

Albert J R Heck

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.

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	Fasting improves therapeutic response in hepatocellular carcinoma through p53-dependent metabolic synergism.. <i>Science Advances</i> , 2022 , 8, eabh2635	14.3	3
775	Label-free visual proteomics: Coupling MS- and EM-based approaches in structural biology.. <i>Molecular Cell</i> , 2022 , 82, 285-303	17.6	3
774	Identifying glycation hot-spots in bovine milk proteins during production and storage of skim milk powder. <i>International Dairy Journal</i> , 2022 , 129, 105340	3.5	0
773	Assessment of genome packaging in AAVs using Orbitrap-based charge-detection mass spectrometry.. <i>Molecular Therapy - Methods and Clinical Development</i> , 2022 , 24, 40-47	6.4	2
772	Proteoform Profiles Reveal That Alpha-1-Antitrypsin in Human Serum and Milk Is Derived From a Common Source.. <i>Frontiers in Molecular Biosciences</i> , 2022 , 9, 858856	5.6	1
771	High Resolution Proteomic Analysis of Subcellular Fractionated Boar Spermatozoa Provides Comprehensive Insights Into Perinuclear Theca-Residing Proteins.. <i>Frontiers in Cell and Developmental Biology</i> , 2022 , 10, 836208	5.7	1
770	Sbk2, a Newly Discovered Atrium-Enriched Regulator of Sarcomere Integrity.. <i>Circulation Research</i> , 2022 , 101161CIRCRESAHA121319300	15.7	
769	Elucidation of the pre-nucleation phase directing metal-organic framework formation. <i>Cell Reports Physical Science</i> , 2021 , 2, 100680	6.1	2
768	Probing Affinity, Avidity, Anticooperativity, and Competition in Antibody and Receptor Binding to the SARS-CoV-2 Spike by Single Particle Mass Analyses. <i>ACS Central Science</i> , 2021 , 7, 1863-1873	16.8	2
767	In-cell structures of conserved supramolecular protein arrays at the mitochondria-cytoskeleton interface in mammalian sperm. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
766	Extending Native Top-Down Electron Capture Dissociation to MDa Immunoglobulin Complexes Provides Useful Sequence Tags Covering Their Critical Variable Complementarity-Determining Regions. <i>Analytical Chemistry</i> , 2021 , 93, 16068-16075	7.8	2
765	The HLA Ligandome Comprises a Limited Repertoire of O-GlcNAcylated Antigens Preferentially Associated With HLA-B*07:02.. <i>Frontiers in Immunology</i> , 2021 , 12, 796584	8.4	0
764	Systems approach reveals distinct and shared signaling networks of the four PGE receptors in T cells. <i>Science Signaling</i> , 2021 , 14, eabc8579	8.8	1
763	Structural basis of soluble membrane attack complex packaging for clearance. <i>Nature Communications</i> , 2021 , 12, 6086	17.4	1
762	Single-particle mass analysis of intact ribosomes by mass photometry and Orbitrap-based charge detection mass spectrometry. <i>iScience</i> , 2021 , 24, 103211	6.1	1
761	Personalized Profiling Reveals Donor- and Lactation-Specific Trends in the Human Milk Proteome and Peptidome. <i>Journal of Nutrition</i> , 2021 , 151, 826-839	4.1	9
760	The lysosomal endopeptidases Cathepsin D and L are selective and effective proteases for the middle-down characterization of antibodies. <i>FEBS Journal</i> , 2021 , 288, 5389-5405	5.7	2

759	Adeno-associated virus capsid assembly is divergent and stochastic. <i>Nature Communications</i> , 2021 , 12, 1642	17.4	22
758	Discrepancies between High-Resolution Native and Glycopeptide-Centric Mass Spectrometric Approaches: A Case Study into the Glycosylation of Erythropoietin Variants. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 2099-2104	3.5	5
757	Human Milk from Previously COVID-19-Infected Mothers: The Effect of Pasteurization on Specific Antibodies and Neutralization Capacity. <i>Nutrients</i> , 2021 , 13,	6.7	18
756	Phosphorylation-Dependent Interactome of Ryanodine Receptor Type 2 in the Heart. <i>Proteomes</i> , 2021 , 9,	4.6	1
755	Optimization of a human milk-directed quantitative sIgA ELISA method substantiated by mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2021 , 413, 5037-5049	4.4	2
754	A serum proteome signature to predict mortality in severe COVID-19 patients. <i>Life Science Alliance</i> , 2021 , 4,	5.8	14
753	Monitoring Human Milk ECasein Phosphorylation and -Glycosylation Over Lactation Reveals Distinct Differences between the Proteome and Endogenous Peptidome. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	3
752	Mild Acid Elution and MHC Immunoaffinity Chromatography Reveal Similar Albeit Not Identical Profiles of the HLA Class I Immunoepitidome. <i>Journal of Proteome Research</i> , 2021 , 20, 289-304	5.6	9
751	Mass Spectrometry-Based Structural Virology. <i>Analytical Chemistry</i> , 2021 , 93, 620-640	7.8	9
750	HLA Class II Presentation Is Specifically Altered at Elevated Temperatures in the B-Lymphoblastic Cell Line JY. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100089	7.6	2
749	Selective cross-linking of coinciding protein assemblies by in-gel cross-linking mass spectrometry. <i>EMBO Journal</i> , 2021 , 40, e106174	13	8
748	Complete and cooperative in vitro assembly of computationally designed self-assembling protein nanomaterials. <i>Nature Communications</i> , 2021 , 12, 883	17.4	7
747	Staphylococcal protein A inhibits complement activation by interfering with IgG hexamer formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	15
746	Generating Informative Sequence Tags from Antigen-Binding Regions of Heavily Glycosylated IgA1 Antibodies by Native Top-Down Electron Capture Dissociation. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 1326-1335	3.5	4
745	HLA-B and cysteinylated ligands distinguish the antigen presentation landscape of extracellular vesicles. <i>Communications Biology</i> , 2021 , 4, 825	6.7	1
744	Similarities and differences in the structures and proteoform profiles of the complement proteins C6 and C7. <i>Proteomics</i> , 2021 , 21, e2000310	4.8	0
743	High-Resolution Native Mass Spectrometry. <i>Chemical Reviews</i> , 2021 ,	68.1	24
742	Neutrophil azurophilic granule glycoproteins are distinctively decorated by atypical pauci- and phosphomannose glycans. <i>Communications Biology</i> , 2021 , 4, 1012	6.7	2

741	Extracellular crosslinking mass spectrometry reveals HLA class I - HLA class II interactions on the cell surface. <i>Molecular Immunology</i> , 2021 , 136, 16-25	4.3	4
740	Recent advancements in mass spectrometry-based tools to investigate newly synthesized proteins. <i>Current Opinion in Chemical Biology</i> , 2021 ,	9.7	4
739	Cas4-Cas1 Is a Protospacer Adjacent Motif-Processing Factor Mediating Half-Site Spacer Integration During CRISPR Adaptation. <i>CRISPR Journal</i> , 2021 , 4, 536-548	2.5	1
738	Allotype-Specific Glycosylation and Cellular Localization of Human Leukocyte Antigen Class I Proteins. <i>Journal of Proteome Research</i> , 2021 , 20, 4518-4528	5.6	0
737	Human plasma IgG1 repertoires are simple, unique, and dynamic. <i>Cell Systems</i> , 2021 ,	10.6	5
736	Molecular characterization of a complex of apoptosis-inducing factor 1 with cytochrome c oxidase of the mitochondrial respiratory chain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	5
735	Editor Profile: Albert Heck. <i>FEBS Journal</i> , 2021 , 288, 5228-5230	5.7	
734	Native Structural and Functional Proteoform Characterization of the Prolyl-Alanyl-Specific Endoprotease EndoPro from. <i>Journal of Proteome Research</i> , 2021 , 20, 4875-4885	5.6	3
733	Quantifying Positional Isomers (QPI) by Top-Down Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100070	7.6	
732	Ion Imaging of Native Protein Complexes Using Orthogonal Time-of-Flight Mass Spectrometry and a Timepix Detector. <i>Journal of the American Society for Mass Spectrometry</i> , 2021 , 32, 569-580	3.5	5
731	Huntingtin structure is orchestrated by HAP40 and shows a polyglutamine expansion-specific interaction with exon 1. <i>Communications Biology</i> , 2021 , 4, 1374	6.7	1
730	A Direct MS-Based Approach to Profile Human Milk Secretory Immunoglobulin A (IgA1) Reveals Donor-Specific Clonal Repertoires With High Longitudinal Stability.. <i>Frontiers in Immunology</i> , 2021 , 12, 789748	8.4	0
729	High-Resolution mRNA and Secretome Atlas of Human Enteroendocrine Cells. <i>Cell</i> , 2020 , 181, 1291-1306	9.19	41
728	A wealth of genotype-specific proteoforms fine-tunes hemoglobin scavenging by haptoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 15554-15564	11.5	17
727	Site-specific functionality and tryptophan mimicry of lipidation in tetraspanin CD9. <i>FEBS Journal</i> , 2020 , 287, 5323-5344	5.7	6
726	Resolving heterogeneous macromolecular assemblies by Orbitrap-based single-particle charge detection mass spectrometry. <i>Nature Methods</i> , 2020 , 17, 395-398	21.6	47
725	Quantitative Longitudinal Inventory of the -Glycoproteome of Human Milk from a Single Donor Reveals the Highly Variable Repertoire and Dynamic Site-Specific Changes. <i>Journal of Proteome Research</i> , 2020 , 19, 1941-1952	5.6	13
724	Fishing for newly synthesized proteins with phosphonate-handles. <i>Nature Communications</i> , 2020 , 11, 3244	17.4	4

723	Ubiquitylation of the ER-Shaping Protein Lunapark via the CRL3 Ubiquitin Ligase Complex. <i>Cell Reports</i> , 2020 , 31, 107664	10.6	6
722	The Orphan Immune Receptor LILRB3 Modulates Fc Receptor-Mediated Functions of Neutrophils. <i>Journal of Immunology</i> , 2020 , 204, 954-966	5.3	7
721	Missing regions within the molecular architecture of human fibrin clots structurally resolved by XL-MS and integrative structural modeling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 1976-1987	11.5	14
720	8T cell diversity and the receptor interface with tumor cells. <i>Journal of Clinical Investigation</i> , 2020 , 130, 4637-4651	15.9	27
719	Targeting proline in (phospho)proteomics. <i>FEBS Journal</i> , 2020 , 287, 2979-2997	5.7	4
718	To Cleave or Not To Cleave in XL-MS?. <i>Journal of the American Society for Mass Spectrometry</i> , 2020 , 31, 196-206	3.5	28
717	Selectivity over coverage in sequencing of IgGs. <i>Chemical Science</i> , 2020 , 11, 11886-11896	9.4	7
716	Single-cell derived tumor organoids display diversity in HLA class I peptide presentation. <i>Nature Communications</i> , 2020 , 11, 5338	17.4	17
715	Loss of SPEG Inhibitory Phosphorylation of Ryanodine Receptor Type-2 Promotes Atrial Fibrillation. <i>Circulation</i> , 2020 , 142, 1159-1172	16.7	20
714	Inhibition of the integrated stress response by viral proteins that block p-eIF2-eIF2B association. <i>Nature Microbiology</i> , 2020 , 5, 1361-1373	26.6	17
713	Malignant tissues produce divergent antibody glycosylation of relevance for cancer gene therapy effectiveness. <i>MAbs</i> , 2020 , 12, 1792084	6.6	6
712	Releasing Nonperipheral Subunits from Protein Complexes in the Gas Phase. <i>Analytical Chemistry</i> , 2020 , 92, 15799-15805	7.8	6
711	Enhancing Top-Down Analysis Using Chromophore-Assisted Infrared Multiphoton Dissociation from (Phospho)peptides to Protein Assemblies. <i>Analytical Chemistry</i> , 2020 , 92, 15506-15516	7.8	4
710	Benefits of Collisional Cross Section Assisted Precursor Selection (caps-PASEF) for Cross-linking Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 1677-1687	7.6	14
709	Targeted LC-ESI-MS characterization of human milk oligosaccharide diversity at 6 to 16 weeks post-partum reveals clear staging effects and distinctive milk groups. <i>Analytical and Bioanalytical Chemistry</i> , 2020 , 412, 6887-6907	4.4	5
708	Mitochondrial CaMKII causes adverse metabolic reprogramming and dilated cardiomyopathy. <i>Nature Communications</i> , 2020 , 11, 4416	17.4	22
707	Dynamic remodelling of the human host cell proteome and phosphoproteome upon enterovirus infection. <i>Nature Communications</i> , 2020 , 11, 4332	17.4	7
706	Activation of Human Monocytes by Colloidal Aluminum Salts. <i>Journal of Pharmaceutical Sciences</i> , 2020 , 109, 750-760	3.9	4

705	NIST Interlaboratory Study on Glycosylation Analysis of Monoclonal Antibodies: Comparison of Results from Diverse Analytical Methods. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 11-30	7.6	49
704	Insights into PPAR β Phosphorylation and Its Inhibition Mechanism. <i>Journal of Medicinal Chemistry</i> , 2020 , 63, 4811-4823	8.3	11
703	Meta-heterogeneity: Evaluating and Describing the Diversity in Glycosylation Between Sites on the Same Glycoprotein. <i>Molecular and Cellular Proteomics</i> , 2020 , 20, 100010	7.6	25
702	Glycoproteoform Profiles of Individual Patients' Plasma Alpha-1-Antichymotrypsin are Unique and Extensively Remodeled Following a Septic Episode. <i>Frontiers in Immunology</i> , 2020 , 11, 608466	8.4	8
701	Functional diversification of hybridoma-produced antibodies by CRISPR/HDR genomic engineering. <i>Science Advances</i> , 2019 , 5, eaaw1822	14.3	5
700	High-Throughput Assessment of Kinome-wide Activation States. <i>Cell Systems</i> , 2019 , 9, 366-374.e5	10.6	12
699	Structure of the inner kinetochore CCAN complex assembled onto a centromeric nucleosome. <i>Nature</i> , 2019 , 574, 278-282	50.4	63
698	Unraveling the Macromolecular Pathways of IgG Oligomerization and Complement Activation on Antigenic Surfaces. <i>Nano Letters</i> , 2019 , 19, 4787-4796	11.5	35
697	Loss of Protein Phosphatase 1 Regulatory Subunit PPP1R3A Promotes Atrial Fibrillation. <i>Circulation</i> , 2019 , 140, 681-693	16.7	28
696	A Colorful Palette of B-Phycoerythrin Proteoforms Exposed by a Multimodal Mass Spectrometry Approach. <i>Chem</i> , 2019 , 5, 1302-1317	16.2	8
695	Glycoproteogenomics: A Frequent Gene Polymorphism Affects the Glycosylation Pattern of the Human Serum Fetuin/B2-HS-Glycoprotein. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 1479-1490	7.6	25
694	Quantitative Proteomics for Differential Protein Expression Profiling 2019 , 1-27		2
693	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
692	Serine 25 phosphorylation inhibits RIPK1 kinase-dependent cell death in models of infection and inflammation. <i>Nature Communications</i> , 2019 , 10, 1729	17.4	69
691	An Integrated Global Analysis of Compartmentalized HRAS Signaling. <i>Cell Reports</i> , 2019 , 26, 3100-3115.e7	20.6	22
690	Gaining Confidence in the Elusive Histidine Phosphoproteome. <i>Analytical Chemistry</i> , 2019 , 91, 5542-5547	7.8	16
689	Actin from the apicomplexan <i>Neospora caninum</i> (NcACT) has different isoforms in 2D electrophoresis. <i>Parasitology</i> , 2019 , 146, 33-41	2.7	0
688	Distinct Stabilities of the Structurally Homologous Heptameric Co-Chaperonins GroES and gp31. <i>Journal of the American Society for Mass Spectrometry</i> , 2019 , 30, 7-15	3.5	3

687	PhoX: An IMAC-Enrichable Cross-Linking Reagent. <i>ACS Central Science</i> , 2019 , 5, 1514-1522	16.8	55
686	Simply Extending the Mass Range in Electron Transfer Higher Energy Collisional Dissociation Increases Confidence in N-Glycopeptide Identification. <i>Analytical Chemistry</i> , 2019 , 91, 10401-10406	7.8	25
685	Reductive methylation labeling, from quantitative to structural proteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2019 , 118, 771-778	14.6	18
684	Recommendations for performing, interpreting and reporting hydrogen deuterium exchange mass spectrometry (HDX-MS) experiments. <i>Nature Methods</i> , 2019 , 16, 595-602	21.6	216
683	Expanding the mass range for UVPD-based native top-down mass spectrometry. <i>Chemical Science</i> , 2019 , 10, 7163-7171	9.4	21
682	Neutrophil myeloperoxidase harbors distinct site-specific peculiarities in its glycosylation. <i>Journal of Biological Chemistry</i> , 2019 , 294, 20233-20245	5.4	20
681	Prostaglandin E2 signaling networks in T cells revealed through a systems approach. <i>FASEB Journal</i> , 2019 , 33, lb258	0.9	
680	Toward an efficient workflow for the analysis of the human milk peptidome. <i>Analytical and Bioanalytical Chemistry</i> , 2019 , 411, 1351-1363	4.4	10
679	Pre-fractionation Extends but also Creates a Bias in the Detectable HLA Class II Ligandome. <i>Journal of Proteome Research</i> , 2019 , 18, 1634-1643	5.6	16
678	Proteomic Profiling of Mouse Helper T Cell Differentiation. <i>Proteomics</i> , 2019 , 19, e1800045	4.8	0
677	Identification of a tumor-specific allo-HLA-restricted pMHC. <i>Blood Advances</i> , 2019 , 3, 2870-2882	7.8	18
676	Loss of CRMP2 O-GlcNAcylation leads to reduced novel object recognition performance in mice. <i>Open Biology</i> , 2019 , 9, 190192	7	9
675	A new perspective on fungal metabolites: identification of bioactive compounds from fungi using zebrafish embryogenesis as read-out. <i>Scientific Reports</i> , 2019 , 9, 17546	4.9	16
674	Label-free targeted LC-ESI-MS analysis of human milk oligosaccharides (HMOS) and related human milk groups with enhanced structural selectivity. <i>Analytical and Bioanalytical Chemistry</i> , 2019 , 411, 231-250	4.4	23
673	Phosphopeptide Fragmentation and Site Localization by Mass Spectrometry: An Update. <i>Analytical Chemistry</i> , 2019 , 91, 126-141	7.8	49
672	PaDuA: A Python Library for High-Throughput (Phospho)proteomics Data Analysis. <i>Journal of Proteome Research</i> , 2019 , 18, 576-584	5.6	7
671	Targeted Analysis of Lysosomal Directed Proteins and Their Sites of Mannose-6-phosphate Modification. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 16-27	7.6	26
670	TREM-1 multimerization is essential for its activation on monocytes and neutrophils. <i>Cellular and Molecular Immunology</i> , 2019 , 16, 460-472	15.4	24

669	Discovery and Quantification of Nonhuman Proteins in Human Milk. <i>Journal of Proteome Research</i> , 2019 , 18, 225-238	5.6	16
668	CTGF/VEGFA-activated Fibroblasts Promote Tumor Migration Through Micro-environmental Modulation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1502-1514	7.6	10
667	Rearrangement of the Protein Phosphatase 1 Interactome During Heart Failure Progression. <i>Circulation</i> , 2018 , 138, 1569-1581	16.7	8
666	Comprehensive Proteoform Characterization of Plasma Complement Component C8b by Hybrid Mass Spectrometry Approaches. <i>Journal of the American Society for Mass Spectrometry</i> , 2018 , 29, 1099-1110	11.5	20
665	TMEM59 potentiates Wnt signaling by promoting signalosome formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E3996-E4005	11.5	26
664	Defeating Major Contaminants in Fe- Immobilized Metal Ion Affinity Chromatography (IMAC) Phosphopeptide Enrichment. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1028-1034	7.6	45
663	Doxorubicin-induced DNA Damage Causes Extensive Ubiquitination of Ribosomal Proteins Associated with a Decrease in Protein Translation. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2297-2308	7.6	13
662	Parsimonious Charge Deconvolution for Native Mass Spectrometry. <i>Journal of Proteome Research</i> , 2018 , 17, 1216-1226	5.6	61
661	Widespread bacterial protein histidine phosphorylation revealed by mass spectrometry-based proteomics. <i>Nature Methods</i> , 2018 , 15, 187-190	21.6	94
660	A search for ceramide binding proteins using bifunctional lipid analogs yields CERT-related protein StarD7. <i>Journal of Lipid Research</i> , 2018 , 59, 515-530	6.3	27
659	The physiology of <i>Agaricus bisporus</i> in semi-commercial compost cultivation appears to be highly conserved among unrelated isolates. <i>Fungal Genetics and Biology</i> , 2018 , 112, 12-20	3.9	7
658	Exploring ECD on a Benchtop Q Exactive Orbitrap Mass Spectrometer. <i>Journal of Proteome Research</i> , 2018 , 17, 926-933	5.6	38
657	Novel identified aluminum hydroxide-induced pathways prove monocyte activation and pro-inflammatory preparedness. <i>Journal of Proteomics</i> , 2018 , 175, 144-155	3.9	20
656	Crosstalk between phosphorylation and O-GlcNAcylation: friend or foe. <i>FEBS Journal</i> , 2018 , 285, 3152-3167	16.7	50
655	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
654	Identification of differentially expressed peptides in high-throughput proteomics data. <i>Briefings in Bioinformatics</i> , 2018 , 19, 971-981	13.4	17
653	Functional Impact of the N-terminal Arm of Proline Dehydrogenase from <i>Thermus thermophilus</i> . <i>Molecules</i> , 2018 , 23,	4.8	3
652	Histone Interaction Landscapes Visualized by Crosslinking Mass Spectrometry in Intact Cell Nuclei. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2018-2033	7.6	56

651	Direct quality control of glycoengineered erythropoietin variants. <i>Nature Communications</i> , 2018 , 9, 334217.4	44
650	Mix and match of the tumor metastasis suppressor Nm23 protein isoforms in vitro and in vivo. <i>FEBS Journal</i> , 2018 , 285, 2856-2868	5.7 10
649	Inheritance of the Golgi Apparatus and Cytokinesis Are Controlled by Degradation of GBF1. <i>Cell Reports</i> , 2018 , 23, 3381-3391.e4	10.6 8
648	Spatial Organization of a cAMP/Ca ²⁺ -Regulated Signaling Complex: A Solution Structural Small-Angle X-ray and Neutron Scattering Study of an AKAP79-Scaffolded Complex Containing Type II PKA and Calcineurin. <i>FASEB Journal</i> , 2018 , 32, 1b56	0.9
647	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	7.6 91
646	Connecting color with assembly in the fluorescent B-phycoerythrin protein complex. <i>FEBS Journal</i> , 2018 , 285, 178-187	5.7 19
645	Efficient and robust proteome-wide approaches for cross-linking mass spectrometry. <i>Nature Protocols</i> , 2018 , 13, 2964-2990	18.8 77
644	Chaperonin CCT checkpoint function in basal transcription factor TFIID assembly. <i>Nature Structural and Molecular Biology</i> , 2018 , 25, 1119-1127	17.6 22
643	A New Tool to Reveal Bacterial Signaling Mechanisms in Antibiotic Treatment and Resistance. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2496-2507	7.6 13
642	The benefits of hybrid fragmentation methods for glycoproteomics. <i>TrAC - Trends in Analytical Chemistry</i> , 2018 , 108, 260-268	14.6 60
641	Effects of Acetylation and Phosphorylation on Subunit Interactions in Three Large Eukaryotic Complexes. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 2387-2401	7.6 10
640	In vivo phosphoproteomics reveals kinase activity profiles that predict treatment outcome in triple-negative breast cancer. <i>Nature Communications</i> , 2018 , 9, 3501	17.4 26
639	Bacterial encapsulins as orthogonal compartments for mammalian cell engineering. <i>Nature Communications</i> , 2018 , 9, 1990	17.4 51
638	Minimal Information About an Immuno-Peptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018 , 18, e18001108	14
637	A Protein-Based Encapsulation System with Calcium-Controlled Cargo Loading and Detachment. <i>Angewandte Chemie - International Edition</i> , 2018 , 57, 11334-11338	16.4 10
636	Vaccine antigens modulate the innate response of monocytes to Al(OH) ₃ . <i>PLoS ONE</i> , 2018 , 13, e0197885.7	6
635	Dissecting ribosomal particles throughout the kingdoms of life using advanced hybrid mass spectrometry methods. <i>Nature Communications</i> , 2018 , 9, 2493	17.4 45
634	Similar Albeit Not the Same: In-Depth Analysis of Proteoforms of Human Serum, Bovine Serum, and Recombinant Human Fetuin. <i>Journal of Proteome Research</i> , 2018 , 17, 2861-2869	5.6 19

633	A System-wide Approach to Monitor Responses to Synergistic BRAF and EGFR Inhibition in Colorectal Cancer Cells. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1892-1908	7.6	7
632	High-fidelity mass analysis unveils heterogeneity in intact ribosomal particles. <i>Nature Methods</i> , 2017 , 14, 283-286	21.6	111
631	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	10.6	96
630	Proteoform Profile Mapping of the Human Serum Complement Component C9 Revealing Unexpected New Features of N-, O-, and C-Glycosylation. <i>Analytical Chemistry</i> , 2017 , 89, 3483-3491	7.8	33
629	Structure and assembly of scalable porous protein cages. <i>Nature Communications</i> , 2017 , 8, 14663	17.4	75
628	Resolving the micro-heterogeneity and structural integrity of monoclonal antibodies by hybrid mass spectrometric approaches. <i>MAbs</i> , 2017 , 9, 638-645	6.6	40
627	Toward an Optimized Workflow for Middle-Down Proteomics. <i>Analytical Chemistry</i> , 2017 , 89, 3318-3325	7.8	67
626	The atheroma plaque secretome stimulates the mobilization of endothelial progenitor cells ex vivo. <i>Journal of Molecular and Cellular Cardiology</i> , 2017 , 105, 12-23	5.8	10
625	Quantitative Map of Proteome Dynamics during Neuronal Differentiation. <i>Cell Reports</i> , 2017 , 18, 1527-1542	14.6	47
624	Cultivation of <i>Podospora anserina</i> on soybean hulls results in an efficient enzyme cocktail for plant biomass hydrolysis. <i>New Biotechnology</i> , 2017 , 37, 162-171	6.4	19
623	Vertex-Specific Proteins pUL17 and pUL25 Mechanically Reinforce Herpes Simplex Virus Capsids. <i>Journal of Virology</i> , 2017 , 91,	6.6	23
622	Microtubule minus-end regulation at spindle poles by an ASPM-katanin complex. <i>Nature Cell Biology</i> , 2017 , 19, 480-492	23.4	85
621	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	5.6	64
620	Native Mass Spectrometry: What is in the Name?. <i>Journal of the American Society for Mass Spectrometry</i> , 2017 , 28, 5-13	3.5	320
619	Glycoproteomics: A Balance between High-Throughput and In-Depth Analysis. <i>Trends in Biotechnology</i> , 2017 , 35, 598-609	15.1	89
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7	Cross-linking/Mass Spectrometry: A Community-Wide, Comparative Study Towards Establishing Best Practice Guidelines		4
6	Functional diversification of hybridoma produced antibodies by CRISPR/HDR genomic engineering		1
5	Resolving heterogeneous high-mass macromolecular machineries by Orbitrap-based single particle charge detection mass spectrometry		1
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1	In-cell structures of a conserved supramolecular array at the mitochondria-cytoskeleton interface in mammalian sperm	2