

Neil L Kelleher

List of Publications by Citations

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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	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
381	Proteoform: a single term describing protein complexity. <i>Nature Methods</i> , 2013 , 10, 186-7	21.6	857
380	Electron capture dissociation for structural characterization of multiply charged protein cations. <i>Analytical Chemistry</i> , 2000 , 72, 563-73	7.8	852
379	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
378	Mapping intact protein isoforms in discovery mode using top-down proteomics. <i>Nature</i> , 2011 , 480, 254-8	30.4	520
377	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
376	Peer Reviewed: Top-Down Proteomics. <i>Analytical Chemistry</i> , 2004 , 76, 196 A-203 A	7.8	445
375	Decoding protein modifications using top-down mass spectrometry. <i>Nature Methods</i> , 2007 , 4, 817-21	21.6	392
374	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
373	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
372	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
371	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
370	Progress in Top-Down Proteomics and the Analysis of Proteoforms. <i>Annual Review of Analytical Chemistry</i> , 2016 , 9, 499-519	12.5	322
369	Top Down proteomics: facts and perspectives. <i>Biochemical and Biophysical Research Communications</i> , 2014 , 445, 683-93	3.4	317
368	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
367	A monovalent streptavidin with a single femtomolar biotin binding site. <i>Nature Methods</i> , 2006 , 3, 267-73	21.6	274
366	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

365	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
364	Gaseous Conformational Structures of Cytochrome c. <i>Journal of the American Chemical Society</i> , 1998 , 120, 4732-4740	16.4	247
363	Loss of BAP1 function leads to EZH2-dependent transformation. <i>Nature Medicine</i> , 2015 , 21, 1344-9	50.5	231
362	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
361	Therapeutic targeting of polycomb and BET bromodomain proteins in diffuse intrinsic pontine gliomas. <i>Nature Medicine</i> , 2017 , 23, 493-500	50.5	225
360	A computational framework to explore large-scale biosynthetic diversity. <i>Nature Chemical Biology</i> , 2020 , 16, 60-68	11.7	211
359	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
358	Attomole-sensitivity electrospray source for large-molecule mass spectrometry. <i>Analytical Chemistry</i> , 1995 , 67, 3802-5	7.8	197
357	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
356	Lacticin 481: in vitro reconstitution of lantibiotic synthetase activity. <i>Science</i> , 2004 , 303, 679-81	33.3	196
355	Pervasive combinatorial modification of histone H3 in human cells. <i>Nature Methods</i> , 2007 , 4, 487-9	21.6	195
354	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
353	Informatics and multiplexing of intact protein identification in bacteria and the archaea. <i>Nature Biotechnology</i> , 2001 , 19, 952-7	44.5	189
352	Deconstruction of iterative multidomain polyketide synthase function. <i>Science</i> , 2008 , 320, 243-6	33.3	185
351	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
350	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
349	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
348	Processing complex mixtures of intact proteins for direct analysis by mass spectrometry. <i>Analytical Chemistry</i> , 2002 , 74, 2923-9	7.8	161

347	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
346	Rapid Sequencing of Oligonucleotides by High-Resolution Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 1994 , 116, 4893-4897	16.4	153
345	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
344	Dichlorination of a pyrrolyl-S-carrier protein by FADH2-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
343	ProSight Lite: Graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015 , 15, 1235-1238	4.8	145
342	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
341	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
340	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
339	On the scalability and requirements of whole protein mass spectrometry. <i>Analytical Chemistry</i> , 2011 , 83, 6868-74	7.8	139
338	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
337	Best practices and benchmarks for intact protein analysis for top-down mass spectrometry. <i>Nature Methods</i> , 2019 , 16, 587-594	21.6	137
336	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
335	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
334	Thiamin biosynthesis in <i>Escherichia coli</i> . 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
333	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
332	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
331	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
330	Detection and localization of protein modifications by high resolution tandem mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2005 , 24, 126-34	11	121

329	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
328	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
327	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
326	A proteomics approach to discovering natural products and their biosynthetic pathways. <i>Nature Biotechnology</i> , 2009 , 27, 951-6	44.5	113
325	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
324	A scalable platform to identify fungal secondary metabolites and their gene clusters. <i>Nature Chemical Biology</i> , 2017 , 13, 895-901	11.7	108
323	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
322	Lactacin 481 synthetase phosphorylates its substrate during lantibiotic production. <i>Journal of the American Chemical Society</i> , 2005 , 127, 15332-3	16.4	108
321	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
320	Heterologous production of fosfomycin and identification of the minimal biosynthetic gene cluster. <i>Chemistry and Biology</i> , 2006 , 13, 1171-82		104
319	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
318	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
317	Proteoforms as the next proteomics currency. <i>Science</i> , 2018 , 359, 1106-1107	33.3	101
316	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
315	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, 1099-1108	3.5	101
314	ProSight Lite: graphical software to analyze top-down mass spectrometry data. <i>Proteomics</i> , 2015 , 15, 1235-8	4.8	100
313	Preferential dimethylation of histone H4 lysine 20 by Suv4-20. <i>Journal of Biological Chemistry</i> , 2008 , 283, 12085-92	5.4	98
312	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

311	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
310	Gene-specific characterization of human histone H2B by electron capture dissociation. <i>Journal of Proteome Research</i> , 2006 , 5, 233-9	5.6	97
309	A protease for @middle-down@proteomics. <i>Nature Methods</i> , 2012 , 9, 822-4	21.6	95
308	Unusual transformations in the biosynthesis of the antibiotic phosphinothricin tripeptide. <i>Nature Chemical Biology</i> , 2007 , 3, 480-5	11.7	94
307	Directed evolution of the nonribosomal peptide synthetase AdmK generates new andrimid derivatives in vivo. <i>Chemistry and Biology</i> , 2011 , 18, 601-7		91
306	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
305	Mutant-IDH1-dependent chromatin state reprogramming, reversibility, and persistence. <i>Nature Genetics</i> , 2018 , 50, 62-72	36.3	86
304	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
303	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
302	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
301	Diversity of Amyloid-beta Proteoforms in the Alzheimer@ Disease Brain. <i>Scientific Reports</i> , 2017 , 7, 95204	4.9	84
300	Analysis of intact protein isoforms by mass spectrometry. <i>Journal of Biological Chemistry</i> , 2011 , 286, 25451-8	5.4	83
299	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
298	Top-down characterization of endogenous protein complexes with native proteomics. <i>Nature Chemical Biology</i> , 2018 , 14, 36-41	11.7	82
297	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
296	A phosphopantetheinylating polyketide synthase producing a linear polyene to initiate enediyne 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
295	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
294	Identification and Quantification of Proteoforms by Mass Spectrometry. <i>Proteomics</i> , 2019 , 19, e180036	14.8	77

293	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
292	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
291	The emergence of top-down proteomics in clinical research. <i>Genome Medicine</i> , 2013 , 5, 53	14.4	74
290	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
289	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
288	Quantitation and Identification of Thousands of Human Proteoforms below 30 kDa. <i>Journal of Proteome Research</i> , 2016 , 15, 976-82	5.6	73
287	The first pilot project of the consortium for top-down proteomics: a status report. <i>Proteomics</i> , 2014 , 14, 1130-40	4.8	73
286	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
285	Applying label-free quantitation to top down proteomics. <i>Analytical Chemistry</i> , 2014 , 86, 4961-8	7.8	72
284	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
283	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
282	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
281	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
280	Ultraviolet photodissociation for characterization of whole proteins on a chromatographic time scale. <i>Analytical Chemistry</i> , 2014 , 86, 2185-92	7.8	69
279	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
278	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
277	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
276	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

275	The biosynthesis of methanobactin. <i>Science</i> , 2018 , 359, 1411-1416	33.3	68
274	Optimizing capillary electrophoresis for top-down proteomics of 30-80 kDa proteins. <i>Proteomics</i> , 2014 , 14, 1158-64	4.8	68
273	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
272	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
271	Interpreting top-down mass spectra using spectral alignment. <i>Analytical Chemistry</i> , 2008 , 80, 2499-505	7.8	65
270	Kinetic and mass spectrometric analysis of p300 histone acetyltransferase domain autoacetylation. <i>Journal of Biological Chemistry</i> , 2006 , 281, 40292-301	5.4	64
269	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
268	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
267	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
266	Top down mass spectrometry of Molecular and Cellular Proteomics, 2006 , 5, 14-25	7.6	61
265	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
264	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
263	The emerging landscape of single-molecule protein sequencing technologies. <i>Nature Methods</i> , 2021 , 18, 604-617	21.6	60
262	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
261	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
260	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
259	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
258	Top down proteomics of human membrane proteins from enriched mitochondrial fractions. <i>Analytical Chemistry</i> , 2013 , 85, 1880-8	7.8	58

257	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
256	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
255	"Proteotyping": population proteomics of human leukocytes using top down mass spectrometry. <i>Analytical Chemistry</i> , 2008 , 80, 2857-66	7.8	57
254	Tissue-specific expression and post-translational modification of histone H3 variants. <i>Journal of Proteome Research</i> , 2008 , 7, 4225-36	5.6	56
253	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
252	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021 , 589, 299-305	50.4	56
251	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
250	Neuropeptidomics of the supraoptic rat nucleus. <i>Journal of Proteome Research</i> , 2008 , 7, 4992-5003	5.6	54
249	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
248	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
247	Toward efficient analysis of >70 kDa proteins with 100% sequence coverage. <i>Proteomics</i> , 2001 , 1, 927-33	4.8	53
246	Expansion for the Brachylophosaurus canadensis 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
245	Kinetics of re-establishing H3K79 methylation marks in global human chromatin. <i>Journal of Biological Chemistry</i> , 2010 , 285, 32778-32786	5.4	52
244	Comprehensive phosphoprotein analysis of linker histone H1 from Tetrahymena thermophila. <i>Molecular and Cellular Proteomics</i> , 2006 , 5, 1593-609	7.6	52
243	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
242	Fungal artificial chromosomes for mining of the fungal secondary metabolome. <i>BMC Genomics</i> , 2015 , 16, 343	4.5	51
241	Multiplexed mass spectrometry of individual ions improves measurement of proteoforms and their complexes. <i>Nature Methods</i> , 2020 , 17, 391-394	21.6	50
240	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

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	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
237	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
236	Genome-wide high-throughput mining of natural-product biosynthetic gene clusters by phage display. <i>Chemistry and Biology</i> , 2007 , 14, 303-12		49
235	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
234	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
233	An informatic framework for decoding protein complexes by top-down mass spectrometry. <i>Nature Methods</i> , 2016 , 13, 237-40	21.6	48
232	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
231	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
230	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
229	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
228	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
227	Mechanism of N Reduction Catalyzed by Fe-Nitrogenase Involves Reductive Elimination of H. <i>Biochemistry</i> , 2018 , 57, 701-710	3.2	47
226	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
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