

Neil L Kelleher

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

382
papers

26,365
citations

83
h-index

147
g-index

452
ext. papers

30,351
ext. citations

9.7
avg, IF

7.13
L-index

#	Paper	IF	Citations
382	The Blood Proteoform Atlas: A reference map of proteoforms in human hematopoietic cells.. <i>Science</i> , 2022 , 375, 411-418	33.3	6
381	Putting Humpty Dumpty Back Together Again: What Does Protein Quantification Mean in Bottom-Up Proteomics?. <i>Journal of Proteome Research</i> , 2022 ,	5.6	3
380	A mixed-valent Fe(II)Fe(III) species converts cysteine to an oxazolone/thioamide pair in methanobactin biosynthesis.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022 , 119, e2123566119	11.5	1
379	ProSight Annotator: Complete control and customization of protein entries in UniProt XML files.. <i>Proteomics</i> , 2022 , e2100209	4.8	1
378	The Human Proteoform Atlas: a FAIR community resource for experimentally derived proteoforms.. <i>Nucleic Acids Research</i> , 2022 , 50, D526-D533	20.1	0
377	Proteomanalyse 2022 , 1013-1063		
376	An efficient cell-free protein synthesis platform for producing proteins with pyrrolysine-based non-canonical amino acids.. <i>Biotechnology Journal</i> , 2022 , e2200096	5.6	1
375	New views of old proteins: clarifying the enigmatic proteome. <i>Molecular and Cellular Proteomics</i> , 2022 , 100254	7.6	0
374	Next-Generation Serology by Mass Spectrometry: Readout of the SARS-CoV-2 Antibody Repertoire. <i>Journal of Proteome Research</i> , 2021 ,	5.6	4
373	Development of novel methods for non-canonical myeloma protein analysis with an innovative adaptation of immunofixation electrophoresis, native top-down mass spectrometry, and middle-down sequencing. <i>Clinical Chemistry and Laboratory Medicine</i> , 2021 , 59, 653-661	5.9	3
372	Spatial mapping of protein composition and tissue organization: a primer for multiplexed antibody-based imaging. <i>Nature Methods</i> , 2021 ,	21.6	6
371	The Human Proteoform Project: Defining the human proteome. <i>Science Advances</i> , 2021 , 7, eabk0734	14.3	19
370	Should LC-MS/MS Be the Reference Measurement Procedure to Determine Protein Concentrations in Human Samples?. <i>Clinical Chemistry</i> , 2021 , 67, 466-471	5.5	0
369	Separation and Characterization of Endogenous Nucleosomes by Native Capillary Zone Electrophoresis-Top-Down Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 5151-5160	7.8	4
368	Deeper Protein Identification Using Field Asymmetric Ion Mobility Spectrometry in Top-Down Proteomics. <i>Analytical Chemistry</i> , 2021 , 93, 6323-6328	7.8	9
367	Remarkable and Unexpected Mechanism for ()-3-Amino-4-(difluoromethylenyl)cyclohex-1-ene-1-carboxylic Acid as a Selective Inactivator of Human Ornithine Aminotransferase. <i>Journal of the American Chemical Society</i> , 2021 , 143, 8193-8207	16.4	3
366	New Interface for Faster Proteoform Analysis: Immunoprecipitation Coupled with SampleStream-Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1659-1670 ²	3.5	2

365	An interpreted atlas of biosynthetic gene clusters from 1,000 fungal genomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	27
364	Turnover and Inactivation Mechanisms for (-)-3-Amino-4,4-difluorocyclopent-1-enecarboxylic Acid, a Selective Mechanism-Based Inactivator of Human Ornithine Aminotransferase. <i>Journal of the American Chemical Society</i> , 2021 , 143, 8689-8703	16.4	4
363	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021 , 18, 604-617	21.6	60
362	Oncogenic KRAS creates an aspartate metabolism signature in colorectal cancer cells. <i>FEBS Journal</i> , 2021 , 288, 6683-6699	5.7	2
361	Reassembling protein complexes after controlled disassembly by top-down mass spectrometry in native mode. <i>International Journal of Mass Spectrometry</i> , 2021 , 465,	1.9	2
360	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021 , 589, 299-305	50.4	56
359	Isotopic Resolution of Protein Complexes up to 466 kDa Using Individual Ion Mass Spectrometry. <i>Analytical Chemistry</i> , 2021 , 93, 2723-2727	7.8	10
358	Standard procedures for native CZE-MS of proteins and protein complexes up to 800kDa. <i>Electrophoresis</i> , 2021 , 42, 1050-1059	3.6	9
357	Metabolomics and genomics in natural products research: complementary tools for targeting new chemical entities. <i>Natural Product Reports</i> , 2021 , 38, 2041-2065	15.1	5
356	-Constructed Ribosomes Enable Multi-site Incorporation of Noncanonical Amino Acids into Proteins. <i>Biochemistry</i> , 2021 , 60, 161-169	3.2	2
355	Precise Characterization of KRAS4B Proteoforms by Combining Immunoprecipitation with Top-Down Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021 , 2262, 47-64	1.4	0
354	Decoding the protein composition of whole nucleosomes with Nuc-MS. <i>Nature Methods</i> , 2021 , 18, 303-308	8.6	13
353	A community resource for paired genomic and metabolomic data mining. <i>Nature Chemical Biology</i> , 2021 , 17, 363-368	11.7	32
352	Elevated N-Linked Glycosylation of IgG V Regions in Myasthenia Gravis Disease Subtypes. <i>Journal of Immunology</i> , 2021 , 207, 2005-2014	5.3	1
351	Spectrum of Apolipoprotein AI and Apolipoprotein AII Proteoforms and Their Associations With Indices of Cardiometabolic Health: The CARDIA Study. <i>Journal of the American Heart Association</i> , 2021 , 10, e019890	6	1
350	Characterization of a Copper-Chelating Natural Product from the Methanotroph sp. LW3. <i>Biochemistry</i> , 2021 , 60, 2845-2850	3.2	1
349	SPT5 stabilization of promoter-proximal RNA polymerase II. <i>Molecular Cell</i> , 2021 , 81, 4413-4424.e5	17.6	4
348	Genome Mining and Metabolomics Uncover a Rare d-Capreomycinide Containing Natural Product and Its Biosynthetic Gene Cluster. <i>ACS Chemical Biology</i> , 2020 , 15, 3013-3020	4.9	3

347	Mutant EZH2 Induces a Pre-malignant Lymphoma Niche by Reprogramming the Immune Response. <i>Cancer Cell</i> , 2020 , 37, 655-673.e11	24.3	47
346	The serine hydroxymethyltransferase-2 (SHMT2) initiates lymphoma development through epigenetic tumor suppressor silencing. <i>Nature Cancer</i> , 2020 , 1, 653-664	15.4	11
345	Individual Ion Mass Spectrometry Enhances the Sensitivity and Sequence Coverage of Top-Down Mass Spectrometry. <i>Journal of Proteome Research</i> , 2020 , 19, 1346-1350	5.6	15
344	Voltage Rollercoaster Filtering of Low-Mass Contaminants During Native Protein Analysis. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 763-767	3.5	3
343	NMT1 and NMT2 are lysine myristoyltransferases regulating the ARF6 GTPase cycle. <i>Nature Communications</i> , 2020 , 11, 1067	17.4	28
342	A Remarkable Difference That One Fluorine Atom Confers on the Mechanisms of Inactivation of Human Ornithine Aminotransferase by Two Cyclohexene Analogues of β -Aminobutyric Acid. <i>Journal of the American Chemical Society</i> , 2020 , 142, 4892-4903	16.4	12
341	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. <i>Nature Methods</i> , 2020 , 17, 391-394	21.6	50
340	Thorough Performance Evaluation of 213 nm Ultraviolet Photodissociation for Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 405-420	7.6	18
339	Elucidating Proteoform Dynamics Underlying the Senescence Associated Secretory Phenotype. <i>Journal of Proteome Research</i> , 2020 , 19, 938-948	5.6	1
338	Native vs Denatured: An in Depth Investigation of Charge State and Isotope Distributions. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 574-581	3.5	14
337	A MUC16 IgG Binding Activity Selects for a Restricted Subset of IgG Enriched for Certain Simian Immunodeficiency Virus Epitope Specificities. <i>Journal of Virology</i> , 2020 , 94,	6.6	2
336	Targeted detection and quantitation of histone modifications from 1,000 cells. <i>PLoS ONE</i> , 2020 , 15, e0240829	3.7	0
335	Mechanism-Based Design of 3-Amino-4-Halocyclopentenecarboxylic Acids as Inactivators of GABA Aminotransferase. <i>ACS Medicinal Chemistry Letters</i> , 2020 , 11, 1949-1955	4.3	4
334	Using 10,000 Fragment Ions to Inform Scoring in Native Top-down Proteomics. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1398-1409	3.5	7
333	Novel Interface for High-Throughput Analysis of Biotherapeutics by Electrospray Mass Spectrometry. <i>Analytical Chemistry</i> , 2020 , 92, 2186-2193	7.8	10
332	Discovery of the Biosynthetic Machinery for Stravidins, Biotin Antimetabolites. <i>ACS Chemical Biology</i> , 2020 , 15, 1134-1140	4.9	2
331	A computational framework to explore large-scale biosynthetic diversity. <i>Nature Chemical Biology</i> , 2020 , 16, 60-68	11.7	211
330	In the fungus where it happens: History and future propelling <i>Aspergillus nidulans</i> as the archetype of natural products research. <i>Fungal Genetics and Biology</i> , 2020 , 144, 103477	3.9	28

329	Streptomyces buecheriae sp. nov., an actinomycete isolated from multiple bat species. <i>Antonie Van Leeuwenhoek</i> , 2020 , 113, 2213-2221	2.1	3
328	Histone tail analysis reveals H3K36me2 and H4K16ac as epigenetic signatures of diffuse intrinsic pontine glioma. <i>Journal of Experimental and Clinical Cancer Research</i> , 2020 , 39, 261	12.8	8
327	Interlaboratory Study for Characterizing Monoclonal Antibodies by Top-Down and Middle-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 1783-1802	3.5	32
326	Heterologous Expression of the Unusual Terreazepine Biosynthetic Gene Cluster Reveals a Promising Approach for Identifying New Chemical Scaffolds. <i>MBio</i> , 2020 , 11,	7.8	6
325	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
324	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
323	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
322	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
321	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
320	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
319	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
318	Targeted detection and quantitation of histone modifications from 1,000 cells 2020 , 15, e0240829		
317	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
316	STORI Plots Enable Accurate Tracking of Individual Ion Signals. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2200-2203	3.5	14
315	Multidimensional Top-Down Proteomics of Brain-Region-Specific Mouse Brain Proteoforms Responsive to Cocaine and Estradiol. <i>Journal of Proteome Research</i> , 2019 , 18, 3999-4012	5.6	5
314	Back Cover: Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, 1970085	4.8	7
313	Native top-down mass spectrometry provides insights into the copper centers of membrane-bound methane monooxygenase. <i>Nature Communications</i> , 2019 , 10, 2675	17.4	45
312	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137

311	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e18003614.8	77
310	Standard Proteoforms and Their Complexes for Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 1190-1198	3.5 20
309	Precision Targeting with EZH2 and HDAC Inhibitors in Epigenetically Dysregulated Lymphomas. <i>Clinical Cancer Research</i> , 2019 , 25, 5271-5283	12.9 38
308	Coupling Fluorescence-Activated Cell Sorting and Targeted Analysis of Histone Modification Profiles in Primary Human Leukocytes. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 2526-2534	3.5 5
307	Mo-, V-, and Fe-Nitrogenases Use a Universal Eight-Electron Reductive-Elimination Mechanism To Achieve N Reduction. <i>Biochemistry</i> , 2019 , 58, 3293-3301	3.2 59
306	A Mutation in Histone H2B Represents a New Class of Oncogenic Driver. <i>Cancer Discovery</i> , 2019 , 9, 1438-1451	14.1 30
305	Mechanism of Inactivation of Ornithine Aminotransferase by (1,3)-3-Amino-4-(hexafluoropropan-2-ylidene)cyclopentane-1-carboxylic Acid. <i>Journal of the American Chemical Society</i> , 2019 , 141, 10711-10721	16.4 9
304	Defining the NSD2 interactome: PARP1 PARylation reduces NSD2 histone methyltransferase activity and impedes chromatin binding. <i>Journal of Biological Chemistry</i> , 2019 , 294, 12459-12471	5.4 9
303	Direct measurement of light and heavy antibody chains using ion mobility and middle-down mass spectrometry. <i>MABs</i> , 2019 , 11, 1351-1357	6.6 11
302	A Highly Productive, One-Pot Cell-Free Protein Synthesis Platform Based on Genomically Recoded <i>Escherichia coli</i> . <i>Cell Chemical Biology</i> , 2019 , 26, 1743-1754.e9	8.2 33
301	Chromatin occupancy and epigenetic analysis reveal new insights into the function of the GATA1 N terminus in erythropoiesis. <i>Blood</i> , 2019 , 134, 1619-1631	2.2 22
300	Proton Transfer Charge Reduction Enables High-Throughput Top-Down Analysis of Large Proteoforms. <i>Analytical Chemistry</i> , 2019 , 91, 15732-15739	7.8 20
299	An activating mutation of the NSD2 histone methyltransferase drives oncogenic reprogramming in acute lymphocytic leukemia. <i>Oncogene</i> , 2019 , 38, 671-686	9.2 23
298	USP7 Cooperates with NOTCH1 to Drive the Oncogenic Transcriptional Program in T-Cell Leukemia. <i>Clinical Cancer Research</i> , 2019 , 25, 222-239	12.9 46
297	A novel crosslinking protocol stabilizes amyloid β oligomers capable of inducing Alzheimer's-associated pathologies. <i>Journal of Neurochemistry</i> , 2019 , 148, 822-836	6 11
296	Accurate Estimation of Context-Dependent False Discovery Rates in Top-Down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 796-805	7.6 17
295	Measurement of Individual Ions Sharply Increases the Resolution of Orbitrap Mass Spectra of Proteins. <i>Analytical Chemistry</i> , 2019 , 91, 2776-2783	7.8 28
294	A comprehensive pipeline for translational top-down proteomics from a single blood draw. <i>Nature Protocols</i> , 2019 , 14, 119-152	18.8 36

293	Discovery of the Tyrobetaine Natural Products and Their Biosynthetic Gene Cluster via Metabologenomics. <i>ACS Chemical Biology</i> , 2018 , 13, 1029-1037	4.9	25
292	Proteoforms as the next proteomics currency. <i>Science</i> , 2018 , 359, 1106-1107	33.3	101
291	Top-Down Proteomics Enables Comparative Analysis of Brain Proteoforms Between Mouse Strains. <i>Analytical Chemistry</i> , 2018 , 90, 3802-3810	7.8	15
290	EGlucocerebrosidase Modulators Promote Dimerization of EGlucocerebrosidase and Reveal an Allosteric Binding Site. <i>Journal of the American Chemical Society</i> , 2018 , 140, 5914-5924	16.4	20
289	Repurposed HisC Aminotransferases Complete the Biosynthesis of Some Methanobactins. <i>Biochemistry</i> , 2018 , 57, 3515-3523	3.2	11
288	Precise characterization of KRAS4b proteoforms in human colorectal cells and tumors reveals mutation/modification cross-talk. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, 4140-4145	11.5	47
287	Identification of the First Diketomorpholine Biosynthetic Pathway Using FAC-MS Technology. <i>ACS Chemical Biology</i> , 2018 , 13, 1142-1147	4.9	21
286	A Targeted, Differential Top-Down Proteomic Methodology for Comparison of ApoA-I Proteoforms in Individuals with High and Low HDL Efflux Capacity. <i>Journal of Proteome Research</i> , 2018 , 17, 2156-2164	5.6	15
285	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
284	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
283	Mechanism of N Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of H. <i>Biochemistry</i> , 2018 , 57, 701-710	3.2	47
282	Total Synthesis of Tambromycin Enabled by Indole C-H Functionalization. <i>Organic Letters</i> , 2018 , 20, 2369-2373	6.2	20
281	The biosynthesis of methanobactin. <i>Science</i> , 2018 , 359, 1411-1416	33.3	68
280	Cell-free protein synthesis from genomically recoded bacteria enables multisite incorporation of noncanonical amino acids. <i>Nature Communications</i> , 2018 , 9, 1203	17.4	110
279	Interrogation of Benzomalvin Biosynthesis Using Fungal Artificial Chromosomes with Metabolomic Scoring (FAC-MS): Discovery of a Benzodiazepine Synthase Activity. <i>Biochemistry</i> , 2018 , 57, 3237-3243	3.2	15
278	The Value of Activated Ion Electron Transfer Dissociation for High-Throughput Top-Down Characterization of Intact Proteins. <i>Analytical Chemistry</i> , 2018 , 90, 8553-8560	7.8	24
277	Accurate Sequence Analysis of a Monoclonal Antibody by Top-Down and Middle-Down Orbitrap Mass Spectrometry Applying Multiple Ion Activation Techniques. <i>Analytical Chemistry</i> , 2018 , 90, 8421-8429	7.8	61
276	Natural products from thioester reductase containing biosynthetic pathways. <i>Natural Product Reports</i> , 2018 , 35, 847-878	15.1	33

275	Development of First-in-Class Histone Acetyltransferase (HAT) Activators for Precision Targeting of Epigenetic Derangements in Lymphoma. <i>Blood</i> , 2018 , 132, 37-37	2.2	1
274	Coupling Fluorescence-Activated Cell Sorting and Targeted LC-MS/MS for Epi-Proteomic Analysis of Normal Leukocytes. <i>FASEB Journal</i> , 2018 , 32, lb96	0.9	
273	Global Chromatin Occupancy and Epigenetic Signature Analysis Reveal New Insights into the Function of GATA1 N-Terminus in Erythropoiesis. <i>Blood</i> , 2018 , 132, 533-533	2.2	1
272	Mutant-IDH1-dependent chromatin state reprogramming, reversibility, and persistence. <i>Nature Genetics</i> , 2018 , 50, 62-72	36.3	86
271	Top-down characterization of endogenous protein complexes with native proteomics. <i>Nature Chemical Biology</i> , 2018 , 14, 36-41	11.7	82
270	Characterization of a long overlooked copper protein from methane- and ammonia-oxidizing bacteria. <i>Nature Communications</i> , 2018 , 9, 4276	17.4	30
269	Stability of histone post-translational modifications in samples derived from liver tissue and primary hepatic cells. <i>PLoS ONE</i> , 2018 , 13, e0203351	3.7	3
268	The unique biomineralization transcriptome and proteome of <i>Lytechinus variegatus</i> teeth. <i>Connective Tissue Research</i> , 2018 , 59, 20-29	3.3	2
267	Estimating the Distribution of Protein Post-Translational Modification States by Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018 , 17, 2727-2734	5.6	15
266	Expansion for the <i>Brachylophosaurus canadensis</i> Collagen I Sequence and Additional Evidence of the Preservation of Cretaceous Protein. <i>Journal of Proteome Research</i> , 2017 , 16, 920-932	5.6	52
265	Chromatographic efficiency and selectivity in top-down proteomics of histones. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017 , 1044-1045, 47-53	3.2	4
264	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017 , 23, 493-500	50.5	225
263	Characterizing the Structure and Oligomerization of Major Royal Jelly Protein 1 (MRJP1) by Mass Spectrometry and Complementary Biophysical Tools. <i>Biochemistry</i> , 2017 , 56, 1645-1655	3.2	21
262	Substrate Trapping in the Siderophore Tailoring Enzyme PvdQ. <i>ACS Chemical Biology</i> , 2017 , 12, 643-647	4.9	4
261	High-Throughput Analysis of Intact Human Proteins Using UVPD and HCD on an Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017 , 16, 2072-2079	5.6	57
260	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017 , 13, 895-901	11.7	108
259	Defining Gas-Phase Fragmentation Propensities of Intact Proteins During Native Top-Down Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1203-1215	3.5	33
258	Modulation of Protein Fragmentation Through Carbamylation of Primary Amines. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 1587-1599	3.5	15

257	Translation system engineering in Escherichia coli enhances non-canonical amino acid incorporation into proteins. <i>Biotechnology and Bioengineering</i> , 2017 , 114, 1074-1086	4.9	37
256	A cryptic Tudor domain links BRWD2/PHIP to COMPASS-mediated histone H3K4 methylation. <i>Genes and Development</i> , 2017 , 31, 2003-2014	12.6	29
255	Histone H3K4 monomethylation catalyzed by Trr and mammalian COMPASS-like proteins at enhancers is dispensable for development and viability. <i>Nature Genetics</i> , 2017 , 49, 1647-1653	36.3	97
254	UTX/KDM6A Loss Enhances the Malignant Phenotype of Multiple Myeloma and Sensitizes Cells to EZH2 inhibition. <i>Cell Reports</i> , 2017 , 21, 628-640	10.6	70
253	Native Electron Capture Dissociation Maps to Iron-Binding Channels in Horse Spleen Ferritin. <i>Analytical Chemistry</i> , 2017 , 89, 10711-10716	7.8	9
252	Selective Targeting by a Mechanism-Based Inactivator against Pyridoxal 5-Phosphate-Dependent Enzymes: Mechanisms of Inactivation and Alternative Turnover. <i>Biochemistry</i> , 2017 , 56, 4951-4961	3.2	12
251	Diversity of Amyloid-beta Proteoforms in the Alzheimer's Disease Brain. <i>Scientific Reports</i> , 2017 , 7, 9520	4.9	84
250	Colibactin assembly line enzymes use S-adenosylmethionine to build a cyclopropane ring. <i>Nature Chemical Biology</i> , 2017 , 13, 1063-1065	11.7	40
249	Cell Surface Proteomics of N-Linked Glycoproteins for Typing of Human Lymphocytes. <i>Proteomics</i> , 2017 , 17, 1700156	4.8	8
248	Identification and Characterization of Human Proteoforms by Top-Down LC-21 Tesla FT-ICR Mass Spectrometry. <i>Journal of Proteome Research</i> , 2017 , 16, 1087-1096	5.6	66
247	Advancing Top-down Analysis of the Human Proteome Using a Benchtop Quadrupole-Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2017 , 16, 609-618	5.6	58
246	In Vitro Reconstruction of Nonribosomal Peptide Biosynthesis Directly from DNA Using Cell-Free Protein Synthesis. <i>ACS Synthetic Biology</i> , 2017 , 6, 39-44	5.7	62
245	A synthetic biology approach to probing nucleosome symmetry. <i>ELife</i> , 2017 , 6,	8.9	10
244	Bioinformatics Analysis of Top-Down Mass Spectrometry Data with ProSight Lite. <i>Methods in Molecular Biology</i> , 2017 , 1558, 381-394	1.4	20
243	High-Throughput Natural Products Discovery in Fungi Using FAC-MS Technology. <i>FASEB Journal</i> , 2017 , 31, 766.6	0.9	
242	Unabridged Analysis of Human Histone H3 by Differential Top-Down Mass Spectrometry Reveals Hypermethylated Proteoforms from MMSET/NSD2 Overexpression. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 776-90	7.6	49
241	A researcher's guide to mass spectrometry-based proteomics. <i>Proteomics</i> , 2016 , 16, 2435-43	4.8	20
240	Characterization of Methanobactin from Methylosinus sp. LW4. <i>Journal of the American Chemical Society</i> , 2016 , 138, 11124-7	16.4	27

239	Epiproteomics: quantitative analysis of histone marks and codes by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2016 , 33, 142-50	9.7	49
238	Elucidating the Rimosamide-Detoxin Natural Product Families and Their Biosynthesis Using Metabolite/Gene Cluster Correlations. <i>ACS Chemical Biology</i> , 2016 , 11, 3452-3460	4.9	29
237	CN-GELFrEE - Clear Native Gel-eluted Liquid Fraction Entrapment Electrophoresis. <i>Journal of Visualized Experiments</i> , 2016 , 53597	1.6	8
236	Reply to "Uveal melanoma cells are resistant to EZH2 inhibition regardless of BAP1 status". <i>Nature Medicine</i> , 2016 , 22, 578-9	50.5	7
235	Progress in Top-Down Proteomics and the Analysis of Proteoforms. <i>Annual Review of Analytical Chemistry</i> , 2016 , 9, 499-519	12.5	322
234	New Aspercryptins, Lipopeptide Natural Products, Revealed by HDAC Inhibition in <i>Aspergillus nidulans</i> . <i>ACS Chemical Biology</i> , 2016 , 11, 2117-23	4.9	31
233	Mapping Proteoforms and Protein Complexes From King Cobra Venom Using Both Denaturing and Native Top-down Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 2423-34	7.6	49
232	An informatic framework for decoding protein complexes by top-down mass spectrometry. <i>Nature Methods</i> , 2016 , 13, 237-40	21.6	48
231	Metabologenomics: Correlation of Microbial Gene Clusters with Metabolites Drives Discovery of a Nonribosomal Peptide with an Unusual Amino Acid Monomer. <i>ACS Central Science</i> , 2016 , 2, 99-108	16.8	73
230	Systems Proteomics View of the Endogenous Human Claudin Protein Family. <i>Journal of Proteome Research</i> , 2016 , 15, 339-59	5.6	17
229	Quantitation and Identification of Thousands of Human Proteoforms below 30 kDa. <i>Journal of Proteome Research</i> , 2016 , 15, 976-82	5.6	73
228	Antigen clasping by two antigen-binding sites of an exceptionally specific antibody for histone methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 2092-7	11.5	30
227	Enhanced binding of antibodies generated during chronic HIV infection to mucus component MUC16. <i>Mucosal Immunology</i> , 2016 , 9, 1549-1558	9.2	41
226	Targeted analysis of recombinant NF kappa B (RelA/p65) by denaturing and native top down mass spectrometry. <i>Journal of Proteomics</i> , 2016 , 134, 76-84	3.9	9
225	Integrated Bottom-Up and Top-Down Proteomics of Patient-Derived Breast Tumor Xenografts. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 45-56	7.6	53
224	Bone protein "extractomics": comparing the efficiency of bone protein extractions of in tandem mass spectrometry, with an eye towards paleoproteomics. <i>PeerJ</i> , 2016 , 4, e2603	3.1	29
223	Screening for Expressed Nonribosomal Peptide Synthetases and Polyketide Synthases Using LC-MS/MS-Based Proteomics. <i>Methods in Molecular Biology</i> , 2016 , 1401, 135-47	1.4	5
222	A Method for Label-Free, Differential Top-Down Proteomics. <i>Methods in Molecular Biology</i> , 2016 , 1410, 121-33	1.4	24

221	Therapeutic Targeting of the Histone Ubiquitination-Methylation Axis in T Cell Leukemia. <i>Blood</i> , 2016 , 128, 1532-1532	2.2	
220	Modern mass spectrometry for synthetic biology and structure-based discovery of natural products. <i>Natural Product Reports</i> , 2016 , 33, 942-50	15.1	39
219	Comparative top down proteomics of peripheral blood mononuclear cells from kidney transplant recipients with normal kidney biopsies or acute rejection. <i>Proteomics</i> , 2016 , 16, 2048-58	4.8	16
218	The Search Engine for Multi-Proteoform Complexes: An Online Tool for the Identification and Stoichiometry Determination of Protein Complexes. <i>Current Protocols in Bioinformatics</i> , 2016 , 56, 13.30.1-13.30.5	24.3	11
217	Mass Spectrometry Imaging and Identification of Peptides Associated with Cephalic Ganglia Regeneration in <i>Schmidtea mediterranea</i> . <i>Journal of Biological Chemistry</i> , 2016 , 291, 8109-20	5.4	16
216	Illuminating the dark matter of shotgun proteomics. <i>Nature Biotechnology</i> , 2015 , 33, 717-8	44.5	25
215	Reducing protein oxidation in low-flow electrospray enables deeper investigation of proteoforms by top down proteomics. <i>EuPA Open Proteomics</i> , 2015 , 8, 40-47	0.1	6
214	Mechanism of Inactivation of Neuronal Nitric Oxide Synthase by (S)-2-Amino-5-(2-(methylthio)acetimidamido)pentanoic Acid. <i>Journal of the American Chemical Society</i> , 2015 , 137, 5980-9	16.4	4
213	Analyzing internal fragmentation of electrosprayed ubiquitin ions during beam-type collisional dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2015 , 26, 782-7	3.5	31
212	Improving cell-free protein synthesis through genome engineering of <i>Escherichia coli</i> lacking release factor 1. <i>ChemBioChem</i> , 2015 , 16, 844-53	3.8	68
211	Design and mechanism of tetrahydrothiophene-based α -aminobutyric acid aminotransferase inactivators. <i>Journal of the American Chemical Society</i> , 2015 , 137, 4525-33	16.4	14
210	Large-scale metabolomics reveals a complex response of <i>Aspergillus nidulans</i> to epigenetic perturbation. <i>ACS Chemical Biology</i> , 2015 , 10, 1535-41	4.9	63
209	Online matrix removal platform for coupling gel-based separations to whole protein electrospray ionization mass spectrometry. <i>Journal of Proteome Research</i> , 2015 , 14, 2199-206	5.6	14
208	Defining the Neuropeptidome of the Spiny Lobster <i>Panulirus interruptus</i> Brain Using a Multidimensional Mass Spectrometry-Based Platform. <i>Journal of Proteome Research</i> , 2015 , 14, 4776-91	5.6	21
207	Fungal artificial chromosomes for mining of the fungal secondary metabolome. <i>BMC Genomics</i> , 2015 , 16, 343	4.5	51
206	Top Down Proteomics Reveals Mature Proteoforms Expressed in Subcellular Fractions of the <i>Echinococcus granulosus</i> Preadult Stage. <i>Journal of Proteome Research</i> , 2015 , 14, 4805-14	5.6	13
205	Loss of BAP1 function leads to EZH2-dependent transformation. <i>Nature Medicine</i> , 2015 , 21, 1344-9	50.5	231
204	Mechanism of Inactivation of GABA Aminotransferase by (E)- and (Z)-(1S,3S)-3-Amino-4-fluoromethylenyl-1-cyclopentanoic Acid. <i>ACS Chemical Biology</i> , 2015 , 10, 2087-98	4.9	8

203	Mass Spectrometry and Antibody-Based Characterization of Blood Vessels from <i>Brachylophosaurus canadensis</i> . <i>Journal of Proteome Research</i> , 2015 , 14, 5252-62	5.6	44
202	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015 , 15, 1235-1238	4.8	145
201	ProSight Lite: graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015 , 15, 1235-8	4.8	100
200	Evolution of translation machinery in recoded bacteria enables multi-site incorporation of nonstandard amino acids. <i>Nature Biotechnology</i> , 2015 , 33, 1272-1279	44.5	172
199	Probing Asymmetric Charge Partitioning of Protein Oligomers during Tandem Mass Spectrometry. <i>International Journal of Mass Spectrometry</i> , 2015 , 390, 132-136	1.9	6
198	Redox metabolites signal polymicrobial biofilm development via the NapA oxidative stress cascade in <i>Aspergillus</i> . <i>Current Biology</i> , 2015 , 25, 29-37	6.3	48
197	Tunable loading of oligonucleotides with secondary structure on gold nanoparticles through a pH-driven method. <i>Bioconjugate Chemistry</i> , 2015 , 26, 279-85	6.3	21
196	Native GELFrEE: a new separation technique for biomolecular assemblies. <i>Analytical Chemistry</i> , 2015 , 87, 3032-8	7.8	30
195	Mechanism of inactivation of β -aminobutyric acid aminotransferase by (1S,3S)-3-amino-4-difluoromethylene-1-cyclopentanoic acid (CPP-115). <i>Journal of the American Chemical Society</i> , 2015 , 137, 2628-40	16.4	23
194	Allele-Specific Crispr Targeting Reveals Epigenetic and Phenotypic Effects of a MMSET Gain of Function Mutation Found in Relapsed Acute Lymphoblastic Leukemia. <i>Blood</i> , 2015 , 126, 437-437	2.2	
193	BAP1 Loss Results in EZH2-Dependent Transformation in Myelodysplastic Syndromes. <i>Blood</i> , 2015 , 126, 713-713	2.2	
192	Top Down proteomics: facts and perspectives. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 683-93	3.4	317
191	The first pilot project of the consortium for top-down proteomics: a status report. <i>Proteomics</i> , 2014 , 14, 1130-40	4.8	73
190	Applying label-free quantitation to top down proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 4961-8	7.8	72
189	Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014 , 14, 1158-64	4.8	68
188	The C-score: a Bayesian framework to sharply improve proteoform scoring in high-throughput top down proteomics. <i>Journal of Proteome Research</i> , 2014 , 13, 3231-40	5.6	60
187	Ultraviolet photodissociation for characterization of whole proteins on a chromatographic time scale. <i>Analytical Chemistry</i> , 2014 , 86, 2185-92	7.8	69
186	Fragmentation of integral membrane proteins in the gas phase. <i>Analytical Chemistry</i> , 2014 , 86, 4627-34	7.8	22

185	Autopilot: an online data acquisition control system for the enhanced high-throughput characterization of intact proteins. <i>Analytical Chemistry</i> , 2014 , 86, 1485-92	7.8	29
184	Comparing label-free quantitative peptidomics approaches to characterize diurnal variation of peptides in the rat suprachiasmatic nucleus. <i>Analytical Chemistry</i> , 2014 , 86, 443-52	7.8	34
183	A roadmap for natural product discovery based on large-scale genomics and metabolomics. <i>Nature Chemical Biology</i> , 2014 , 10, 963-8	11.7	343
182	Cell-free protein synthesis from a release factor 1 deficient <i>Escherichia coli</i> activates efficient and multiple site-specific nonstandard amino acid incorporation. <i>ACS Synthetic Biology</i> , 2014 , 3, 398-409	5.7	114
181	Top-down proteomics with mass spectrometry imaging: a pilot study towards discovery of biomarkers for neurodevelopmental disorders. <i>PLoS ONE</i> , 2014 , 9, e92831	3.7	33
180	Histone methyltransferase MMSET/NSD2 alters EZH2 binding and reprograms the myeloma epigenome through global and focal changes in H3K36 and H3K27 methylation. <i>PLoS Genetics</i> , 2014 , 10, e1004566	6	137
179	Site-specific human histone H3 methylation stability: fast K4me3 turnover. <i>Proteomics</i> , 2014 , 14, 2190-9	4.8	20
178	Strain-specific proteogenomics accelerates the discovery of natural products via their biosynthetic pathways. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014 , 41, 451-9	4.2	30
177	Loss of the Histone Demethylase UTX Contributes to Multiple Myeloma and Sensitizes Cells to EZH2 Inhibitors. <i>Blood</i> , 2014 , 124, 611-611	2.2	3
176	Measurement of acetylation turnover at distinct lysines in human histones identifies long-lived acetylation sites. <i>Nature Communications</i> , 2013 , 4, 2203	17.4	76
175	Large-scale top-down proteomics of the human proteome: membrane proteins, mitochondria, and senescence. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3465-73	7.6	118
174	The emergence of top-down proteomics in clinical research. <i>Genome Medicine</i> , 2013 , 5, 53	14.4	74
173	Developing top down proteomics to maximize proteome and sequence coverage from cells and tissues. <i>Current Opinion in Chemical Biology</i> , 2013 , 17, 787-94	9.7	42
172	Discovery of the antibiotic phosacetamycin via a new mass spectrometry-based method for phosphonic acid detection. <i>ACS Chemical Biology</i> , 2013 , 8, 908-13	4.9	23
171	Proteomics guided discovery of flavopeptins: anti-proliferative aldehydes synthesized by a reductase domain-containing non-ribosomal peptide synthetase. <i>Journal of the American Chemical Society</i> , 2013 , 135, 10449-56	16.4	22
170	Complete protein characterization using top-down mass spectrometry and ultraviolet photodissociation. <i>Journal of the American Chemical Society</i> , 2013 , 135, 12646-51	16.4	255
169	Status of mass spectrometry-based proteomics and metabolomics in basic and translational research. <i>Biochemistry</i> , 2013 , 52, 3794-6	3.2	4
168	Top down proteomics of human membrane proteins from enriched mitochondrial fractions. <i>Analytical Chemistry</i> , 2013 , 85, 1880-8	7.8	58

167	Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013 , 10, 186-7	21.6	857
166	Oncogene-induced cellular senescence elicits an anti-Warburg effect. <i>Proteomics</i> , 2013 , 13, 2585-96	4.8	33
165	EZH2 is required for germinal center formation and somatic EZH2 mutations promote lymphoid transformation. <i>Cancer Cell</i> , 2013 , 23, 677-92	24.3	547
164	Quantitative peptidomics for discovery of circadian-related peptides from the rat suprachiasmatic nucleus. <i>Journal of Proteome Research</i> , 2013 , 12, 585-93	5.6	44
163	From protein complexes to subunit backbone fragments: a multi-stage approach to native mass spectrometry. <i>Analytical Chemistry</i> , 2013 , 85, 11163-73	7.8	126
162	Metabolic perturbation of an essential pathway: evaluation of a glycine precursor of coenzyme A. <i>Journal of the American Chemical Society</i> , 2013 , 135, 5962-5	16.4	5
161	Gobichelin A and B: Mixed-Ligand Siderophores Discovered Using Proteomics. <i>MedChemComm</i> , 2013 , 4, 233-238	5	20
160	Comparative peptidomics analysis of neural adaptations in rats repeatedly exposed to amphetamine. <i>Journal of Neurochemistry</i> , 2012 , 123, 276-87	6	22
159	High-definition de novo sequencing of crustacean hyperglycemic hormone (CHH)-family neuropeptides. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1951-64	7.6	28
158	Analysis of intact monoclonal antibody IgG1 by electron transfer dissociation Orbitrap FTMS. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1758-67	7.6	124
157	A cell-based approach to the human proteome project. <i>Journal of the American Society for Mass Spectrometry</i> , 2012 , 23, 1617-24	3.5	37
156	Ion mobility separation of variant histone tails extending to the "middle-down" range. <i>Analytical Chemistry</i> , 2012 , 84, 4271-6	7.8	39
155	Robust analysis of the yeast proteome under 50 kDa by molecular-mass-based fractionation and top-down mass spectrometry. <i>Analytical Chemistry</i> , 2012 , 84, 209-15	7.8	54
154	Separation of variant methylated histone tails by differential ion mobility. <i>Analytical Chemistry</i> , 2012 , 84, 6317-20	7.8	40
153	Nano-LC FTICR tandem mass spectrometry for top-down proteomics: routine baseline unit mass resolution of whole cell lysate proteins up to 72 kDa. <i>Analytical Chemistry</i> , 2012 , 84, 2111-7	7.8	35
152	Interrogation of global active site occupancy of a fungal iterative polyketide synthase reveals strategies for maintaining biosynthetic fidelity. <i>Journal of the American Chemical Society</i> , 2012 , 134, 6865-77	16.4	39
151	A protease for @middle-down@proteomics. <i>Nature Methods</i> , 2012 , 9, 822-4	21.6	95
150	Evaluation of the compact high-field orbitrap for top-down proteomics of human cells. <i>Journal of Proteome Research</i> , 2012 , 11, 4308-14	5.6	75

149	A proteomic survey of nonribosomal peptide and polyketide biosynthesis in actinobacteria. <i>Journal of Proteome Research</i> , 2012 , 11, 85-94	5.6	30
148	Total kinetic analysis reveals how combinatorial methylation patterns are established on lysines 27 and 36 of histone H3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 13549-54	11.5	102
147	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011 , 480, 254-8	5.4	520
146	Nine enzymes are required for assembly of the pacidamycin group of peptidyl nucleoside antibiotics. <i>Journal of the American Chemical Society</i> , 2011 , 133, 5240-3	16.4	85
145	Surveys of non-ribosomal peptide and polyketide assembly lines in fungi and prospects for their analysis in vitro and in vivo. <i>Fungal Genetics and Biology</i> , 2011 , 48, 49-61	3.9	44
144	Structure determination and interception of biosynthetic intermediates for the plantazolicin class of highly discriminating antibiotics. <i>ACS Chemical Biology</i> , 2011 , 6, 1307-13	4.9	71
143	tRNA-dependent peptide bond formation by the transferase PacB in biosynthesis of the pacidamycin group of pentapeptidyl nucleoside antibiotics. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011 , 108, 12249-53	11.5	74
142	The MMSET histone methyl transferase switches global histone methylation and alters gene expression in t(4;14) multiple myeloma cells. <i>Blood</i> , 2011 , 117, 211-20	2.2	257
141	Identification of Phosphorylated Human Peptides by Accurate Mass Measurement Alone. <i>International Journal of Mass Spectrometry</i> , 2011 , 308, 357-361	1.9	5
140	Analysis of intact protein isoforms by mass spectrometry. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25451-8	5.4	83
139	Directed evolution of the nonribosomal peptide synthetase AdmK generates new andrimid derivatives in vivo. <i>Chemistry and Biology</i> , 2011 , 18, 601-7		91
138	Proteomics-based discovery of koranimine, a cyclic imine natural product. <i>Journal of the American Chemical Society</i> , 2011 , 133, 7316-9	16.4	43
137	On the scalability and requirements of whole protein mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 6868-74	7.8	139
136	MMSET Contributes to Multiple Myeloma Oncogenesis Through Induction of Global Epigenetic Changes and Alteration of the DNA Damage Response. <i>Blood</i> , 2011 , 118, 3475-3475	2.2	
135	Endogenous peptide discovery of the rat circadian clock: a focused study of the suprachiasmatic nucleus by ultrahigh performance tandem mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 285-97	7.6	69
134	Kinetics of re-establishing H3K79 methylation marks in global human chromatin. <i>Journal of Biological Chemistry</i> , 2010 , 285, 32778-32786	5.4	52
133	Histone H1 phosphorylation is associated with transcription by RNA polymerases I and II. <i>Journal of Cell Biology</i> , 2010 , 189, 407-15	7.3	72
132	Size-sorting combined with improved nanocapillary liquid chromatography-mass spectrometry for identification of intact proteins up to 80 kDa. <i>Analytical Chemistry</i> , 2010 , 82, 1234-44	7.8	83

131	The nonribosomal peptide synthetase enzyme DdaD tethers N-(β -fumaramoyl-L-2,3-diaminopropionate for Fe(II)/ α -ketoglutarate-dependent epoxidation by DdaC during dapdiamide antibiotic biosynthesis. <i>Journal of the American Chemical Society</i> , 2010 , 132, 15773-81	16.4	33
130	The emerging process of Top Down mass spectrometry for protein analysis: biomarkers, protein-therapeutics, and achieving high throughput. <i>Molecular BioSystems</i> , 2010 , 6, 1532-9		79
129	Mass spectrometry screening reveals peptides modulated differentially in the medial prefrontal cortex of rats with disparate initial sensitivity to cocaine. <i>AAPS Journal</i> , 2010 , 12, 443-54	3.7	23
128	Efficient readout of posttranslational codes on the 50-residue tail of histone H3 by high-resolution MS/MS. <i>Analytical Biochemistry</i> , 2010 , 396, 180-7	3.1	11
127	Deciphering the late biosynthetic steps of antimalarial compound FR-900098. <i>Chemistry and Biology</i> , 2010 , 17, 57-64		27
126	Intact mass detection, interpretation, and visualization to automate Top-Down proteomics on a large scale. <i>Proteomics</i> , 2010 , 10, 3589-97	4.8	44
125	Negative regulation of NF-kappaB action by Set9-mediated lysine methylation of the RelA subunit. <i>EMBO Journal</i> , 2009 , 28, 1055-66	13	159
124	A proteomics approach to discovering natural products and their biosynthetic pathways. <i>Nature Biotechnology</i> , 2009 , 27, 951-6	44.5	113
123	Top-down proteomics reveals novel protein forms expressed in <i>Methanosarcina acetivorans</i> . <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 1743-50	3.5	32
122	A robust two-dimensional separation for top-down tandem mass spectrometry of the low-mass proteome. <i>Journal of the American Society for Mass Spectrometry</i> , 2009 , 20, 2183-91	3.5	81
121	Global histone profiling by LC-FTMS after inhibition and knockdown of deacetylases in human cells. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2009 , 877, 3885-92	3.3	19
120	In vitro biosynthesis of unnatural enterocin and wailupemycin polyketides. <i>Journal of Natural Products</i> , 2009 , 72, 469-72	4.9	36
119	Distributive and directional behavior of lantibiotic synthetases revealed by high-resolution tandem mass spectrometry. <i>Journal of the American Chemical Society</i> , 2009 , 131, 12258-64	16.4	47
118	To cyclize or not to cyclize: catching enzyme evolution in the act. <i>ACS Chemical Biology</i> , 2009 , 4, 495-7	4.9	1
117	Tandem mass spectrometry with ultrahigh mass accuracy clarifies peptide identification by database retrieval. <i>Journal of Proteome Research</i> , 2009 , 8, 374-9	5.6	59
116	Global amine and acid functional group modification of proteins. <i>Analytical Chemistry</i> , 2008 , 80, 713-20	7.8	22
115	"Proteotyping": population proteomics of human leukocytes using top down mass spectrometry. <i>Analytical Chemistry</i> , 2008 , 80, 2857-66	7.8	57
114	Deconstruction of iterative multidomain polyketide synthase function. <i>Science</i> , 2008 , 320, 243-6	33.3	185

113	Interpreting top-down mass spectra using spectral alignment. <i>Analytical Chemistry</i> , 2008 , 80, 2499-505	7.8	65
112	Combinatorial modification of human histone H4 quantitated by two-dimensional liquid chromatography coupled with top down mass spectrometry. <i>Journal of Biological Chemistry</i> , 2008 , 283, 14927-37	5.4	149
111	Gatekeeping versus promiscuity in the early stages of the andrimid biosynthetic assembly line. <i>ACS Chemical Biology</i> , 2008 , 3, 542-54	4.9	33
110	Polyunsaturated fatty-acid-like trans-enoyl reductases utilized in polyketide biosynthesis. <i>Journal of the American Chemical Society</i> , 2008 , 130, 11614-6	16.4	49
109	Neuropeptidomics of the supraoptic rat nucleus. <i>Journal of Proteome Research</i> , 2008 , 7, 4992-5003	5.6	54
108	Tissue-specific expression and post-translational modification of histone H3 variants. <i>Journal of Proteome Research</i> , 2008 , 7, 4225-36	5.6	56
107	Versatile online-offline engine for automated acquisition of high-resolution tandem mass spectra. <i>Analytical Chemistry</i> , 2008 , 80, 8055-63	7.8	26
106	Certain and progressive methylation of histone H4 at lysine 20 during the cell cycle. <i>Molecular and Cellular Biology</i> , 2008 , 28, 468-86	4.8	226
105	Precision proteomics: the case for high resolution and high mass accuracy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 18132-8	11.5	348
104	Mass spectrometry-based discovery of circadian peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 12527-32	11.5	88
103	Preferential dimethylation of histone H4 lysine 20 by Suv4-20. <i>Journal of Biological Chemistry</i> , 2008 , 283, 12085-92	5.4	98
102	A phosphopantetheinylating polyketide synthase producing a linear polyene to initiate enediene antitumor antibiotic biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 1460-5	11.5	80
101	A ketoreductase domain in the PksJ protein of the bacillaene assembly line carries out both alpha- and beta-ketone reduction during chain growth. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 12809-14	11.5	37
100	Accessing natural product biosynthetic processes by mass spectrometry. <i>Current Opinion in Chemical Biology</i> , 2008 , 12, 475-82	9.7	25
99	Cloning, expression, and biochemical characterization of <i>Streptomyces rubellomurinus</i> genes required for biosynthesis of antimalarial compound FR900098. <i>Chemistry and Biology</i> , 2008 , 15, 765-70		70
98	The loading module of mycosubtilin: an adenylation domain with fatty acid selectivity. <i>Journal of the American Chemical Society</i> , 2007 , 129, 6366-7	16.4	59
97	Top-down proteomics on a chromatographic time scale using linear ion trap fourier transform hybrid mass spectrometers. <i>Analytical Chemistry</i> , 2007 , 79, 7984-91	7.8	107
96	A selective chemical probe for coenzyme A-requiring enzymes. <i>Angewandte Chemie - International Edition</i> , 2007 , 46, 7621-4	16.4	41

95	Reassignment of the structure of the antibiotic A53868 reveals an unusual amino dehydrophosphonic acid. <i>Angewandte Chemie - International Edition</i> , 2007 , 46, 9089-92	16.4	32
94	Genome-wide high-throughput mining of natural-product biosynthetic gene clusters by phage display. <i>Chemistry and Biology</i> , 2007 , 14, 303-12		49
93	Incorporation of nonmethyl branches by isoprenoid-like logic: multiple beta-alkylation events in the biosynthesis of myxovirescin A1. <i>Chemistry and Biology</i> , 2007 , 14, 835-46		67
92	Characterization of neurohistone variants and post-translational modifications by electron capture dissociation mass spectrometry. <i>International Journal of Mass Spectrometry</i> , 2007 , 259, 184-196	1.9	38
91	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007 , 3, 480-5	11.7	94
90	Pervasive combinatorial modification of histone H3 in human cells. <i>Nature Methods</i> , 2007 , 4, 487-9	21.6	195
89	Decoding protein modifications using top-down mass spectrometry. <i>Nature Methods</i> , 2007 , 4, 817-21	21.6	392
88	Using ProSight PTM and related tools for targeted protein identification and characterization with high mass accuracy tandem MS data. <i>Current Protocols in Bioinformatics</i> , 2007 , Chapter 13, Unit 13.6	24.2	35
87	ProSight PTM 2.0: improved protein identification and characterization for top down mass spectrometry. <i>Nucleic Acids Research</i> , 2007 , 35, W701-6	20.1	196
86	Mild performic acid oxidation enhances chromatographic and top down mass spectrometric analyses of histones. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1510-26	7.6	47
85	Global assessment of combinatorial post-translational modification of core histones in yeast using contemporary mass spectrometry. LYS4 trimethylation correlates with degree of acetylation on the same H3 tail. <i>Journal of Biological Chemistry</i> , 2007 , 282, 27923-34	5.4	73
84	Characterization of proteomic and metabolomic responses to dietary factors and supplements. <i>Journal of Nutrition</i> , 2007 , 137, 2787-93	4.1	27
83	Investigating nonribosomal peptide and polyketide biosynthesis by direct detection of intermediates on >70 kDa polypeptides by using Fourier-transform mass spectrometry. <i>ChemBioChem</i> , 2006 , 7, 904-7	3.8	19
82	Identification and characterization of homologues of vertebrate beta-thymosin in the marine mollusk <i>Aplysia californica</i> . <i>Journal of Mass Spectrometry</i> , 2006 , 41, 1030-40	2.2	24
81	Nuclear localization of the <i>Saccharomyces cerevisiae</i> ribonucleotide reductase small subunit requires a karyopherin and a WD40 repeat protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 1422-7	11.5	37
80	Kinetic and mass spectrometric analysis of p300 histone acetyltransferase domain autoacetylation. <i>Journal of Biological Chemistry</i> , 2006 , 281, 40292-301	5.4	64
79	Substrate specificity of the adenylation enzyme SgcC1 involved in the biosynthesis of the enediyne antitumor antibiotic C-1027. <i>Journal of Biological Chemistry</i> , 2006 , 281, 29633-40	5.4	27
78	Convergence of isoprene and polyketide biosynthetic machinery: isoprenyl-S-carrier proteins in the pksX pathway of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 8977-82	11.5	144

77	Discovery and in vitro biosynthesis of haloduracin, a two-component lantibiotic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 17243-8	11.5	190
76	Top down mass spectrometry of Molecular and Cellular Proteomics, 2006 , 5, 14-25	7.6	61
75	Comprehensive phosphoprotein analysis of linker histone H1 from <i>Tetrahymena thermophila</i> . <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1593-609	7.6	52
74	Hydroxymalonyl-acyl carrier protein (ACP) and aminomalonyl-ACP are two additional type I polyketide synthase extender units. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 14349-54	11.5	108
73	Protein assembly line components in prodigiosin biosynthesis: characterization of PigA,G,H,I,J. <i>Journal of the American Chemical Society</i> , 2006 , 128, 12600-1	16.4	56
72	Dissecting non-ribosomal and polyketide biosynthetic machineries using electrospray ionization Fourier-Transform mass spectrometry. <i>Natural Product Reports</i> , 2006 , 23, 893-918	15.1	53
71	Facile detection of acyl and peptidyl intermediates on thiotemplate carrier domains via phosphopantetheinyl elimination reactions during tandem mass spectrometry. <i>Biochemistry</i> , 2006 , 45, 12756-66	3.2	132
70	Probing intra- versus interchain kinetic preferences of L-Thr acylation on dimeric VibF with mass spectrometry. <i>Biophysical Journal</i> , 2006 , 91, 2609-19	2.9	4
69	Biosynthesis of pipercolic acid by RapL, a lysine cyclodeaminase encoded in the rapamycin gene cluster. <i>Journal of the American Chemical Society</i> , 2006 , 128, 3838-47	16.4	101
68	Structural characterization of in vitro and in vivo intermediates on the loading module of microcystin synthetase. <i>ACS Chemical Biology</i> , 2006 , 1, 93-102	4.9	42
67	Top-down approaches for measuring expression ratios of intact yeast proteins using Fourier transform mass spectrometry. <i>Analytical Chemistry</i> , 2006 , 78, 686-94	7.8	69
66	The dehydratase activity of lactacin 481 synthetase is highly processive. <i>Journal of the American Chemical Society</i> , 2006 , 128, 1420-1	16.4	28
65	Mass spectrometric characterization of human histone H3: a bird's eye view. <i>Journal of Proteome Research</i> , 2006 , 5, 240-7	5.6	173
64	Quantitative analysis of modified proteins and their positional isomers by tandem mass spectrometry: human histone H4. <i>Analytical Chemistry</i> , 2006 , 78, 4271-80	7.8	205
63	Precise characterization of human histones in the H2A gene family by top down mass spectrometry. <i>Journal of Proteome Research</i> , 2006 , 5, 248-53	5.6	142
62	Gene-specific characterization of human histone H2B by electron capture dissociation. <i>Journal of Proteome Research</i> , 2006 , 5, 233-9	5.6	97
61	The bifunctional glyceryl transferase/phosphatase OzmB belonging to the HAD superfamily that diverts 1,3-bisphosphoglycerate into polyketide biosynthesis. <i>Journal of the American Chemical Society</i> , 2006 , 128, 10386-7	16.4	49
60	A monovalent streptavidin with a single femtomolar biotin binding site. <i>Nature Methods</i> , 2006 , 3, 267-73	21.6	274

59	Heterologous production of fosfomycin and identification of the minimal biosynthetic gene cluster. <i>Chemistry and Biology</i> , 2006 , 13, 1171-82		104
58	Genetically encoded short peptide tag for versatile protein labeling by Sfp phosphopantetheinyl transferase. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 15815-20	11.5	291
57	Characterization of a new tailoring domain in polyketide biogenesis: the amine transferase domain of MycA in the mycosubtilin gene cluster. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14986-7	16.4	52
56	Elucidating the substrate specificity and condensation domain activity of FkBP, the FK520 pipecolate-incorporating enzyme. <i>Biochemistry</i> , 2005 , 44, 5993-6002	3.2	58
55	Monitoring multiple active sites on thiotemplate enzymes in parallel: a molecular movie of yersiniabactin bioassembly. <i>Journal of the American Chemical Society</i> , 2005 , 127, 14984-5	16.4	10
54	Biosynthesis of the beta-amino acid moiety of the enediyne antitumor antibiotic C-1027 featuring beta-amino acyl-S-carrier protein intermediates. <i>Journal of the American Chemical Society</i> , 2005 , 127, 11594-5	16.4	47
53	New and automated MSn approaches for top-down identification of modified proteins. <i>Journal of the American Society for Mass Spectrometry</i> , 2005 , 16, 2027-38	3.5	61
52	Contemporary mass spectrometry for the direct detection of enzyme intermediates. <i>Current Opinion in Chemical Biology</i> , 2005 , 9, 424-30	9.7	19
51	Parallel interrogation of covalent intermediates in the biosynthesis of gramicidin S using high-resolution mass spectrometry. <i>Protein Science</i> , 2005 , 14, 2702-12	6.3	18
50	Lactacin 481 synthetase phosphorylates its substrate during lantibiotic production. <i>Journal of the American Chemical Society</i> , 2005 , 127, 15332-3	16.4	108
49	Detection and localization of protein modifications by high resolution tandem mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2005 , 24, 126-34	11	121
48	Dichlorination of a pyrrolyl-S-carrier protein by FADH ₂ -dependent halogenase PltA during pyoluteorin biosynthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 13843-8	11.5	149
47	Precise and parallel characterization of coding polymorphisms, alternative splicing, and modifications in human proteins by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1002-8	7.6	85
46	Targeted analysis and discovery of posttranslational modifications in proteins from methanogenic archaea by top-down MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004 , 101, 2678-83	11.5	85
45	ProSight PTM: an integrated environment for protein identification and characterization by top-down mass spectrometry. <i>Nucleic Acids Research</i> , 2004 , 32, W340-5	20.1	167
44	Strategies for automating top-down protein analysis with Q-FTICR MS. <i>International Journal of Mass Spectrometry</i> , 2004 , 234, 175-184	1.9	19
43	Construction of a hybrid quadrupole/Fourier transform ion cyclotron resonance mass spectrometer for versatile MS/MS above 10 kDa. <i>Journal of the American Society for Mass Spectrometry</i> , 2004 , 15, 1099-108	3.5	101
42	Mass spectrometric interrogation of thioester-bound intermediates in the initial stages of epothilone biosynthesis. <i>Chemistry and Biology</i> , 2004 , 11, 327-35		38

41	Improved molecular weight-based processing of intact proteins for interrogation by quadrupole-enhanced FT MS/MS. <i>Journal of Proteome Research</i> , 2004 , 3, 801-6	5.6	25
40	Kinetic and regiospecific interrogation of covalent intermediates in the nonribosomal peptide synthesis of yersiniabactin. <i>Journal of the American Chemical Society</i> , 2004 , 126, 13265-75	16.4	27
39	Molecular-level description of proteins from <i>saccharomyces cerevisiae</i> using quadrupole FT hybrid mass spectrometry for top down proteomics. <i>Analytical Chemistry</i> , 2004 , 76, 2852-8	7.8	69
38	Shotgun annotation of histone modifications: a new approach for streamlined characterization of proteins by top down mass spectrometry. <i>Journal of the American Chemical Society</i> , 2004 , 126, 3386-7	16.4	141
37	Lacticin 481: in vitro reconstitution of lantibiotic synthetase activity. <i>Science</i> , 2004 , 303, 679-81	33.3	196
36	Peer Reviewed: Top-Down Proteomics. <i>Analytical Chemistry</i> , 2004 , 76, 196 A-203 A	7.8	445
35	Fourier-transform mass spectrometry for detection of thioester-bound intermediates in unfractionated proteolytic mixtures of 80 and 191 kDa portions of Bacitracin A synthetase. <i>Analytica Chimica Acta</i> , 2003 , 496, 217-224	6.6	8
34	Electron capture dissociation and ¹³ C, ¹⁵ N depletion for deuterium localization in intact proteins after solution-phase exchange. <i>Analytical Chemistry</i> , 2003 , 75, 3263-6	7.8	30
33	Web and database software for identification of intact proteins using "top down" mass spectrometry. <i>Analytical Chemistry</i> , 2003 , 75, 4081-6	7.8	126
32	Facile synthesis of site-specifically acetylated and methylated histone proteins: reagents for evaluation of the histone code hypothesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 12033-8	11.5	104
31	Fourier-transform mass spectrometry for automated fragmentation and identification of 5-20 kDa proteins in mixtures. <i>Electrophoresis</i> , 2002 , 23, 3217-23	3.6	40
30	Processing complex mixtures of intact proteins for direct analysis by mass spectrometry. <i>Analytical Chemistry</i> , 2002 , 74, 2923-9	7.8	161
29	Toward efficient analysis of >70 kDa proteins with 100% sequence coverage. <i>Proteomics</i> , 2001 , 1, 927-33	4.8	53
28	Informatics and multiplexing of intact protein identification in bacteria and the archaea. <i>Nature Biotechnology</i> , 2001 , 19, 952-7	44.5	189
27	From primary structure to function: biological insights from large-molecule mass spectra. <i>Chemistry and Biology</i> , 2000 , 7, R37-45		24
26	Electron capture dissociation for structural characterization of multiply charged protein cations. <i>Analytical Chemistry</i> , 2000 , 72, 563-73	7.8	852
25	Assembly line enzymology by multimodular nonribosomal peptide synthetases: the thioesterase domain of <i>E. coli</i> EntF catalyzes both elongation and cyclolactonization. <i>Chemistry and Biology</i> , 1999 , 6, 385-400		138
24	In vivo processing and antibiotic activity of microcin B17 analogs with varying ring content and altered bisheterocyclic sites. <i>Chemistry and Biology</i> , 1999 , 6, 305-18		49

23	Top Down versus Bottom Up Protein Characterization by Tandem High-Resolution Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1999 , 121, 806-812	16.4	496
22	Localization of labile posttranslational modifications by electron capture dissociation: the case of gamma-carboxyglutamic acid. <i>Analytical Chemistry</i> , 1999 , 71, 4250-3	7.8	346
21	Gaseous Conformational Structures of Cytochrome c. <i>Journal of the American Chemical Society</i> , 1998 , 120, 4732-4740	16.4	247
20	Kinetics and regioselectivity of peptide-to-heterocycle conversions by microcin B17 synthetase. <i>Chemistry and Biology</i> , 1998 , 5, 373-84		36
19	Two-dimensional mass spectrometry of biomolecules at the subfemtomole level. <i>Current Opinion in Chemical Biology</i> , 1998 , 2, 571-8	9.7	36
18	Efficient sequence analysis of the six gene products (7-74 kDa) from the Escherichia coli thiamin biosynthetic operon by tandem high-resolution mass spectrometry. <i>Protein Science</i> , 1998 , 7, 1796-801	6.3	97
17	Overexpression of recombinant proteins with a C-terminal thiocarboxylate: implications for protein semisynthesis and thiamin biosynthesis. <i>Protein Science</i> , 1998 , 7, 1839-42	6.3	46
16	Thiamin biosynthesis in Escherichia coli. Identification of ThiS thiocarboxylate as the immediate sulfur donor in the thiazole formation. <i>Journal of Biological Chemistry</i> , 1998 , 273, 16555-60	5.4	128
15	Regioselectivity and Chemoselectivity Analysis of Oxazole and Thiazole Ring Formation by the Peptide-Heterocyclizing Microcin B17 Synthetase Using High-Resolution MS/MS. <i>Journal of the American Chemical Society</i> , 1998 , 120, 9716-9717	16.4	26
14	Electron Capture Dissociation of Multiply Charged Protein Cations. A Nonergodic Process. <i>Journal of the American Chemical Society</i> , 1998 , 120, 3265-3266	16.4	1658
13	Identification of modification sites in large biomolecules by stable isotope labeling and tandem high resolution mass spectrometry. The active site nucleophile of thiaminase I. <i>Journal of Biological Chemistry</i> , 1997 , 272, 32215-20	5.4	43
12	Unit resolution mass spectra of 112 kDa molecules with 3 Da accuracy. <i>Journal of the American Society for Mass Spectrometry</i> , 1997 , 8, 380-383	3.5	117
11	Mechanistic studies on thiaminase I. Overexpression and identification of the active site nucleophile. <i>Journal of Biological Chemistry</i> , 1996 , 271, 3445-52	5.4	48
10	Accurate base composition of double-strand DNA by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1996 , 7, 1266-9	3.5	29
9	Complete large-molecule high-resolution mass spectra from 50-femtomole microvolume injection. <i>Journal of the American Society for Mass Spectrometry</i> , 1995 , 6, 220-1	3.5	12
8	Thiaminase I (42 kDa) heterogeneity, sequence refinement, and active site location from high-resolution tandem mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 1995 , 6, 981-4	3.5	48
7	Attomole-sensitivity electrospray source for large-molecule mass spectrometry. <i>Analytical Chemistry</i> , 1995 , 67, 3802-5	7.8	197
6	Rapid Sequencing of Oligonucleotides by High-Resolution Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1994 , 116, 4893-4897	16.4	153

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