

# Albert J R Heck

## 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.

776 papers	46,734 citations	103 h-index	180 g-index
844 ext. papers	53,842 ext. citations	8.6 avg, IF	7.73 L-index

#	Paper	IF	Citations
776	Multiplex peptide stable isotope dimethyl labeling for quantitative proteomics. <i>Nature Protocols</i> , <b>2009</b> , 4, 484-94	18.8	1072
775	Lgr5 homologues associate with Wnt receptors and mediate R-spondin signalling. <i>Nature</i> , <b>2011</b> , 476, 293-7	50.4	903
774	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. <i>Nature Methods</i> , <b>2013</b> , 10, 730-6	21.6	894
773	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> , <b>2004</b> , 76, 3935-43	7.8	835
772	Wnt signaling through inhibition of E-catenin degradation in an intact Axin1 complex. <i>Cell</i> , <b>2012</b> , 149, 1245-56	56.2	619
771	Tumour suppressor RNF43 is a stem-cell E3 ligase that induces endocytosis of Wnt receptors. <i>Nature</i> , <b>2012</b> , 488, 665-9	50.4	599
770	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 887-93	44.5	583
769	Native mass spectrometry: a bridge between interactomics and structural biology. <i>Nature Methods</i> , <b>2008</b> , 5, 927-33	21.6	577
768	Next-generation proteomics: towards an integrative view of proteome dynamics. <i>Nature Reviews Genetics</i> , <b>2013</b> , 14, 35-48	30.1	530
767	Quantitative phosphoproteomics of early elicitor signaling in Arabidopsis. <i>Molecular and Cellular Proteomics</i> , <b>2007</b> , 6, 1198-214	7.6	528
766	The Lgr5 intestinal stem cell signature: robust expression of proposed quiescent N4Ncell markers. <i>EMBO Journal</i> , <b>2012</b> , 31, 3079-91	13	523
765	Investigation of intact protein complexes by mass spectrometry. <i>Mass Spectrometry Reviews</i> , <b>2004</b> , 23, 368-89	11	503
764	Structural basis for CRISPR RNA-guided DNA recognition by Cascade. <i>Nature Structural and Molecular Biology</i> , <b>2011</b> , 18, 529-36	17.6	425
763	Complement is activated by IgG hexamers assembled at the cell surface. <i>Science</i> , <b>2014</b> , 343, 1260-3	33.3	424
762	Ion mobility mass spectrometry of proteins and protein assemblies. <i>Chemical Society Reviews</i> , <b>2010</b> , 39, 1633-55	58.5	369
761	Metabolic labeling of <i>C. elegans</i> and <i>D. melanogaster</i> for quantitative proteomics. <i>Nature Biotechnology</i> , <b>2003</b> , 21, 927-31	44.5	362
760	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> , <b>2003</b> , 100, 7480-5	11.5	347

759	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> , <b>2011</b> , 108, 10092-7	11.5	345
758	Regulation of retromer recruitment to endosomes by sequential action of Rab5 and Rab7. <i>Journal of Cell Biology</i> , <b>2008</b> , 183, 513-26	7.3	328
757	Mass spectrometry-based proteomics and network biology. <i>Annual Review of Biochemistry</i> , <b>2012</b> , 81, 379-405	29.1	326
756	Native Mass Spectrometry: What is in the Name?. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2017</b> , 28, 5-13	3.5	320
755	Identification of CMTM6 and CMTM4 as PD-L1 protein regulators. <i>Nature</i> , <b>2017</b> , 549, 106-110	50.4	309
754	High-sensitivity Orbitrap mass analysis of intact macromolecular assemblies. <i>Nature Methods</i> , <b>2012</b> , 9, 1084-6	21.6	303
753	Proteome-wide profiling of protein assemblies by cross-linking mass spectrometry. <i>Nature Methods</i> , <b>2015</b> , 12, 1179-84	21.6	302
752	Sequential waves of functionally related proteins are expressed when B cells prepare for antibody secretion. <i>Immunity</i> , <b>2003</b> , 18, 243-53	32.3	300
751	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> , <b>2004</b> , 101, 8455-60	11.5	291
750	Phosphopeptide fragmentation and analysis by mass spectrometry. <i>Journal of Mass Spectrometry</i> , <b>2009</b> , 44, 861-78	2.2	290
749	Imaging techniques for the study of chemical reaction dynamics. <i>Annual Review of Physical Chemistry</i> , <b>1995</b> , 46, 335-72	15.7	289
748	Toward a comprehensive characterization of a human cancer cell phosphoproteome. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 260-71	5.6	276
747	Phosphorylation dynamics during early differentiation of human embryonic stem cells. <i>Cell Stem Cell</i> , <b>2009</b> , 5, 214-26	18	271
746	Robust phosphoproteome enrichment using monodisperse microsphere-based immobilized titanium (IV) ion affinity chromatography. <i>Nature Protocols</i> , <b>2013</b> , 8, 461-80	18.8	270
745	Lipid II is an intrinsic component of the pore induced by nisin in bacterial membranes. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 19898-903	5.4	251
744	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> , <b>2015</b> , 60, 63-76	17.6	250
743	Improved peptide identification by targeted fragmentation using CID, HCD and ETD on an LTQ-Orbitrap Velos. <i>Journal of Proteome Research</i> , <b>2011</b> , 10, 2377-88	5.6	248
742	Native protein mass spectrometry: from intact oligomers to functional machineries. <i>Current Opinion in Chemical Biology</i> , <b>2004</b> , 8, 519-26	9.7	247

741	Six alternative proteases for mass spectrometry-based proteomics beyond trypsin. <i>Nature Protocols</i> , <b>2016</b> , 11, 993-1006	18.8	245
740	A large fraction of HLA class I ligands are proteasome-generated spliced peptides. <i>Science</i> , <b>2016</b> , 354, 354-358	33.3	232
739	A high-quality catalog of the <i>Drosophila melanogaster</i> proteome. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 576-83	44.5	230
738	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> , <b>2012</b> , 11, 5145-56	5.6	227
737	Lys-N and trypsin cover complementary parts of the phosphoproteome in a refined SCX-based approach. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 4493-501	7.8	226
736	MSQuant, an open source platform for mass spectrometry-based quantitative proteomics. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 393-403	5.6	225
735	GATA-1 forms distinct activating and repressive complexes in erythroid cells. <i>EMBO Journal</i> , <b>2005</b> , 24, 2354-66	13	223
734	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , <b>2019</b> , 16, 595-602	21.6	216
733	Improving the performance of a quadrupole time-of-flight instrument for macromolecular mass spectrometry. <i>Analytical Chemistry</i> , <b>2006</b> , 78, 7473-83	7.8	213
732	GMP synthetase stimulates histone H2B deubiquitylation by the epigenetic silencer USP7. <i>Molecular Cell</i> , <b>2005</b> , 17, 695-707	17.6	208
731	On terminal alkynes that can react with active-site cysteine nucleophiles in proteases. <i>Journal of the American Chemical Society</i> , <b>2013</b> , 135, 2867-70	16.4	207
730	Hydrophilic interaction liquid chromatography (HILIC) in proteomics. <i>Analytical and Bioanalytical Chemistry</i> , <b>2008</b> , 391, 151-9	4.4	206
729	Toward full peptide sequence coverage by dual fragmentation combining electron-transfer and higher-energy collision dissociation tandem mass spectrometry. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 9668-73	7.8	203
728	Interrogating viral capsid assembly with ion mobility-mass spectrometry. <i>Nature Chemistry</i> , <b>2011</b> , 3, 126-32	32.6	203
727	RNA targeting by the type III-A CRISPR-Cas Csm complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , <b>2014</b> , 56, 518-30	17.6	202
726	Direct Determination of Solution Binding Constants for Noncovalent Complexes between Bacterial Cell Wall Peptide Analogues and Vancomycin Group Antibiotics by Electrospray Ionization Mass Spectrometry. <i>Analytical Chemistry</i> , <b>1998</b> , 70, 4427-4432	7.8	201
725	The generating function of CID, ETD, and CID/ETD pairs of tandem mass spectra: applications to database search. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 2840-52	7.6	193
724	The fluxes through glycolytic enzymes in <i>Saccharomyces cerevisiae</i> are predominantly regulated at posttranscriptional levels. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 15753-8	11.5	192

723	MHC class II-associated proteins in B-cell exosomes and potential functional implications for exosome biogenesis. <i>Immunology and Cell Biology</i> , <b>2010</b> , 88, 851-6	5	186
722	The effect of the source pressure on the abundance of ions of noncovalent protein assemblies in an electrospray ionization orthogonal time-of-flight instrument. <i>Rapid Communications in Mass Spectrometry</i> , <b>2001</b> , 15, 596-601	2.2	182
721	High-resolution mass spectrometry of viral assemblies: molecular composition and stability of dimorphic hepatitis B virus capsids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2008</b> , 105, 9216-20	11.5	181
720	Proteomics beyond trypsin. <i>FEBS Journal</i> , <b>2015</b> , 282, 2612-26	5.7	180
719	Munc13-4 is an effector of rab27a and controls secretion of lysosomes in hematopoietic cells. <i>Molecular Biology of the Cell</i> , <b>2005</b> , 16, 731-41	3.5	179
718	Microtubule minus-end stabilization by polymerization-driven CAMSAP deposition. <i>Developmental Cell</i> , <b>2014</b> , 28, 295-309	10.2	175
717	Triplex protein quantification based on stable isotope labeling by peptide dimethylation applied to cell and tissue lysates. <i>Proteomics</i> , <b>2008</b> , 8, 4624-32	4.8	174
716	Structure and activity of the RNA-targeting Type III-B CRISPR-Cas complex of <i>Thermus thermophilus</i> . <i>Molecular Cell</i> , <b>2013</b> , 52, 135-145	17.6	173
715	Evaluation and optimization of ZIC-HILIC-RP as an alternative MudPIT strategy. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 937-46	5.6	169
714	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> , <b>2008</b> , 7, 687-97	5.6	164
713	Comprehensive analysis of the secreted proteins of the parasite <i>Haemonchus contortus</i> reveals extensive sequence variation and differential immune recognition. <i>Journal of Biological Chemistry</i> , <b>2003</b> , 278, 16941-51	5.4	164
712	The diverse and expanding role of mass spectrometry in structural and molecular biology. <i>EMBO Journal</i> , <b>2016</b> , 35, 2634-2657	13	160
711	Genome-wide characterization of the routes to pluripotency. <i>Nature</i> , <b>2014</b> , 516, 198-206	50.4	153
710	Nuclear PtdIns5P as a transducer of stress signaling: an in vivo role for PIP4Kbeta. <i>Molecular Cell</i> , <b>2006</b> , 23, 685-95	17.6	147
709	Expanding the detectable HLA peptide repertoire using electron-transfer/higher-energy collision dissociation (ETHcD). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 4507-12	11.5	145
708	The phosphoproteomics data explosion. <i>Current Opinion in Chemical Biology</i> , <b>2009</b> , 13, 414-20	9.7	145
707	Optimized fragmentation schemes and data analysis strategies for proteome-wide cross-link identification. <i>Nature Communications</i> , <b>2017</b> , 8, 15473	17.4	144
706	Cross-talk between phosphorylation and lysine acetylation in a genome-reduced bacterium. <i>Molecular Systems Biology</i> , <b>2012</b> , 8, 571	12.2	144

705	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> , <b>2010</b> , 9, 84-99	7.6	142
704	Studying 18 MDa virus assemblies with native mass spectrometry. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 4020-3	16.4	140
703	Differential targeting of two distinct SWI/SNF-related Drosophila chromatin-remodeling complexes. <i>Molecular and Cellular Biology</i> , <b>2004</b> , 24, 3077-88	4.8	140
702	Mass spectrometric analysis of the Schistosoma mansoni tegumental sub-proteome. <i>Journal of Proteome Research</i> , <b>2005</b> , 4, 958-66	5.6	139
701	Human Ccr4-Not complexes contain variable deadenylase subunits. <i>Biochemical Journal</i> , <b>2009</b> , 422, 443-53	5.3	134
700	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , <b>2013</b> , 31, 557-64	44.5	132
699	Chaperonin complexes monitored by ion mobility mass spectrometry. <i>Journal of the American Chemical Society</i> , <b>2009</b> , 131, 1452-9	16.4	132
698	The kinase TNK1 is an essential activator of Wnt target genes. <i>EMBO Journal</i> , <b>2009</b> , 28, 3329-40	13	130
697	Unambiguous phosphosite localization using electron-transfer/higher-energy collision dissociation (ETHCD). <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 1520-5	5.6	125
696	Recent advances in peptide separation by multidimensional liquid chromatography for proteome analysis. <i>Journal of Proteomics</i> , <b>2012</b> , 75, 3791-813	3.9	124
695	Homodimeric galectin-7 (p53-induced gene 1) is a negative growth regulator for human neuroblastoma cells. <i>Oncogene</i> , <b>2003</b> , 22, 6277-88	9.2	123
694	Trends in ultrasensitive proteomics. <i>Current Opinion in Chemical Biology</i> , <b>2012</b> , 16, 206-13	9.7	120
693	Quantitative proteomics by metabolic labeling of model organisms. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 11-24	7.6	120
692	An experimental correction for arginine-to-proline conversion artifacts in SILAC-based quantitative proteomics. <i>Nature Methods</i> , <b>2007</b> , 4, 677-8	21.6	120
691	Exploring an orbitrap analyzer for the characterization of intact antibodies by native mass spectrometry. <i>Angewandte Chemie - International Edition</i> , <b>2012</b> , 51, 12992-6	16.4	117
690	Zwitterionic hydrophilic interaction liquid chromatography (ZIC-HILIC and ZIC-cHILIC) provide high resolution separation and increase sensitivity in proteome analysis. <i>Analytical Chemistry</i> , <b>2011</b> , 83, 3440-7	7.8	117
689	Encapsulation of phthalocyanine supramolecular stacks into virus-like particles. <i>Journal of the American Chemical Society</i> , <b>2011</b> , 133, 6878-81	16.4	116
688	Activation of FoxM1 during G2 requires cyclin A/Cdk-dependent relief of autorepression by the FoxM1 N-terminal domain. <i>Molecular and Cellular Biology</i> , <b>2008</b> , 28, 3076-87	4.8	116

687	Guest encapsulation and self-assembly of molecular capsules in polar solvents via multiple ionic interactions. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 6569-75	16.4	112
686	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> , <b>1991</b> , 5, 406-414	2.2	112
685	High-fidelity mass analysis unveils heterogeneity in intact ribosomal particles. <i>Nature Methods</i> , <b>2017</b> , 14, 283-286	21.6	111
684	EGFR Dynamics Change during Activation in Native Membranes as Revealed by NMR. <i>Cell</i> , <b>2016</b> , 167, 1241-1251.e11	56.2	110
683	Dis3-like 1: a novel exoribonuclease associated with the human exosome. <i>EMBO Journal</i> , <b>2010</b> , 29, 2358-67	13.7	109
682	Defining the stoichiometry and cargo load of viral and bacterial nanoparticles by Orbitrap mass spectrometry. <i>Journal of the American Chemical Society</i> , <b>2014</b> , 136, 7295-9	16.4	108
681	A quest for human and mouse embryonic stem cell-specific proteins. <i>Molecular and Cellular Proteomics</i> , <b>2006</b> , 5, 1261-73	7.6	107
680	Revealing promiscuous drug-target interactions by chemical proteomics. <i>Drug Discovery Today</i> , <b>2009</b> , 14, 1021-9	8.8	106
679	Hybrid mass spectrometry approaches in glycoprotein analysis and their usage in scoring biosimilarity. <i>Nature Communications</i> , <b>2016</b> , 7, 13397	17.4	105
678	Probing the biophysical interplay between a viral genome and its capsid. <i>Nature Chemistry</i> , <b>2013</b> , 5, 502-9	27.6	104
677	The quantitative proteomes of human-induced pluripotent stem cells and embryonic stem cells. <i>Molecular Systems Biology</i> , <b>2011</b> , 7, 550	12.2	104
676	RNA polymerase I contains a TFIIF-related DNA-binding subcomplex. <i>Molecular Cell</i> , <b>2010</b> , 39, 583-94	17.6	103
675	Straightforward ladder sequencing of peptides using a Lys-N metalloendopeptidase. <i>Nature Methods</i> , <b>2008</b> , 5, 405-7	21.6	103
674	Proteome analysis of yeast response to various nutrient limitations. <i>Molecular Systems Biology</i> , <b>2006</b> , 2, 2006.0026	12.2	103
673	Norwalk virus assembly and stability monitored by mass spectrometry. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 1742-51	7.6	102
672	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> , <b>2006</b> , 5, 1435-47	5.6	101
671	In-gel isoelectric focusing of peptides as a tool for improved protein identification. <i>Journal of Proteome Research</i> , <b>2006</b> , 5, 1721-30	5.6	101
670	Benchmarking stable isotope labeling based quantitative proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 88, 14-26	3.9	100



669	Plasma membrane proteomics of human embryonic stem cells and human embryonal carcinoma cells. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 2936-51	5.6	100
668	Differential oxidation of protein-tyrosine phosphatases. <i>Journal of Biological Chemistry</i> , <b>2005</b> , 280, 10298-304	5.4	100
667	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> , <b>2016</b> , 14, e1002344	9.7	100
666	Talin-KANK1 interaction controls the recruitment of cortical microtubule stabilizing complexes to focal adhesions. <i>ELife</i> , <b>2016</b> , 5,	8.9	100
665	Stability and shape of hepatitis B virus capsids in vacuo. <i>Angewandte Chemie - International Edition</i> , <b>2008</b> , 47, 6247-51	16.4	99
664	Quantitative proteomics and transcriptomics of anaerobic and aerobic yeast cultures reveals post-transcriptional regulation of key cellular processes. <i>Microbiology (United Kingdom)</i> , <b>2007</b> , 153, 3864-3878	2.9	99
663	Factors affecting gas-phase deuterium scrambling in peptide ions and their implications for protein structure determination. <i>Journal of the American Chemical Society</i> , <b>2002</b> , 124, 11191-8	16.4	99
662	Protein acetylation affects acetate metabolism, motility and acid stress response in Escherichia coli. <i>Molecular Systems Biology</i> , <b>2014</b> , 10, 762	12.2	98
661	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> , <b>2011</b> , 108, 580-5	11.5	98
660	Exploring the membrane proteome--challenges and analytical strategies. <i>Journal of Proteomics</i> , <b>2010</b> , 73, 868-78	3.9	98
659	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> , <b>2011</b> , 187, 3238-46	5.3	97
658	Personalized Proteome Profiles of Healthy and Tumor Human Colon Organoids Reveal Both Individual Diversity and Basic Features of Colorectal Cancer. <i>Cell Reports</i> , <b>2017</b> , 18, 263-274	10.6	96
657	Quantitative and qualitative proteome characteristics extracted from in-depth integrated genomics and proteomics analysis. <i>Cell Reports</i> , <b>2013</b> , 5, 1469-78	10.6	96
656	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> , <b>2012</b> , 11, 1682-9	7.6	96
655	De novo discovery of phenotypic intratumour heterogeneity using imaging mass spectrometry. <i>Journal of Pathology</i> , <b>2015</b> , 235, 3-13	9.4	95
654	Detailed mass analysis of structural heterogeneity in monoclonal antibodies using native mass spectrometry. <i>Nature Protocols</i> , <b>2014</b> , 9, 967-76	18.8	95
653	Widespread bacterial protein histidine phosphorylation revealed by mass spectrometry-based proteomics. <i>Nature Methods</i> , <b>2018</b> , 15, 187-190	21.6	94
652	Structure of the yeast vacuolar ATPase. <i>Journal of Biological Chemistry</i> , <b>2008</b> , 283, 35983-95	5.4	93



651	Boundaries of mass resolution in native mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2014</b> , 25, 906-17	3.5	92
650	Profiling of N-acetylated protein termini provides in-depth insights into the N-terminal nature of the proteome. <i>Molecular and Cellular Proteomics</i> , <b>2010</b> , 9, 928-39	7.6	92
649	Molecular Basis of Assembly and Activation of Complement Component C1 in Complex with Immunoglobulin G1 and Antigen. <i>Molecular Cell</i> , <b>2016</b> , 63, 135-45	17.6	91
648	The interactome of intact mitochondria by cross-linking mass spectrometry provides evidence for coexisting respiratory supercomplexes. <i>Molecular and Cellular Proteomics</i> , <b>2018</b> , 17, 216-232	7.6	91
647	Glycoproteomics: A Balance between High-Throughput and In-Depth Analysis. <i>Trends in Biotechnology</i> , <b>2017</b> , 35, 598-609	15.1	89
646	Elucidating crosstalk mechanisms between phosphorylation and O-GlcNAcylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, E7255-E7261	11.5	89
645	Mass spectrometric analysis of intact human monoclonal antibody aggregates fractionated by size-exclusion chromatography. <i>Pharmaceutical Research</i> , <b>2010</b> , 27, 2197-204	4.5	88
644	Benchmarking multiple fragmentation methods on an orbitrap fusion for top-down phospho-proteoform characterization. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 4152-8	7.8	87
643	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D1237-D1247	20.1	87
642	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. <i>Amino Acids</i> , <b>2012</b> , 43, 1087-108	3.5	87
641	Monitoring macromolecular complexes involved in the chaperonin-assisted protein folding cycle by mass spectrometry. <i>Nature Methods</i> , <b>2005</b> , 2, 371-6	21.6	87
640	In vivo profiling and visualization of cellular protein-lipid interactions using bifunctional fatty acids. <i>Angewandte Chemie - International Edition</i> , <b>2013</b> , 52, 4033-8	16.4	86
639	Microtubule minus-end regulation at spindle poles by an ASPM-katanin complex. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 480-492	23.4	85
638	Proteasome Activation by Small Molecules. <i>Cell Chemical Biology</i> , <b>2017</b> , 24, 725-736.e7	8.2	85
637	Targeted analysis of protein termini. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 4634-45	5.6	85
636	The two biosynthetic routes leading to phosphatidylcholine in yeast produce different sets of molecular species. Evidence for lipid remodeling. <i>Biochemistry</i> , <b>2003</b> , 42, 3054-9	3.2	85
635	Lipase active-site-directed anchoring of organometallics: metallopincer/protein hybrids. <i>Chemistry - A European Journal</i> , <b>2005</b> , 11, 6869-77	4.8	85
634	Squeezing protein shells: how continuum elastic models, molecular dynamics simulations, and experiments coalesce at the nanoscale. <i>Biophysical Journal</i> , <b>2010</b> , 99, 1175-81	2.9	84

633	Identification of cell surface proteins for antibody-based selection of human embryonic stem cell-derived cardiomyocytes. <i>Journal of Proteome Research</i> , <b>2010</b> , 9, 1610-8	5.6	84
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