

# Albert J R Heck

## List of Publications by Year in descending order

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782  
papers

58,607  
citations

1094

112  
h-index

2558

195  
g-index

844  
all docs

844  
docs citations

844  
times ranked

61302  
citing authors

#	ARTICLE	IF	CITATIONS
1	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	9.0	1,353
2	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , 2009, 4, 484-494.	5.5	1,247
3	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , 2011, 476, 293-297.	13.7	1,096
4	Selective Isolation at the Femtomole Level of Phosphopeptides from Proteolytic Digests Using 2D-NanoLC-ESI-MS/MS and Titanium Oxide Precolumns. <i>Analytical Chemistry</i> , 2004, 76, 3935-3943.	3.2	884
5	Tumour suppressor RNF43 is a stem-cell E3 ligase that induces endocytosis of Wnt receptors. <i>Nature</i> , 2012, 488, 665-669.	13.7	791
6	Wnt Signaling through Inhibition of $\beta^2$ -Catenin Degradation in an Intact Axin1 Complex. <i>Cell</i> , 2012, 149, 1245-1256.	13.5	747
7	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694
8	Native mass spectrometry: a bridge between interactomics and structural biology. <i>Nature Methods</i> , 2008, 5, 927-933.	9.0	656
9	Next-generation proteomics: towards an integrative view of proteome dynamics. <i>Nature Reviews Genetics</i> , 2013, 14, 35-48.	7.7	656
10	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent $\beta^4$ cell markers. <i>EMBO Journal</i> , 2012, 31, 3079-3091.	3.5	634
11	Quantitative Phosphoproteomics of Early Elicitor Signaling in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1198-1214.	2.5	614
12	Complement Is Activated by IgG Hexamers Assembled at the Cell Surface. <i>Science</i> , 2014, 343, 1260-1263.	6.0	602
13	Investigation of intact protein complexes by mass spectrometry. <i>Mass Spectrometry Reviews</i> , 2004, 23, 368-389.	2.8	541
14	Identification of CMTM6 and CMTM4 as PD-L1 protein regulators. <i>Nature</i> , 2017, 549, 106-110.	13.7	501
15	Structural basis for CRISPR RNA-guided DNA recognition by Cascade. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 529-536.	3.6	498
16	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019, 16, 595-602.	9.0	452
17	Native Mass Spectrometry: What is in the Name?. <i>Journal of the American Society for Mass Spectrometry</i> , 2017, 28, 5-13.	1.2	437
18	Ion mobility mass spectrometry of proteins and protein assemblies. <i>Chemical Society Reviews</i> , 2010, 39, 1633-1655.	18.7	420

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19	RNA-guided complex from a bacterial immune system enhances target recognition through seed sequence interactions. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 10092-10097.	3.3	413
20	Proteome-wide profiling of protein assemblies by cross-linking mass spectrometry. <i>Nature Methods</i> , 2015, 12, 1179-1184.	9.0	408
21	Efficient biotinylation and single-step purification of tagged transcription factors in mammalian cells and transgenic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 7480-7485.	3.3	400
22	Regulation of retromer recruitment to endosomes by sequential action of Rab5 and Rab7. <i>Journal of Cell Biology</i> , 2008, 183, 513-526.	2.3	395
23	Metabolic labeling of <i>C. elegans</i> and <i>D. melanogaster</i> for quantitative proteomics. <i>Nature Biotechnology</i> , 2003, 21, 927-931.	9.4	391
24	Mass Spectrometry-Based Proteomics and Network Biology. <i>Annual Review of Biochemistry</i> , 2012, 81, 379-405.	5.0	382
25	Toward a Comprehensive Characterization of a Human Cancer Cell Phosphoproteome. <i>Journal of Proteome Research</i> , 2013, 12, 260-271.	1.8	363
26	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2009, 44, 861-878.	0.7	349
27	Severe acute respiratory syndrome coronavirus (SARS-CoV) infection inhibition using spike protein heptad repeat-derived peptides. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 8455-8460.	3.3	348
28	High-sensitivity Orbitrap mass analysis of intact macromolecular assemblies. <i>Nature Methods</i> , 2012, 9, 1084-1086.	9.0	347
29	NF- $\kappa$ B-Independent Role of IKK $\alpha$ /IKK $\beta$ in Preventing RIPK1 Kinase-Dependent Apoptotic and Necroptotic Cell Death during TNF Signaling. <i>Molecular Cell</i> , 2015, 60, 63-76.	4.5	345
30	Sequential Waves of Functionally Related Proteins Are Expressed When B Cells Prepare for Antibody Secretion. <i>Immunity</i> , 2003, 18, 243-253.	6.6	341
31	Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. <i>Nature Protocols</i> , 2016, 11, 993-1006.	5.5	341
32	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , 2013, 8, 461-480.	5.5	340
33	A large fraction of HLA class I ligands are proteasome-generated spliced peptides. <i>Science</i> , 2016, 354, 354-358.	6.0	322
34	Imaging Techniques for the Study of Chemical Reaction Dynamics. <i>Annual Review of Physical Chemistry</i> , 1995, 46, 335-372.	4.8	314
35	Phosphorylation Dynamics during Early Differentiation of Human Embryonic Stem Cells. <i>Cell Stem Cell</i> , 2009, 5, 214-226.	5.2	301
36	Large-Scale Quantitative Assessment of Different In-Solution Protein Digestion Protocols Reveals Superior Cleavage Efficiency of Tandem Lys-C/Trypsin Proteolysis over Trypsin Digestion. <i>Journal of Proteome Research</i> , 2012, 11, 5145-5156.	1.8	298

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37	On Terminal Alkynes That Can React with Active-Site Cysteine Nucleophiles in Proteases. <i>Journal of the American Chemical Society</i> , 2013, 135, 2867-2870.	6.6	290
38	Lipid II Is an Intrinsic Component of the Pore Induced by Nisin in Bacterial Membranes. <i>Journal of Biological Chemistry</i> , 2003, 278, 19898-19903.	1.6	284
39	Improved Peptide Identification by Targeted Fragmentation Using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , 2011, 10, 2377-2388.	1.8	277
40	Native protein mass spectrometry: from intact oligomers to functional machineries. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 519-526.	2.8	274
41	Proteomics beyond trypsin. <i>FEBS Journal</i> , 2015, 282, 2612-2626.	2.2	268
42	RNA Targeting by the Type III-A CRISPR-Cas Csm Complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , 2014, 56, 518-530.	4.5	267
43	GATA-1 forms distinct activating and repressive complexes in erythroid cells. <i>EMBO Journal</i> , 2005, 24, 2354-2366.	3.5	255
44	Lys-N and Trypsin Cover Complementary Parts of the Phosphoproteome in a Refined SCX-Based Approach. <i>Analytical Chemistry</i> , 2009, 81, 4493-4501.	3.2	251
45	A high-quality catalog of the <i>Drosophila melanogaster</i> proteome. <i>Nature Biotechnology</i> , 2007, 25, 576-583.	9.4	247
46	MHC class II-associated proteins in B cell exosomes and potential functional implications for exosome biogenesis. <i>Immunology and Cell Biology</i> , 2010, 88, 851-856.	1.0	247
47	Toward Full Peptide Sequence Coverage by Dual Fragmentation Combining Electron-Transfer and Higher-Energy Collision Dissociation Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2012, 84, 9668-9673.	3.2	246
48	GMP Synthetase Stimulates Histone H2B Deubiquitylation by the Epigenetic Silencer USP7. <i>Molecular Cell</i> , 2005, 17, 695-707.	4.5	241
49	Improving the Performance of a Quadrupole Time-of-Flight Instrument for Macromolecular Mass Spectrometry. <i>Analytical Chemistry</i> , 2006, 78, 7473-7483.	3.2	240
50	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	1.8	237
51	Microtubule Minus-End Stabilization by Polymerization-Driven CAMSAP Deposition. <i>Developmental Cell</i> , 2014, 28, 295-309.	3.1	235
52	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2008, 391, 151-159.	1.9	234
53	Interrogating viral capsid assembly with ion mobility mass spectrometry. <i>Nature Chemistry</i> , 2011, 3, 126-132.	6.6	234
54	The Generating Function of CID, ETD, and CID/ETD Pairs of Tandem Mass Spectra: Applications to Database Search. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2840-2852.	2.5	226

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55	The fluxes through glycolytic enzymes in <i>Saccharomyces cerevisiae</i> are predominantly regulated at posttranscriptional levels. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 15753-15758.	3.3	223
56	Optimized fragmentation schemes and data analysis strategies for proteome-wide cross-link identification. Nature Communications, 2017, 8, 15473.	5.8	223
57	Structure and Activity of the RNA-Targeting Type III-B CRISPR-Cas Complex of <i>Thermus thermophilus</i> . Molecular Cell, 2013, 52, 135-145.	4.5	212
58	Direct Determination of Solution Binding Constants for Noncovalent Complexes between Bacterial Cell Wall Peptide Analogues and Vancomycin Group Antibiotics by Electrospray Ionization Mass Spectrometry. Analytical Chemistry, 1998, 70, 4427-4432.	3.2	210
59	High-resolution mass spectrometry of viral assemblies: Molecular composition and stability of dimorphic hepatitis B virus capsids. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 9216-9220.	3.3	204
60	The diverse and expanding role of mass spectrometry in structural and molecular biology. EMBO Journal, 2016, 35, 2634-2657.	3.5	198
61	The effect of the source pressure on the abundance of ions of noncovalent protein assemblies in an electrospray ionization orthogonal time-of-flight instrument. Rapid Communications in Mass Spectrometry, 2001, 15, 596-601.	0.7	194
62	Nuclear PtdIns5P as a Transducer of Stress Signaling: An In Vivo Role for PIP4Kbeta. Molecular Cell, 2006, 23, 685-695.	4.5	194
63	Triplex protein quantification based on stable isotope labeling by peptide dimethylation applied to cell and tissue lysates. Proteomics, 2008, 8, 4624-4632.	1.3	192
64	Munc13-4 Is an Effector of Rab27a and Controls Secretion of Lysosomes in Hematopoietic Cells. Molecular Biology of the Cell, 2005, 16, 731-741.	0.9	190
65	Expanding the detectable HLA peptide repertoire using electron-transfer/higher-energy collision dissociation (EThcD). Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 4507-4512.	3.3	189
66	Comprehensive Analysis of the Secreted Proteins of the Parasite <i>Haemonchus contortus</i> Reveals Extensive Sequence Variation and Differential Immune Recognition. Journal of Biological Chemistry, 2003, 278, 16941-16951.	1.6	188
67	Genome-wide characterization of the routes to pluripotency. Nature, 2014, 516, 198-206.	13.7	187
68	Evaluation and Optimization of ZIC-HILIC-RP as an Alternative MudPIT Strategy. Journal of Proteome Research, 2007, 6, 937-946.	1.8	182
69	The phosphoproteomics data explosion. Current Opinion in Chemical Biology, 2009, 13, 414-420.	2.8	170
70	The kinase TNIK is an essential activator of Wnt target genes. EMBO Journal, 2009, 28, 3329-3340.	3.5	169
71	Crosstalk between phosphorylation and lysine acetylation in a genome-reduced bacterium. Molecular Systems Biology, 2012, 8, 571.	3.2	169
72	Human Ccr4-Not complexes contain variable deadenylase subunits. Biochemical Journal, 2009, 422, 443-453.	1.7	166

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73	Highly Robust, Automated, and Sensitive Online TiO <sub>2</sub> -Based Phosphoproteomics Applied To Study Endogenous Phosphorylation in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2008, 7, 687-697.	1.8	165
74	Studying 18â€¦MDa Virus Assemblies with Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4020-4023.	7.2	164
75	A large synthetic peptide and phosphopeptide reference library for mass spectrometryâ€‘based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	9.4	164
76	High-Resolution Native Mass Spectrometry. <i>Chemical Reviews</i> , 2022, 122, 7269-7326.	23.0	164
77	Differential Targeting of Two Distinct SWI/SNF-Related <i>Drosophila</i> Chromatin-Remodeling Complexes. <i>Molecular and Cellular Biology</i> , 2004, 24, 3077-3088.	1.1	159
78	Protein acetylation affects acetate metabolism, motility and acid stress response in <i>Escherichia coli</i> . <i>Molecular Systems Biology</i> , 2014, 10, 762.	3.2	159
79	In-depth Qualitative and Quantitative Profiling of Tyrosine Phosphorylation Using a Combination of Phosphopeptide Immunoaffinity Purification and Stable Isotope Dimethyl Labeling. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 84-99.	2.5	155
80	A Novel Platform for the Potentiation of Therapeutic Antibodies Based on Antigen-Dependent Formation of IgG Hexamers at the Cell Surface. <i>PLoS Biology</i> , 2016, 14, e1002344.	2.6	154
81	EGFR Dynamics Change during Activation in Native Membranes as Revealed by NMR. <i>Cell</i> , 2016, 167, 1241-1251.e11.	13.5	153
82	Efficient and robust proteome-wide approaches for cross-linking mass spectrometry. <i>Nature Protocols</i> , 2018, 13, 2964-2990.	5.5	153
83	Mass Spectrometric Analysis of the <i>Schistosoma mansoni</i> Tegumental Sub-proteome. <i>Journal of Proteome Research</i> , 2005, 4, 958-966.	1.8	150
84	Talin-KANK1 interaction controls the recruitment of cortical microtubule stabilizing complexes to focal adhesions. <i>Elife</i> , 2016, 5, .	2.8	150
85	Microtubule minus-end regulation at spindle poles by an ASPMâ€‘katanin complex. <i>Nature Cell Biology</i> , 2017, 19, 480-492.	4.6	147
86	Unambiguous Phosphosite Localization using Electron-Transfer/Higher-Energy Collision Dissociation (EThcD). <i>Journal of Proteome Research</i> , 2013, 12, 1520-1525.	1.8	145
87	High-fidelity mass analysis unveils heterogeneity in intact ribosomal particles. <i>Nature Methods</i> , 2017, 14, 283-286.	9.0	145
88	Homodimeric galectin-7 (p53-induced gene 1) is a negative growth regulator for human neuroblastoma cells. <i>Oncogene</i> , 2003, 22, 6277-6288.	2.6	142
89	The interactome of intact mitochondria by cross-linking mass spectrometry provides evidence for coexisting respiratory supercomplexes. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 216-232.	2.5	142
90	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , 2012, 75, 3791-3813.	1.2	141

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91	Widespread bacterial protein histidine phosphorylation revealed by mass spectrometry-based proteomics. <i>Nature Methods</i> , 2018, 15, 187-190.	9.0	140
92	Chaperonin Complexes Monitored by Ion Mobility Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2009, 131, 1452-1459.	6.6	139
93	Hybrid mass spectrometry approaches in glycoprotein analysis and their usage in scoring biosimilarity. <i>Nature Communications</i> , 2016, 7, 13397.	5.8	139
94	Molecular Basis of Assembly and Activation of Complement Component C1 in Complex with Immunoglobulin G1 and Antigen. <i>Molecular Cell</i> , 2016, 63, 135-145.	4.5	139
95	Revealing promiscuous drug-target interactions by chemical proteomics. <i>Drug Discovery Today</i> , 2009, 14, 1021-1029.	3.2	134
96	Dis3-like 1: a novel exoribonuclease associated with the human exosome. <i>EMBO Journal</i> , 2010, 29, 2358-2367.	3.5	134
97	Trends in ultrasensitive proteomics. <i>Current Opinion in Chemical Biology</i> , 2012, 16, 206-213.	2.8	134
98	Defining the Stoichiometry and Cargo Load of Viral and Bacterial Nanoparticles by Orbitrap Mass Spectrometry. <i>Journal of the American Chemical Society</i> , 2014, 136, 7295-7299.	6.6	134
99	Quantitative Proteomics by Metabolic Labeling of Model Organisms. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 11-24.	2.5	133
100	An experimental correction for arginine-to-proline conversion artifacts in SILAC-based quantitative proteomics. <i>Nature Methods</i> , 2007, 4, 677-678.	9.0	132
101	Elucidating crosstalk mechanisms between phosphorylation and O-GlcNAcylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7255-E7261.	3.3	132
102	Activation of FoxM1 during G <sub>2</sub> Requires Cyclin A/Cdk-Dependent Relief of Autorepression by the FoxM1 N-Terminal Domain. <i>Molecular and Cellular Biology</i> , 2008, 28, 3076-3087.	1.1	131
103	Exploring an Orbitrap Analyzer for the Characterization of Intact Antibodies by Native Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2012, 51, 12992-12996.	7.2	130
104	Zwitterionic Hydrophilic Interaction Liquid Chromatography (ZIC-HILIC and ZIC-cHILIC) Provide High Resolution Separation and Increase Sensitivity in Proteome Analysis. <i>Analytical Chemistry</i> , 2011, 83, 3440-3447.	3.2	128
105	Species-Specific Determinants in the IgG CH3 Domain Enable Fab-Arm Exchange by Affecting the Noncovalent CH3-CH3 Interaction Strength. <i>Journal of Immunology</i> , 2011, 187, 3238-3246.	0.4	128
106	Personalized Proteome Profiles of Healthy and Tumor Human Colon Organoids Reveal Both Individual Diversity and Basic Features of Colorectal Cancer. <i>Cell Reports</i> , 2017, 18, 263-274.	2.9	126
107	Proteome analysis of yeast response to various nutrient limitations. <i>Molecular Systems Biology</i> , 2006, 2, 2006.0026.	3.2	125
108	The quantitative proteomes of human-induced pluripotent stem cells and embryonic stem cells. <i>Molecular Systems Biology</i> , 2011, 7, 550.	3.2	125

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109	Guest Encapsulation and Self-Assembly of Molecular Capsules in Polar Solvents via Multiple Ionic Interactions. <i>Journal of the American Chemical Society</i> , 2002, 124, 6569-6575.	6.6	122
110	Encapsulation of Phthalocyanine Supramolecular Stacks into Virus-like Particles. <i>Journal of the American Chemical Society</i> , 2011, 133, 6878-6881.	6.6	122
111	Serine 25 phosphorylation inhibits RIPK1 kinase-dependent cell death in models of infection and inflammation. <i>Nature Communications</i> , 2019, 10, 1729.	5.8	121
112	Resolving heterogeneous macromolecular assemblies by Orbitrap-based single-particle charge detection mass spectrometry. <i>Nature Methods</i> , 2020, 17, 395-398.	9.0	121
113	Mass-specific selection of ions in Fourier-transform ion cyclotron resonance mass spectrometry. Unintentional off-resonance cyclotron excitation of selected ions. <i>Rapid Communications in Mass Spectrometry</i> , 1991, 5, 406-414.	0.7	120
114	A Quest for Human and Mouse Embryonic Stem Cell-specific Proteins. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1261-1273.	2.5	120
115	RNA Polymerase I Contains a TFIIF-Related DNA-Binding Subcomplex. <i>Molecular Cell</i> , 2010, 39, 583-594.	4.5	120
116	Exploring the membrane proteome—Challenges and analytical strategies. <i>Journal of Proteomics</i> , 2010, 73, 868-878.	1.2	119
117	The System MHC Atlas project. <i>Nucleic Acids Research</i> , 2018, 46, D1237-D1247.	6.5	119
118	Norwalk Virus Assembly and Stability Monitored by Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1742-1751.	2.5	118
119	Probing the biophysical interplay between a viral genome and its capsid. <i>Nature Chemistry</i> , 2013, 5, 502-509.	6.6	117
120	Robust, Sensitive, and Automated Phosphopeptide Enrichment Optimized for Low Sample Amounts Applied to Primary Hippocampal Neurons. <i>Journal of Proteome Research</i> , 2017, 16, 728-737.	1.8	117
121	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , 2008, 5, 405-407.	9.0	116
122	<i>De novo</i> discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , 2015, 235, 3-13.	2.1	116
123	In Vivo Profiling and Visualization of Cellular Protein-Lipid Interactions Using Bifunctional Fatty Acids. <i>Angewandte Chemie - International Edition</i> , 2013, 52, 4033-4038.	7.2	114
124	Detailed mass analysis of structural heterogeneity in monoclonal antibodies using native mass spectrometry. <i>Nature Protocols</i> , 2014, 9, 967-976.	5.5	114
125	Differential Oxidation of Protein-tyrosine Phosphatases. <i>Journal of Biological Chemistry</i> , 2005, 280, 10298-10304.	1.6	113
126	Profiling of N-Acetylated Protein Termini Provides In-depth Insights into the N-terminal Nature of the Proteome. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 928-939.	2.5	113

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127	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478.	2.9	113
128	Proteasome Activation by Small Molecules. <i>Cell Chemical Biology</i> , 2017, 24, 725-736.e7.	2.5	113
129	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. <i>Nature</i> , 2019, 574, 278-282.	13.7	113
130	Plasma Membrane Proteomics of Human Embryonic Stem Cells and Human Embryonal Carcinoma Cells. <i>Journal of Proteome Research</i> , 2008, 7, 2936-2951.	1.8	112
131	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , 2013, 88, 14-26.	1.2	112
132	Boundaries of Mass Resolution in Native Mass Spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2014, 25, 906-917.	1.2	111
133	Structure of the Yeast Vacuolar ATPase. <i>Journal of Biological Chemistry</i> , 2008, 283, 35983-35995.	1.6	110
134	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020, 181, 1291-1306.e19.	13.5	110
135	N-terminal domain of human Hsp90 triggers binding to the cochaperone p23. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 580-585.	3.3	109
136	Molecular Basis of Transcription-Coupled Pre-mRNA Capping. <i>Molecular Cell</i> , 2015, 58, 1079-1089.	4.5	109
137	Glycoproteomics: A Balance between High-Throughput and In-Depth Analysis. <i>Trends in Biotechnology</i> , 2017, 35, 598-609.	4.9	109
138	Quantitative proteomics and transcriptomics of anaerobic and aerobic yeast cultures reveals post-transcriptional regulation of key cellular processes. <i>Microbiology (United Kingdom)</i> , 2007, 153, 3864-3878.	0.7	108
139	Analysis of the cGMP/cAMP Interactome Using a Chemical Proteomics Approach in Mammalian Heart Tissue Validates Sphingosine Kinase Type 1-interacting Protein as a Genuine and Highly Abundant AKAP. <i>Journal of Proteome Research</i> , 2006, 5, 1435-1447.	1.8	107
140	Factors Affecting Gas-Phase Deuterium Scrambling in Peptide Ions and Their Implications for Protein Structure Determination. <i>Journal of the American Chemical Society</i> , 2002, 124, 11191-11198.	6.6	106
141	In-Gel Isoelectric Focusing of Peptides as a Tool for Improved Protein Identification. <i>Journal of Proteome Research</i> , 2006, 5, 1721-1730.	1.8	106
142	Structures of the cyanobacterial circadian oscillator frozen in a fully assembled state. <i>Science</i> , 2017, 355, 1181-1184.	6.0	106
143	The PRoteomics IDentification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1682-1689.	2.5	105
144	Histone Interaction Landscapes Visualized by Crosslinking Mass Spectrometry in Intact Cell Nuclei. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2018-2033.	2.5	103

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145	Interrogating the architecture of protein assemblies and protein interaction networks by cross-linking mass spectrometry. <i>Current Opinion in Structural Biology</i> , 2015, 35, 100-108.	2.6	102
146	Structure and assembly of scalable porous protein cages. <i>Nature Communications</i> , 2017, 8, 14663.	5.8	102
147	Stability and Shape of Hepatitis B Virus Capsids In Vacuo. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 6247-6251.	7.2	101
148	Squeezing Protein Shells: How Continuum Elastic Models, Molecular Dynamics Simulations, and Experiments Coalesce at the Nanoscale. <i>Biophysical Journal</i> , 2010, 99, 1175-1181.	0.2	101
149	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. <i>Amino Acids</i> , 2012, 43, 1087-1108.	1.2	101
150	Depletion of Phosphatidylcholine in Yeast Induces Shortening and Increased Saturation of the Lipid Acyl Chains: Evidence for Regulation of Intrinsic Membrane Curvature in a Eukaryote. <i>Molecular Biology of the Cell</i> , 2006, 17, 1006-1017.	0.9	100
151	Mass Spectrometric Analysis of Intact Human Monoclonal Antibody Aggregates Fractionated by Size-Exclusion Chromatography. <i>Pharmaceutical Research</i> , 2010, 27, 2197-2204.	1.7	100
152	Self-Sorting of Foreign Proteins in a Bacterial Nanocompartment. <i>Journal of the American Chemical Society</i> , 2014, 136, 3828-3832.	6.6	100
153	PhoX: An IMAC-Enrichable Cross-Linking Reagent. <i>ACS Central Science</i> , 2019, 5, 1514-1522.	5.3	100
154	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019, 91, 6953-6961.	3.2	100
155	Identification of Cell Surface Proteins for Antibody-Based Selection of Human Embryonic Stem Cell-Derived Cardiomyocytes. <i>Journal of Proteome Research</i> , 2010, 9, 1610-1618.	1.8	99
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