

Richard D Smith

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1,308 papers	80,359 citations	132 h-index	204 g-index
1,377 ext. papers	89,568 ext. citations	6.9 avg, IF	7.86 L-index

#	Paper	IF	Citations
1308	Genomic responses in mouse models poorly mimic human inflammatory diseases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 3507-12	11.5	2076
1307	New developments in biochemical mass spectrometry: electrospray ionization. <i>Analytical Chemistry</i> , 1990 , 62, 882-99	7.8	947
1306	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004 , 22, 1459-66	44.5	632
1305	Toward a human blood serum proteome: analysis by multidimensional separation coupled with mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2002 , 1, 947-55	7.6	622
1304	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016 , 166, 755-765	56.2	544
1303	On-line mass spectrometric detection for capillary zone electrophoresis. <i>Analytical Chemistry</i> , 1987 , 59, 1230-1232	7.8	513
1302	Principles and practice of electrospray ionization mass spectrometry for large polypeptides and proteins. <i>Mass Spectrometry Reviews</i> , 1991 , 10, 359-452	11	506
1301	Identification of proteins in human cytomegalovirus (HCMV) particles: the HCMV proteome. <i>Journal of Virology</i> , 2004 , 78, 10960-6	6.6	460
1300	Improved electrospray ionization interface for capillary zone electrophoresis-mass spectrometry. <i>Analytical Chemistry</i> , 1988 , 60, 1948-1952	7.8	452
1299	Activated ClpP kills persisters and eradicates a chronic biofilm infection. <i>Nature</i> , 2013 , 503, 365-70	50.4	451
1298	Responding to global infectious disease outbreaks: lessons from SARS on the role of risk perception, communication and management. <i>Social Science and Medicine</i> , 2006 , 63, 3113-23	5.1	446
1297	Omic data from evolved E. coli are consistent with computed optimal growth from genome-scale models. <i>Molecular Systems Biology</i> , 2010 , 6, 390	12.2	419
1296	Comparative analysis of proteome and transcriptome variation in mouse. <i>PLoS Genetics</i> , 2011 , 7, e1001363	13.3	417
1295	Reversed-phase chromatography with multiple fraction concatenation strategy for proteome profiling of human MCF10A cells. <i>Proteomics</i> , 2011 , 11, 2019-26	4.8	387
1294	An accurate mass tag strategy for quantitative and high-throughput proteome measurements. <i>Proteomics</i> , 2002 , 2, 513-23	4.8	386
1293	Proteomics by FTICR mass spectrometry: top down and bottom up. <i>Mass Spectrometry Reviews</i> , 2005 , 24, 168-200	11	375
1292	Fundamentals of traveling wave ion mobility spectrometry. <i>Analytical Chemistry</i> , 2008 , 80, 9689-99	7.8	368

1291	Human plasma N-glycoproteome analysis by immunoaffinity subtraction, hydrazide chemistry, and mass spectrometry. <i>Journal of Proteome Research</i> , 2005 , 4, 2070-80	5.6	365
1290	Global analysis of the <i>Deinococcus radiodurans</i> proteome by using accurate mass tags. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11049-54	11.5	355
1289	DAnTE: a statistical tool for quantitative analysis of -omics data. <i>Bioinformatics</i> , 2008 , 24, 1556-8	7.2	333
1288	Phosphoprotein isotope-coded affinity tag approach for isolating and quantitating phosphopeptides in proteome-wide analyses. <i>Analytical Chemistry</i> , 2001 , 73, 2578-86	7.8	320
1287	Capillary zone electrophoresis-mass spectrometry using an electrospray ionization interface. <i>Analytical Chemistry</i> , 1988 , 60, 436-441	7.8	316
1286	Rapid expansion of supercritical fluid solutions: solute formation of powders, thin films, and fibers. <i>Industrial & Engineering Chemistry Research</i> , 1987 , 26, 2298-2306	3.9	304
1285	Temporal proteome and lipidome profiles reveal hepatitis C virus-associated reprogramming of hepatocellular metabolism and bioenergetics. <i>PLoS Pathogens</i> , 2010 , 6, e1000719	7.6	302
1284	Probability-based evaluation of peptide and protein identifications from tandem mass spectrometry and SEQUEST analysis: the human proteome. <i>Journal of Proteome Research</i> , 2005 , 4, 53-62	5.6	293
1283	Normalization approaches for removing systematic biases associated with mass spectrometry and label-free proteomics. <i>Journal of Proteome Research</i> , 2006 , 5, 277-86	5.6	287
1282	Theory versus practice: a review of Willingness-to-pay in health and health care. <i>Health Economics (United Kingdom)</i> , 2001 , 10, 39-52	2.4	287
1281	Observations on the solubility of surfactants and related molecules in carbon dioxide at 50°C. <i>Journal of Supercritical Fluids</i> , 1990 , 3, 51-65	4.2	284
1280	Advances and challenges in liquid chromatography-mass spectrometry-based proteomics profiling for clinical applications. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1727-44	7.6	281
1279	Mass spectrometry-based proteomics: existing capabilities and future directions. <i>Chemical Society Reviews</i> , 2012 , 41, 3912-28	58.5	277
1278	Ultra-high-efficiency strong cation exchange LC/RPLC/MS/MS for high dynamic range characterization of the human plasma proteome. <i>Analytical Chemistry</i> , 2004 , 76, 1134-44	7.8	273
1277	Advances in proteomics data analysis and display using an accurate mass and time tag approach. <i>Mass Spectrometry Reviews</i> , 2006 , 25, 450-82	11	272
1276	Quantitative analysis of bacterial and mammalian proteomes using a combination of cysteine affinity tags and ¹⁵ N-metabolic labeling. <i>Analytical Chemistry</i> , 2001 , 73, 2132-9	7.8	272
1275	A perspective on the Maillard reaction and the analysis of protein glycation by mass spectrometry: probing the pathogenesis of chronic disease. <i>Journal of Proteome Research</i> , 2009 , 8, 754-69	5.6	261
1274	Use of artificial neural networks for the accurate prediction of peptide liquid chromatography elution times in proteome analyses. <i>Analytical Chemistry</i> , 2003 , 75, 1039-48	7.8	261

1273	Utility of accurate mass tags for proteome-wide protein identification. <i>Analytical Chemistry</i> , 2000 , 72, 3349-54	7.8	252
1272	Solvent-induced conformational changes of polypeptides probed by electrospray-ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1991 , 5, 101-5	2.2	251
1271	Observation of the Noncovalent Quaternary Associations of Proteins by Electrospray Ionization Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1994 , 116, 5271-5278	16.4	250
1270	Effect of reducing disulfide-containing proteins on electrospray ionization mass spectra. <i>Analytical Chemistry</i> , 1990 , 62, 693-8	7.8	250
1269	High-efficiency nanoscale liquid chromatography coupled on-line with mass spectrometry using nanoelectrospray ionization for proteomics. <i>Analytical Chemistry</i> , 2002 , 74, 4235-49	7.8	249
1268	Primary sequence information from intact proteins by electrospray ionization tandem mass spectrometry. <i>Science</i> , 1990 , 248, 201-4	33.3	249
1267	Utilizing human blood plasma for proteomic biomarker discovery. <i>Journal of Proteome Research</i> , 2005 , 4, 1073-85	5.6	240
1266	Ischemia in tumors induces early and sustained phosphorylation changes in stress kinase pathways but does not affect global protein levels. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1690-704	7.6	239
1265	Proteogenomic Analysis of Human Colon Cancer Reveals New Therapeutic Opportunities. <i>Cell</i> , 2019 , 177, 1035-1049.e19	56.2	237
1264	The observation of non-covalent interactions in solution by electrospray ionization mass spectrometry: Promise, pitfalls and prognosis. <i>Biological Mass Spectrometry</i> , 1993 , 22, 493-501		237
1263	Transport functions dominate the SAR11 metaproteome at low-nutrient extremes in the Sargasso Sea. <i>ISME Journal</i> , 2009 , 3, 93-105	11.9	235
1262	Tandem mass spectrometry identifies many mouse brain O-GlcNAcylated proteins including EGF domain-specific O-GlcNAc transferase targets. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 7280-5	11.5	234
1261	An Interlaboratory Evaluation of Drift Tube Ion Mobility-Mass Spectrometry Collision Cross Section Measurements. <i>Analytical Chemistry</i> , 2017 , 89, 9048-9055	7.8	233
1260	Tandem mass spectrometry of very large molecules. 2. Dissociation of multiply charged proline-containing proteins from electrospray ionization. <i>Analytical Chemistry</i> , 1993 , 65, 425-38	7.8	227
1259	High-sensitivity ion mobility spectrometry/mass spectrometry using electrodynamic ion funnel interfaces. <i>Analytical Chemistry</i> , 2005 , 77, 3330-9	7.8	225
1258	An IMS-IMS analogue of MS-MS. <i>Analytical Chemistry</i> , 2006 , 78, 4161-74	7.8	221
1257	Probing proteomes using capillary isoelectric focusing-electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry. <i>Analytical Chemistry</i> , 1999 , 71, 2076-84	7.8	220
1256	A novel ion funnel for focusing ions at elevated pressure using electrospray ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1997 , 11, 1813-1817	2.2	219

1255	Automated 20 kpsi RPLC-MS and MS/MS with chromatographic peak capacities of 1000-1500 and capabilities in proteomics and metabolomics. <i>Analytical Chemistry</i> , 2005 , 77, 3090-100	7.8	218
1254	Enrichment of integral membrane proteins for proteomic analysis using liquid chromatography-tandem mass spectrometry. <i>Journal of Proteome Research</i> , 2002 , 1, 351-60	5.6	216
1253	Chemically etched open tubular and monolithic emitters for nanoelectrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 2006 , 78, 7796-801	7.8	214
1252	Nanodroplet processing platform for deep and quantitative proteome profiling of 10-100 mammalian cells. <i>Nature Communications</i> , 2018 , 9, 882	17.4	213
1251	Charge competition and the linear dynamic range of detection in electrospray ionization mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2004 , 15, 1416-1423	3.5	208
1250	Collisional activation and collision-activated dissociation of large multiply charged polypeptides and proteins produced by electrospray ionization. <i>Journal of the American Society for Mass Spectrometry</i> , 1990 , 1, 53-65	3.5	207
1249	An ion funnel interface for improved ion focusing and sensitivity using electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 1998 , 70, 4111-9	7.8	206
1248	Packed capillary reversed-phase liquid chromatography with high-performance electrospray ionization Fourier transform ion cyclotron resonance mass spectrometry for proteomics. <i>Analytical Chemistry</i> , 2001 , 73, 1766-75	7.8	205
1247	Collisional effects on the charge distribution of ions from large molecules, formed by electrospray-ionization mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 1988 , 2, 207-210	10.2	205
1246	Mechanisms of severe acute respiratory syndrome coronavirus-induced acute lung injury. <i>MBio</i> , 2013 , 4,	7.8	204
1245	Statistical characterization of the charge state and residue dependence of low-energy CID peptide dissociation patterns. <i>Analytical Chemistry</i> , 2005 , 77, 5800-13	7.8	203
1244	Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon-stimulated gene responses. <i>MBio</i> , 2014 , 5, e01174-14	7.8	199
1243	Peptide and protein analysis by electrospray ionization-mass spectrometry and capillary electrophoresis-mass spectrometry. <i>Analytical Biochemistry</i> , 1989 , 179, 404-12	3.1	198
1242	In silico method for modelling metabolism and gene product expression at genome scale. <i>Nature Communications</i> , 2012 , 3, 929	17.4	194
1241	High Throughput Proteome-Wide Precision Measurements of Protein Expression Using Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999 , 121, 7949-7950	16.4	194
1240	Extraction of metal ions from liquid and solid materials by supercritical carbon dioxide. <i>Analytical Chemistry</i> , 1992 , 64, 2875-2878	7.8	191
1239	<i>Synechococcus elongatus</i> UTEX 2973, a fast growing cyanobacterial chassis for biosynthesis using light and CO ₂ <i>Scientific Reports</i> , 2015 , 5, 8132	4.9	190
1238	High-pH reversed-phase chromatography with fraction concatenation for 2D proteomic analysis. <i>Expert Review of Proteomics</i> , 2012 , 9, 129-34	4.2	189

1237	Evaluation of multiprotein immunoaffinity subtraction for plasma proteomics and candidate biomarker discovery using mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 2167-74	7.6	188
1236	Normalization and missing value imputation for label-free LC-MS analysis. <i>BMC Bioinformatics</i> , 2012 , 13 Suppl 16, S5	3.6	187
1235	Clustering millions of tandem mass spectra. <i>Journal of Proteome Research</i> , 2008 , 7, 113-22	5.6	187
1234	Binding MOAD (Mother Of All Databases). <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 333-40	4.0	187
1233	Ionization and transmission efficiency in an electrospray ionization-mass spectrometry interface. <i>Journal of the American Society for Mass Spectrometry</i> , 2007 , 18, 1582-90	3.5	182
1232	The ion funnel: theory, implementations, and applications. <i>Mass Spectrometry Reviews</i> , 2010 , 29, 294-312	4.1	180
1231	Does trypsin cut before proline?. <i>Journal of Proteome Research</i> , 2008 , 7, 300-5	5.6	180
1230	VIPER: an advanced software package to support high-throughput LC-MS peptide identification. <i>Bioinformatics</i> , 2007 , 23, 2021-3	7.2	178
1229	Tandem mass spectrometry of very large molecules: serum albumin sequence information from multiply charged ions formed by electrospray ionization. <i>Analytical Chemistry</i> , 1991 , 63, 2488-99	7.8	178
1228	Antibody-free, targeted mass-spectrometric approach for quantification of proteins at low picogram per milliliter levels in human plasma/serum. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 15395-400	11.5	177
1227	Reproducible workflow for multiplexed deep-scale proteome and phosphoproteome analysis of tumor tissues by liquid chromatography-mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 1632-1661	18.8	176
1226	High throughput quantitative analysis of serum proteins using glycopeptide capture and liquid chromatography mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 144-55	7.6	176
1225	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983.e31	9.1	173
1224	Decon2LS: An open-source software package for automated processing and visualization of high resolution mass spectrometry data. <i>BMC Bioinformatics</i> , 2009 , 10, 87	3.6	173
1223	Ultrasensitive proteomics using high-efficiency on-line micro-SPE-nanoLC-nanoESI MS and MS/MS. <i>Analytical Chemistry</i> , 2004 , 76, 144-54	7.8	173
1222	Design and implementation of a new electrodynamic ion funnel. <i>Analytical Chemistry</i> , 2000 , 72, 2247-55	7.8	173
1221	High-throughput proteomics using high-efficiency multiple-capillary liquid chromatography with on-line high-performance ESI FTICR mass spectrometry. <i>Analytical Chemistry</i> , 2001 , 73, 3011-21	7.8	173
1220	Enhanced detection of low abundance human plasma proteins using a tandem IgY12-SuperMix immunoaffinity separation strategy. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 1963-73	7.6	172

1219	Using Electrospray Ionization FTICR Mass Spectrometry To Study Competitive Binding of Inhibitors to Carbonic Anhydrase. <i>Journal of the American Chemical Society</i> , 1995 , 117, 8859-8860	16.4	172
1218	The challenge of antimicrobial resistance: What economics can contribute. <i>Science</i> , 2019 , 364,	33.3	171
1217	Advancing the sensitivity of selected reaction monitoring-based targeted quantitative proteomics. <i>Proteomics</i> , 2012 , 12, 1074-92	4.8	170
1216	Probing qualitative conformation differences of multiply protonated gas-phase proteins via hydrogen/deuterium isotopic exchange with water-d2. <i>Journal of the American Chemical Society</i> , 1992 , 114, 5897-5898	16.4	170
1215	Combining capillary electrophoresis with mass spectrometry for applications in proteomics. <i>Electrophoresis</i> , 2005 , 26, 1291-305	3.6	168
1214	Stable isotope-coded proteomic mass spectrometry. <i>Current Opinion in Biotechnology</i> , 2003 , 14, 101-9	11.4	167
1213	Sheathless capillary electrophoresis-electrospray ionization mass spectrometry using 10 μ m I.D. capillaries: analyses of tryptic digests of cytochrome c. <i>Journal of Chromatography A</i> , 1994 , 659, 217-22	4.5	166
1212	Integrative analysis of the mitochondrial proteome in yeast. <i>PLoS Biology</i> , 2004 , 2, e160	9.7	165
1211	Direct mass spectrometric analysis of intact proteins of the yeast large ribosomal subunit using capillary LC/FTICR. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 5942-7	11.5	165
1210	Characterization of the human blood plasma proteome. <i>Proteomics</i> , 2005 , 5, 4034-45	4.8	164
1209	New mass spectrometric methods for the study of noncovalent associations of biopolymers. <i>Chemical Society Reviews</i> , 1997 , 26, 191	58.5	163
1208	Connecting genomic alterations to cancer biology with proteomics: the NCI Clinical Proteomic Tumor Analysis Consortium. <i>Cancer Discovery</i> , 2013 , 3, 1108-12	24.4	162
1207	Solubility of fluorinated metal diethyldithiocarbamates in Supercritical carbon dioxide. <i>Journal of Supercritical Fluids</i> , 1991 , 4, 194-198	4.2	158
1206	Small volume and low flow-rate electrospray ionization mass spectrometry of aqueous samples. <i>Rapid Communications in Mass Spectrometry</i> , 1993 , 7, 1017-1021	2.2	156
1205	Whole proteome analysis of post-translational modifications: applications of mass-spectrometry for proteogenomic annotation. <i>Genome Research</i> , 2007 , 17, 1362-77	9.7	155
1204	Precautionary behavior in response to perceived threat of pandemic influenza. <i>Emerging Infectious Diseases</i> , 2007 , 13, 1307-13	10.2	155
1203	Proteomics based on high-efficiency capillary separations. <i>Electrophoresis</i> , 2002 , 23, 3106-24	3.6	152
1202	Observation of a small oligonucleotide duplex by electrospray ionization mass spectrometry. <i>Journal of the American Chemical Society</i> , 1993 , 115, 803-804	16.4	152

1201	High-resolution field asymmetric waveform ion mobility spectrometry using new planar geometry analyzers. <i>Analytical Chemistry</i> , 2006 , 78, 3706-14	7.8	151
1200	Microfabricated isoelectric focusing device for direct electrospray ionization-mass spectrometry. <i>Electrophoresis</i> , 2000 , 21, 191-7	3.6	151
1199	Establishing the proteome of normal human cerebrospinal fluid. <i>PLoS ONE</i> , 2010 , 5, e10980	3.7	150
1198	Liquid chromatography-mass spectrometry-based quantitative proteomics. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25443-9	5.4	147
1197	Robust algorithm for alignment of liquid chromatography-mass spectrometry analyses in an accurate mass and time tag data analysis pipeline. <i>Analytical Chemistry</i> , 2006 , 78, 7397-409	7.8	147
1196	Improved peptide elution time prediction for reversed-phase liquid chromatography-MS by incorporating peptide sequence information. <i>Analytical Chemistry</i> , 2006 , 78, 5026-39	7.8	147
1195	Uncovering biologically significant lipid isomers with liquid chromatography, ion mobility spectrometry and mass spectrometry. <i>Analyst, The</i> , 2016 , 141, 1649-59	5	146
1194	A microfabricated dialysis device for sample cleanup in electrospray ionization mass spectrometry. <i>Analytical Chemistry</i> , 1998 , 70, 3553-6	7.8	146
1193	Head-to-head comparison of serum fractionation techniques. <i>Journal of Proteome Research</i> , 2007 , 6, 828-36	5.6	144
1192	Quantitative proteome analysis of human plasma following in vivo lipopolysaccharide administration using ¹⁶ O/ ¹⁸ O labeling and the accurate mass and time tag approach. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 700-9	7.6	144
1191	Phosphoprotein isotope-coded affinity tags: application to the enrichment and identification of low-abundance phosphoproteins. <i>Analytical Chemistry</i> , 2002 , 74, 607-16	7.8	144
1190	Zeptomole-sensitivity electrospray ionization--Fourier transform ion cyclotron resonance mass spectrometry of proteins. <i>Analytical Chemistry</i> , 2000 , 72, 2271-9	7.8	144
1189	Generation of multiple electrosprays using microfabricated emitter arrays for improved mass spectrometric sensitivity. <i>Analytical Chemistry</i> , 2001 , 73, 1658-63	7.8	143
1188	Enrichment and analysis of nonenzymatically glycosylated peptides: boronate affinity chromatography coupled with electron-transfer dissociation mass spectrometry. <i>Journal of Proteome Research</i> , 2007 , 6, 2323-30	5.6	142
1187	The trace element chemistry of coal during combustion and the emissions from coal-fired plants. <i>Progress in Energy and Combustion Science</i> , 1980 , 6, 53-119	33.6	142
1186	Review, evaluation, and discussion of the challenges of missing value imputation for mass spectrometry-based label-free global proteomics. <i>Journal of Proteome Research</i> , 2015 , 14, 1993-2001	5.6	141
1185	Development and evaluation of a micro- and nanoscale proteomic sample preparation method. <i>Journal of Proteome Research</i> , 2005 , 4, 2397-403	5.6	141
1184	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139

1183	Human Proteinpedia enables sharing of human protein data. <i>Nature Biotechnology</i> , 2008 , 26, 164-7	44.5	138
1182	Proteome analyses using accurate mass and elution time peptide tags with capillary LC time-of-flight mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2003 , 14, 980-93	3.5	136
1181	Recommendations for the Generation, Quantification, Storage, and Handling of Peptides Used for Mass Spectrometry-Based Assays. <i>Clinical Chemistry</i> , 2016 , 62, 48-69	5.5	135
1180	Proteomic analyses using an accurate mass and time tag strategy. <i>BioTechniques</i> , 2004 , 37, 621-4, 626-33, 636 passim	2.5	135
1179	Toward plasma proteome profiling with ion mobility-mass spectrometry. <i>Journal of Proteome Research</i> , 2006 , 5, 2977-84	5.6	134
1178	High-throughput comparative proteome analysis using a quantitative cysteinyl-peptide enrichment technology. <i>Analytical Chemistry</i> , 2004 , 76, 5345-53	7.8	134
1177	Advances in targeted proteomics and applications to biomedical research. <i>Proteomics</i> , 2016 , 16, 2160-82	4.8	134
1176	SerpinB1 Promotes Pancreatic β -Cell Proliferation. <i>Cell Metabolism</i> , 2016 , 23, 194-205	24.6	132
1175	Clinical microfluidics for neutrophil genomics and proteomics. <i>Nature Medicine</i> , 2010 , 16, 1042-7	50.5	132
1174	Preparation of 20-microm-i.d. silica-based monolithic columns and their performance for proteomics analyses. <i>Analytical Chemistry</i> , 2005 , 77, 5028-35	7.8	132
1173	Ultrasensitive and quantitative analyses from combined separations-mass spectrometry for the characterization of proteomes. <i>Accounts of Chemical Research</i> , 2004 , 37, 269-78	24.3	132
1172	Preservation of non-covalent associations in electrospray ionization mass spectrometry: Multiply charged polypeptide and protein dimers. <i>Organic Mass Spectrometry</i> , 1992 , 27, 811-821		132
1171	High dynamic range characterization of the trauma patient plasma proteome. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1899-913	7.6	131
1170	Screening derivatized peptide libraries for tight binding inhibitors to carbonic anhydrase II by electrospray ionization-mass spectrometry. <i>Journal of Medicinal Chemistry</i> , 1996 , 39, 1949-55	8.3	131
1169	Trade in health-related services. <i>Lancet, The</i> , 2009 , 373, 593-601	40	130
1168	Creating nanocavities of tunable sizes: hollow helices. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99, 11583-8	11.5	130
1167	Proteome analysis using selective incorporation of isotopically labeled amino acids. <i>Journal of the American Society for Mass Spectrometry</i> , 2000 , 11, 78-82	3.5	130
1166	Trapping, Detection, and Mass Determination of Coliphage T4 DNA Ions by Electrospray Ionization Fourier Transform Ion Cyclotron Resonance Mass Spectrometry. <i>Analytical Chemistry</i> , 1995 , 67, 1159-1163	7.8	130

1165	The genome of <i>Cyanothece</i> 51142, a unicellular diazotrophic cyanobacterium important in the marine nitrogen cycle. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 15094-9	11.5	129
1164	Phosphoprotein isotope-coded solid-phase tag approach for enrichment and quantitative analysis of phosphopeptides from complex mixtures. <i>Analytical Chemistry</i> , 2003 , 75, 5441-50	7.8	129
1163	Characterization of supercritical fluid solvents using solvatochromic shifts. <i>The Journal of Physical Chemistry</i> , 1986 , 90, 3022-3026		129
1162	DeconMSn: a software tool for accurate parent ion monoisotopic mass determination for tandem mass spectra. <i>Bioinformatics</i> , 2008 , 24, 1021-3	7.2	128
1161	Protein identification with a single accurate mass of a cysteine-containing peptide and constrained database searching. <i>Analytical Chemistry</i> , 2000 , 72, 1112-8	7.8	128
1160	Endogenously nitrated proteins in mouse brain: links to neurodegenerative disease. <i>Biochemistry</i> , 2006 , 45, 8009-22	3.2	127
1159	Application of peptide LC retention time information in a discriminant function for peptide identification by tandem mass spectrometry. <i>Journal of Proteome Research</i> , 2004 , 3, 760-9	5.6	127
1158	Construction of the contingent valuation market in health care: a critical assessment. <i>Health Economics (United Kingdom)</i> , 2003 , 12, 609-28	2.4	127
1157	Perspective: a program to improve protein biomarker discovery for cancer. <i>Journal of Proteome Research</i> , 2005 , 4, 1104-9	5.6	125
1156	On-line microdialysis sample cleanup for electrospray ionization mass spectrometry of nucleic acid samples. <i>Analytical Chemistry</i> , 1996 , 68, 3295-9	7.8	125
1155	Transition-Metal-Mediated Rational Design and Self-Assembly of Chiral, Nanoscale Supramolecular Polyhedra with Unique T Symmetry. <i>Organometallics</i> , 1997 , 16, 3094-3096	3.8	124
1154	Capillary Electrophoresis/Mass Spectrometry. <i>Analytical Chemistry</i> , 1993 , 65, 574A-584A	7.8	124
1153	Free 25-Hydroxyvitamin D: Impact of Vitamin D Binding Protein Assays on Racial-Genotypic Associations. <i>Journal of Clinical Endocrinology and Metabolism</i> , 2016 , 101, 2226-34	5.6	123
1152	Analytical supercritical fluid extraction of adsorbent materials. <i>Analytical Chemistry</i> , 1987 , 59, 38-44	7.8	123
1151	Concentration dependence upon particle size of volatilized elements in fly ash. <i>Environmental Science & Technology</i> , 1979 , 13, 553-558	10.3	123
1150	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
1149	Characterization of the mouse brain proteome using global proteomic analysis complemented with cysteinyl-peptide enrichment. <i>Journal of Proteome Research</i> , 2006 , 5, 361-9	5.6	122
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