-resolution full-scan Orbitrap mass spectrometry data in anti-doping screening of human urine. <i>Rapid Communications in Mass Spectrometry</i> , 2019, 33, 1578-1588.	1.5	9
94	Novel functional proteins coded by the human genome discovered in metastases of melanoma patients. <i>Cell Biology and Toxicology</i> , 2020, 36, 261-272.	5.3	9
95	Quantification of the soluble Receptor of Advanced Glycation End-Products (sRAGE) by LC-MS after enrichment by strong cation exchange (SCX) solid-phase extraction (SPE) at the protein level. <i>Analytica Chimica Acta</i> , 2018, 1043, 45-51.	5.4	8
96	Clusterwise Peak Detection and Filtering Based on Spatial Distribution To Efficiently Mine Mass Spectrometry Imaging Data. <i>Analytical Chemistry</i> , 2019, 91, 11888-11896.	6.5	8
97	Exact hypothesis testing for shrinkage-based Gaussian graphical models. <i>Bioinformatics</i> , 2019, 35, 5011-5017.	4.1	8
98	Label-Free Proteomics of Serum. <i>Methods in Molecular Biology</i> , 2008, 484, 67-77.	0.9	8
99	Pre- and Post-analytical Factors in Biomarker Discovery. <i>Methods in Molecular Biology</i> , 2019, 1959, 1-22.	0.9	7
100	MSIWarp: A General Approach to Mass Alignment in Mass Spectrometry Imaging. <i>Analytical Chemistry</i> , 2020, 92, 16138-16148.	6.5	7
101	Plasma sRAGE levels strongly associate with centrilobular emphysema assessed by HRCT scans. <i>Respiratory Research</i> , 2022, 23, 15.	3.6	7
102	Effect estimate comparison between the prescription sequence symmetry analysis (PSSA) and parallel group study designs: A systematic review. <i>PLoS ONE</i> , 2018, 13, e0208389.	2.5	6
103	Pipelines and Systems for Threshold-Avoiding Quantification of LC-MS/MS Data. <i>Analytical Chemistry</i> , 2021, 93, 11215-11224.	6.5	6
104	Reply to Biswas: Acute and Chronic Effects of Cigarette Smoking on sRAGE. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2019, 199, 806-807.	5.6	5
105	Inversion of peak elution order prevents uniform time alignment of complex liquid-chromatography coupled to mass spectrometry datasets. <i>Journal of Chromatography A</i> , 2014, 1373, 61-72.	3.7	4
106	Analysis of Multiple Mycotoxins in the Qatari Population and Their Relation to Markers of Oxidative Stress. <i>Toxins</i> , 2021, 13, 267.	3.4	4
107	Dynamic binning peak detection and assessment of various lipidomics liquid chromatography-mass spectrometry pre-processing platforms. <i>Analytica Chimica Acta</i> , 2021, 1173, 338674.	5.4	4
108	Prioritization of COPD protein biomarkers, based on a systematic study of the literature. <i>Advances in Precision Medicine</i> , 2016, 1, 4.	0.3	4

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109	Determination of multiple mycotoxins in Qatari population serum samples by LC-MS/MS. World Mycotoxin Journal, 2020, 13, 57-65.	1.4	3
110	Female Specific Association of Low Insulin-Like Growth Factor 1 (IGF1) Levels with Increased Risk of Premature Mortality in Renal Transplant Recipients. Journal of Clinical Medicine, 2020, 9, 293.	2.4	3
111	Angiogenic regulatory influence of extracellular matrix deposited by resting state asthmatic and non-asthmatic airway smooth muscle cells is similar. Journal of Cellular and Molecular Medicine, 2021, 25, 6438-6447.	3.6	3
112	Adsorptive Microtiter Plates As Solid Supports in Affinity Purification Workflows. Journal of Proteome Research, 2021, 20, 5218-5221.	3.7	3
113	Deep Proteomic Analysis on Biobanked Paraffine-Archived Melanoma with Prognostic/Predictive Biomarker Read-Out. Cancers, 2021, 13, 6105.	3.7	3
114	Proteomics Landscape of Host-Pathogen Interaction in Acinetobacter baumannii Infected Mouse Lung. Frontiers in Genetics, 2021, 12, 563516.	2.3	2
115	Ultra-fast retroactive processing by MetAlign of liquid chromatography/high-resolution full-scan Orbitrap mass spectrometry data in WADA Human Urine Sample Monitoring Program. Rapid Communications in Mass Spectrometry, 2021, 35, e9141.	1.5	2
116	Combined Metabolic and Chemical (CoMetChem) Labeling Using Stable Isotopes—a Strategy to Reveal Site-Specific Histone Acetylation and Deacetylation Rates by LC-MS. Analytical Chemistry, 2021, 93, 12872-12880.	6.5	2
117	Olympic anti-doping laboratory: the analytical technological road from 2016 Rio De Janeiro to 2021 Tokyo. Bioanalysis, 2021, 13, 1511-1527.	1.5	1
118	Omics Technology: Lipidomics and Its Pitfalls During the Preanalytical Stage. , 2018, , .		0
119	The “un-shrunk” partial correlation in Gaussian graphical models. BMC Bioinformatics, 2021, 22, 424.	2.6	0
120	Cigarette smoking prior to blood sampling acutely affects serum levels of the chronic obstructive pulmonary disease biomarker surfactant protein D. Clinical Chemistry and Laboratory Medicine, 2020, 58, e138-e141.	2.3	0
121	Accurate Prediction of Protein Sequences for Proteogenomics Data Integration. Methods in Molecular Biology, 2022, 2420, 233-260.	0.9	0