

# Petr Man

## List of Publications by Year in descending order

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127  
papers

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citations

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135  
docs citations

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times ranked

5368  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Cysteine <i>S</i> -glycosylation, a new post-translational modification found in glycopeptide bacteriocins. <i>FEBS Letters</i> , 2011, 585, 645-650.	1.3	132
3	MSTools™ Web based application for visualization and presentation of HXMS data. <i>International Journal of Mass Spectrometry</i> , 2011, 302, 53-58.	0.7	126
4	Identification of the N-glycosylation sites on glutamate carboxypeptidase II necessary for proteolytic activity. <i>Protein Science</i> , 2004, 13, 1627-1635.	3.1	93
5	Protein Patterns of Pig Oocytes During In Vitro Maturation1. <i>Biology of Reproduction</i> , 2004, 71, 1533-1539.	1.2	89
6	Structural insights and in vitro reconstitution of membrane targeting and activation of human PI4KB by the ACBD3 protein. <i>Scientific Reports</i> , 2016, 6, 23641.	1.6	81
7	Effective Removal of Nonionic Detergents in Protein Mass Spectrometry, Hydrogen/Deuterium Exchange, and Proteomics. <i>Analytical Chemistry</i> , 2010, 82, 5107-5116.	3.2	63
8	Aspartic Protease Nepenthesin-1 as a Tool for Digestion in Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2014, 86, 4287-4294.	3.2	63
9	Activation of macrophages by gliadin fragments: isolation and characterization of active peptide. <i>Journal of Leukocyte Biology</i> , 2002, 71, 625-31.	1.5	56
10	Sequence analysis and heterologous expression of the lincomycin biosynthetic cluster of the type strain <i>Streptomyces lincolnensis</i> ATCC 25466. <i>Folia Microbiologica</i> , 2008, 53, 395-401.	1.1	55
11	Recombinant Nepenthesin II for Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Analytical Chemistry</i> , 2015, 87, 6681-6687.	3.2	54
12	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. <i>Scientific Reports</i> , 2016, 6, 30980.	1.6	54
13	The H <sub>2</sub> O <sub>2</sub> -dependent activity of a fungal lytic polysaccharide monooxygenase investigated with a turbidimetric assay. <i>Biotechnology for Biofuels</i> , 2020, 13, 37.	6.2	50
14	Recombinant immobilized rhizopuspepsin as a new tool for protein digestion in hydrogen/deuterium exchange mass spectrometry. <i>Rapid Communications in Mass Spectrometry</i> , 2009, 23, 3431-3438.	0.7	49
15	Defining the Interacting Regions between Apomyoglobin and Lipid Membrane by Hydrogen/Deuterium Exchange Coupled to Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2007, 368, 464-472.	2.0	45
16	Structural Insight into the 14-3-3 Protein-dependent Inhibition of Protein Kinase ASK1 (Apoptosis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.6	45
17	The tick plasma lectin, Dorin M, is a fibrinogen-related molecule. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 291-299.	1.2	44
18	Impact of Chemical Cross-Linking on Protein Structure and Function. <i>Analytical Chemistry</i> , 2018, 90, 1104-1113.	3.2	44

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19	The Assembly and Intermolecular Properties of the Hsp70-Tomm34-Hsp90 Molecular Chaperone Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 9887-9901.	1.6	42
20	p47 Molecular Activation for Assembly of the Neutrophil NADPH Oxidase Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 28980-28990.	1.6	41
21	Characterization of the lectin from females of <i>Phlebotomus duboscqi</i> sand flies. <i>FEBS Journal</i> , 2002, 269, 6294-6301.	0.2	39
22	Conformational Dynamics of the Bovine Mitochondrial ADP/ATP Carrier Isoform 1 Revealed by Hydrogen/Deuterium Exchange Coupled to Mass Spectrometry. <i>Journal of Biological Chemistry</i> , 2010, 285, 34981-34990.	1.6	39
23	Human Stress-inducible Hsp70 Has a High Propensity to Form ATP-dependent Antiparallel Dimers That Are Differentially Regulated by Cochaperone Binding*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 320-337.	2.5	35
24	Structural basis of the 14-3-3 protein-dependent activation of yeast neutral trehalase Nth1. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2013, 1830, 4491-4499.	1.1	34
25	Neprosin, a Selective Prolyl Endoprotease for Bottom-up Proteomics and Histone Mapping. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1162-1171.	2.5	34
26	Interdomain electron transfer in cellobiose dehydrogenase is governed by surface electrostatics. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2017, 1861, 157-167.	1.1	34
27	Molecular Characterization of Binding of Calcium and Carbohydrates by an Early Activation Antigen of Lymphocytes CD69. <i>Biochemistry</i> , 2003, 42, 9295-9306.	1.2	33
28	Native proteomic analysis of protein complexes in murine intestinal brush border membranes. <i>Proteomics</i> , 2007, 7, 121-129.	1.3	33
29	Expression and characterization of plant aspartic protease nepenthesin-1 from <i>Nepenthes gracilis</i> . <i>Protein Expression and Purification</i> , 2014, 95, 121-128.	0.6	33
30	Proteomic analysis of hepatic iron overload in mice suggests dysregulation of urea cycle, impairment of fatty acid oxidation, and changes in the methylation cycle. <i>American Journal of Physiology - Renal Physiology</i> , 2007, 292, G1490-G1498.	1.6	32
31	Asymmetric Preorganization of Inverted Pair Residues in the Sodium-Calcium Exchanger. <i>Scientific Reports</i> , 2016, 6, 20753.	1.6	32
32	Mass spectrometric analysis of the glycosphingolipid-enriched microdomains of rat natural killer cells. <i>Proteomics</i> , 2005, 5, 113-122.	1.3	31
33	Modified electrophoretic and digestion conditions allow a simplified mass spectrometric evaluation of disulfide bonds. <i>Journal of Mass Spectrometry</i> , 2009, 44, 1571-1578.	0.7	31
34	The vaccinia virus DNA polymerase structure provides insights into the mode of processivity factor binding. <i>Nature Communications</i> , 2017, 8, 1455.	5.8	31
35	Identification of heme binding protein complexes in murine erythroleukemic cells: Study by a novel two-dimensional native separation - liquid chromatography and electrophoresis. <i>Proteomics</i> , 2005, 5, 340-350.	1.3	30
36	Chemical Cross-Linking and H/D Exchange for Fast Refinement of Protein Crystal Structure. <i>Analytical Chemistry</i> , 2012, 84, 867-870.	3.2	30

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37	Purification and characterization of a saccharide-binding protein from penetration glands of <i>Diplostomum pseudospathaceum</i> a bifunctional molecule with cysteine protease activity. <i>Parasitology</i> , 2003, 127, 69-77.	0.7	29
38	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, .	2.8	29
39	Separation of nuclear protein complexes by blue native polyacrylamide gel electrophoresis. <i>Electrophoresis</i> , 2006, 27, 1277-1287.	1.3	28
40	High-throughput quantification of lincomycin traces in fermentation broth of genetically modified <i>Streptomyces</i> spp.. <i>Journal of Chromatography A</i> , 2007, 1139, 214-220.	1.8	28
41	Identification of a second Nutlin-3 responsive interaction site in the N-terminal domain of MDM2 using hydrogen/deuterium exchange mass spectrometry. <i>Proteomics</i> , 2013, 13, 2512-2525.	1.3	28
42	Fluorescent Labelled Thiourea-Bridged Glycodendrons. <i>ChemBioChem</i> , 2004, 5, 445-452.	1.3	27
43	Cysteine residues mediate high affinity binding of thioredoxin to <i>ASK1</i> . <i>FEBS Journal</i> , 2016, 283, 3821-3838.	2.2	27
44	Dynamic distinctions in the Na <sup>+</sup> /Ca <sup>2+</sup> exchanger adopting the inward- and outward-facing conformational states. <i>Journal of Biological Chemistry</i> , 2017, 292, 12311-12323.	1.6	27
45	Proteomic analysis of iron overload in human hepatoma cells. <i>American Journal of Physiology - Renal Physiology</i> , 2006, 290, G1059-G1066.	1.6	25
46	Structural Basis for the 14-3-3 Protein-dependent Inhibition of the Regulator of G Protein Signaling 3 (RGS3) Function. <i>Journal of Biological Chemistry</i> , 2011, 286, 43527-43536.	1.6	25
47	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. <i>Journal of Immunology</i> , 2015, 195, 3273-3283.	0.4	25
48	Structure of the dimeric N-glycosylated form of fungal $\beta$ -N-acetylhexosaminidase revealed by computer modeling, vibrational spectroscopy, and biochemical studies. <i>BMC Structural Biology</i> , 2007, 7, 32.	2.3	24
49	Large Propeptides of Fungal $\beta$ -N-Acetylhexosaminidases Are Novel Enzyme Regulators That Must Be Intracellularly Processed to Control Activity, Dimerization, and Secretion into the Extracellular Environment. <i>Biochemistry</i> , 2007, 46, 2719-2734.	1.2	23
50	Characterization of the NADH:ubiquinone oxidoreductase (complex I) in the trypanosomatid <i>Phytomonas serpens</i> (Kinetoplastida). <i>FEBS Journal</i> , 2007, 274, 3150-3158.	2.2	23
51	Hydroxylated anthraquinones produced by <i>Geosmithia</i> species. <i>Folia Microbiologica</i> , 2009, 54, 179-187.	1.1	23
52	Accessibility changes within diphtheria toxin T domain when in the functional molten globule state, as determined using hydrogen/deuterium exchange measurements. <i>FEBS Journal</i> , 2010, 277, 653-662.	2.2	23
53	Role of the EF-hand-like Motif in the 14-3-3 Protein-mediated Activation of Yeast Neutral Trehalase Nth1. <i>Journal of Biological Chemistry</i> , 2014, 289, 13948-13961.	1.6	23
54	Structural basis of heterotetrameric assembly and disease mutations in the human cis-prenyltransferase complex. <i>Nature Communications</i> , 2020, 11, 5273.	5.8	23

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55	Conformational changes in p47 <sup>phox</sup> upon activation highlighted by mass spectrometry coupled to hydrogen/deuterium exchange and limited proteolysis. <i>FEBS Letters</i> , 2009, 583, 835-840.	1.3	22
56	High-performance liquid chromatography–off line mass spectrometry analysis of anthraquinones produced by <i>Geosmithia lavendula</i> . <i>Journal of Chromatography A</i> , 2010, 1217, 6296-6302.	1.8	22
57	Interaction of Late Apoptotic and Necrotic Cells with Vitronectin. <i>PLoS ONE</i> , 2011, 6, e19243.	1.1	22
58	Structural insight into the calcium ion modulated interdomain electron transfer in cellobiose dehydrogenase. <i>FEBS Letters</i> , 2015, 589, 1194-1199.	1.3	22
59	Improving the Sequence Coverage of Integral Membrane Proteins during Hydrogen/Deuterium Exchange Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2019, 91, 10970-10978.	3.2	22
60	Structural basis of the pleiotropic and specific phenotypic consequences of missense mutations in the multifunctional NAD(P)H:quinone oxidoreductase 1 and their pharmacological rescue. <i>Redox Biology</i> , 2021, 46, 102112.	3.9	22
61	Mouse Clr-g, a Ligand for NK Cell Activation Receptor NKR-P1F: Crystal Structure and Biophysical Properties. <i>Journal of Immunology</i> , 2012, 189, 4881-4889.	0.4	21
62	A Dynamic Core in Human NQO1 Controls the Functional and Stability Effects of Ligand Binding and Their Communication across the Enzyme Dimer. <i>Biomolecules</i> , 2019, 9, 728.	1.8	21
63	Biologically Active Metabolites Produced by the Basidiomycete <i>Quambalaria cyanescens</i> . <i>PLoS ONE</i> , 2015, 10, e0118913.	1.1	20
64	Structural Characterization of Phosducin and Its Complex with the 14-3-3 Protein. <i>Journal of Biological Chemistry</i> , 2015, 290, 16246-16260.	1.6	20
65	Recombinant Tyrosinase from <i>Polyporus arcularius</i> : Overproduction in <i>Escherichia coli</i> , Characterization, and Use in a Study of Aurones as Tyrosinase Effectors. <i>Journal of Agricultural and Food Chemistry</i> , 2016, 64, 2925-2931.	2.4	20
66	N-glycosylated catalytic unit meets O-glycosylated propeptide: complex protein architecture in a fungal hexosaminidase. <i>Biochemical Society Transactions</i> , 2004, 32, 764-765.	1.6	19
67	The combination of hydrogen/deuterium exchange or chemical cross-linking techniques with mass spectrometry: Mapping of human 14-3-3 $\eta$ homodimer interface. <i>Journal of Structural Biology</i> , 2012, 179, 10-17.	1.3	19
68	Structural Model of Lymphocyte Receptor NKR-P1C Revealed by Mass Spectrometry and Molecular Modeling. <i>Analytical Chemistry</i> , 2013, 85, 1597-1604.	3.2	19
69	Novel Entropically Driven Conformation-specific Interactions with Tomm34 Protein Modulate Hsp70 Protein Folding and ATPase Activities. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1710-1727.	2.5	19
70	Coordination and redox state–dependent structural changes of the heme-based oxygen sensor AfGcHK associated with intraprotein signal transduction. <i>Journal of Biological Chemistry</i> , 2017, 292, 20921-20935.	1.6	19
71	Chimeric Cellobiose Dehydrogenases Reveal the Function of Cytochrome Domain Mobility for the Electron Transfer to Lytic Polysaccharide Monoxygenase. <i>ACS Catalysis</i> , 2021, 11, 517-532.	5.5	19
72	A highly diverse spectrum of naphthoquinone derivatives produced by the endophytic fungus <i>Biatriospora</i> sp. CCF 4378. <i>Folia Microbiologica</i> , 2015, 60, 259-267.	1.1	18

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73	Structural characterization of the heme-based oxygen sensor, AfGcHK, its interactions with the cognate response regulator, and their combined mechanism of action in a bacterial two-component signaling system. <i>Proteins: Structure, Function and Bioinformatics</i> , 2016, 84, 1375-1389.	1.5	18
74	Isolation and characterization of novel pl 4.8 MnP isoenzyme from white-rot fungus <i>Irpex lacteus</i> . <i>Enzyme and Microbial Technology</i> , 2010, 46, 550-556.	1.6	16
75	Human procaspase-2 phosphorylation at both S139 and S164 is required for 14-3-3 binding. <i>Biochemical and Biophysical Research Communications</i> , 2017, 493, 940-945.	1.0	15
76	Accessibility Changes within Diphtheria Toxin T Domain upon Membrane Penetration Probed by Hydrogen Exchange and Mass Spectrometry. <i>Journal of Molecular Biology</i> , 2011, 414, 123-134.	2.0	14
77	Different Reaction Specificities of F <sub>420</sub> H <sub>2</sub> -Dependent Reductases Facilitate Pyrrolobenzodiazepines and Lincomycin To Fit Their Biological Targets. <i>Journal of the American Chemical Society</i> , 2020, 142, 3440-3448.	6.6	14
78	14-3-3 protein binding blocks the dimerization interface of caspase-2. <i>FEBS Journal</i> , 2020, 287, 3494-3510.	2.2	14
79	Cloning of the first human anti-JCPyV/MP1 neutralizing monoclonal antibody: Epitope definition and implications in risk stratification of patients under natalizumab therapy. <i>Antiviral Research</i> , 2014, 108, 94-103.	1.9	13
80	Comparison of amino acid compositions of peptides eluted from HLA-B27 molecules of healthy individuals and patients with ankylosing spondylitis. <i>Immunology Letters</i> , 2006, 103, 135-141.	1.1	12
81	Large-scale identification of membrane proteins based on analysis of trypsin-protected transmembrane segments. <i>Journal of Proteomics</i> , 2016, 149, 15-22.	1.2	12
82	VP1, the major capsid protein of the mouse polyomavirus, binds microtubules, promotes their acetylation and blocks the host cell cycle. <i>FEBS Journal</i> , 2017, 284, 301-323.	2.2	12
83	Crystal structure of native N-acetylhexosaminidase isolated from <i>Aspergillus oryzae</i> sheds light onto its substrate specificity, high stability, and regulation by propeptide. <i>FEBS Journal</i> , 2018, 285, 580-598.	2.2	12
84	The interaction of the mitochondrial protein importer TOMM34 with HSP70 is regulated by TOMM34 phosphorylation and binding to 14-3-3 adaptors. <i>Journal of Biological Chemistry</i> , 2020, 295, 8928-8944.	1.6	12
85	Structural Dynamics of Lytic Polysaccharide Monooxygenase during Catalysis. <i>Biomolecules</i> , 2020, 10, 242.	1.8	12
86	Allosteric Communication in the Multifunctional and Redox NQO1 Protein Studied by Cavity-Making Mutations. <i>Antioxidants</i> , 2022, 11, 1110.	2.2	12
87	Monitoring of in vitro deamidation of gliadin peptic fragment by mass spectrometry may reflect one of the molecular mechanisms taking place in celiac disease development. <i>Journal of Mass Spectrometry</i> , 2002, 37, 507-511.	0.7	11
88	Introduction of water into the heme distal side by Leu65 mutations of an oxygen sensor, YddV, generates verdoheme and carbon monoxide, exerting the heme oxygenase reaction. <i>Journal of Inorganic Biochemistry</i> , 2014, 140, 29-38.	1.5	11
89	Ergochromes: Heretofore Neglected Side of Ergot Toxicity. <i>Toxins</i> , 2019, 11, 439.	1.5	11
90	Conversion of a heme-based oxygen sensor to a heme oxygenase by hydrogen sulfide: effects of mutations in the heme distal side of a heme-based oxygen sensor phosphodiesterase (Ec DOS). <i>BioMetals</i> , 2013, 26, 839-852.	1.8	10

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91	Thiopurine intolerance-causing mutations in NUDT15 induce temperature-dependent destabilization of the catalytic site. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2019, 1867, 376-381.	1.1	10
92	Bacteriocin ASM1 is an O / S ã€diglycosylated, plasmidã€encoded homologue of glycocin F. <i>FEBS Letters</i> , 2020, 594, 1196-1206.	1.3	10
93	Photoinduced damage of AsLOV2 domain is accompanied by increased singlet oxygen production due to flavin dissociation. <i>Scientific Reports</i> , 2020, 10, 4119.	1.6	10
94	Identification of HL60 Proteins Affected by 5-Aminolevulinic Acid-Based Photodynamic Therapy Using Mass Spectrometric Approach. <i>Collection of Czechoslovak Chemical Communications</i> , 2001, 66, 1720-1728.	1.0	10
95	VDAC2 and aldolase A identified as membrane proteins of K562 cells with increased expression under iron deprivation. <i>Molecular and Cellular Biochemistry</i> , 2008, 311, 225-231.	1.4	9
96	Deciphering Dorin M Glycosylation by Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2008, 14, 345-354.	0.5	9
97	Oligomeric interface modulation causes misregulation of purine 5Â²-nucleotidase in relapsed leukemia. <i>BMC Biology</i> , 2016, 14, 91.	1.7	9
98	MS-Based Approaches Enable the Structural Characterization of Transcription Factor/DNA Response Element Complex. <i>Biomolecules</i> , 2019, 9, 535.	1.8	9
99	Catalytic enhancement of the heme-based oxygen-sensing phosphodiesterase EcDOS by hydrogen sulfide is caused by changes in heme coordination structure. <i>BioMetals</i> , 2015, 28, 637-652.	1.8	8
100	Conformational Dynamics and Interactions of Membrane Proteins by Hydrogen/Deuterium Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2016, 1432, 269-279.	0.4	8
101	Structural Basis for the 14-3-3 Protein-Dependent Inhibition of Phosducin Function. <i>Biophysical Journal</i> , 2017, 112, 1339-1349.	0.2	8
102	Functional expression and characterization of two laccases from the brown rot <i>Fomitopsis pinicola</i> . <i>Enzyme and Microbial Technology</i> , 2021, 148, 109801.	1.6	8
103	Application of Proteomics in the Search for Novel Proteins Associated with the Anti-cancer Effect of the Synthetic Cyclin-dependent Kinases Inhibitor, Bohemine. <i>Technology in Cancer Research and Treatment</i> , 2002, 1, 247-256.	0.8	7
104	Proteomic analysis of erythroid differentiation induced by hexamethylene bisacetamide in murine erythroleukemia cells. <i>Experimental Hematology</i> , 2007, 35, 193-202.	0.2	7
105	LC MALDI-TOF MS/MS and LC ESI FTMS analyses of HLA-B27 associated peptides isolated from peripheral blood cells. <i>Immunology Letters</i> , 2008, 116, 79-85.	1.1	7
106	Effects of hydrogen sulfide on the heme coordination structure and catalytic activity of the globin-coupled oxygen sensor AfGcHK. <i>BioMetals</i> , 2016, 29, 715-729.	1.8	7
107	Early modification of cytochrome c by hydrogen peroxide triggers its fast degradation. <i>International Journal of Biological Macromolecules</i> , 2021, 174, 413-423.	3.6	7
108	The Isoforms of Rat Natural Killer Cell Receptor NKR-P1 Display a Distinct Binding of Complex Saccharide Ligands - RETRACTED. <i>Collection of Czechoslovak Chemical Communications</i> , 2004, 69, 631-644.	1.0	7



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109	HSPA1A conformational mutants reveal a conserved structural unit in Hsp70 proteins. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2020, 1864, 129458.	1.1	6
110	Studying Proteinâ€“DNA Interactions by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2247, 193-219.	0.4	6
111	Characterization of the rplB Gene from <i>Streptomyces collinus</i> and Its Protein Product by Mass Spectrometry. <i>Biochemical and Biophysical Research Communications</i> , 2001, 285, 1344-1349.	1.0	5
112	Facile production of <i>Aspergillus niger</i> Î±-N-acetylgalactosaminidase in yeast. <i>Protein Expression and Purification</i> , 2012, 81, 106-114.	0.6	5
113	Crystallization of nepenthesin I using a low-pH crystallization screen. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2016, 72, 24-28.	0.4	5
114	Utilization of highâ€“accuracy FTICRâ€“MS data in protein quantitation experiments. <i>Journal of Mass Spectrometry</i> , 2009, 44, 1565-1570.	0.7	4
115	Blue native protein electrophoresis for studies of mouse polyomavirus morphogenesis and interactions between the major capsid protein VP1 and cellular proteins. <i>Journal of Virological Methods</i> , 2011, 178, 229-234.	1.0	4
116	<i>Bordetella pertussis</i> and <i>Bordetella bronchiseptica</i> filamentous hemagglutinins are processed at different sites. <i>FEBS Open Bio</i> , 2018, 8, 1256-1266.	1.0	4
117	Conserved cysteine dioxidation enhances membrane interaction of human Cl <sup>sup&gt;â€“</sup> intracellular channel 5. <i>FASEB Journal</i> , 2020, 34, 9925-9940.	0.2	4
118	Peptides eluted from HLA-B27 of human splenocytes and blood cells reveal a similar but partially different profile compared to in vitro grown cell lines. <i>Immunology Letters</i> , 2004, 94, 261-265.	1.1	3
119	A three-pronged â€œPitchforkâ€“strategy enables an extensive description of the human membrane proteome and the identification of missing proteins. <i>Journal of Proteomics</i> , 2019, 204, 103411.	1.2	3
120	Structural basis for long-chain isoprenoid synthesis by <i>cis</i> -prenyltransferases. <i>Science Advances</i> , 2022, 8, eabn1171.	4.7	3
121	Motif orientation matters: Structural characterization of TEAD1 recognition of genomic DNA. <i>Structure</i> , 2021, 29, 345-356.e8.	1.6	2
122	A single evolutionarily divergent mutation determines the different FADâ€“binding affinities of human and rat NQO1 due to siteâ€“specific phosphorylation. <i>FEBS Letters</i> , 2021, 596, 29.	1.3	2
123	153-P: Analysis of HLA-B27 peptides form healthy individuals and ankylosing spodylitis patients. <i>Human Immunology</i> , 2008, 69, S84.	1.2	0
124	Membrane Interaction of Human CLIC5 is Facilitated by Dioxidation of a Conserved Cysteine and Drives Membrane Fusion. <i>Biophysical Journal</i> , 2021, 120, 291a.	0.2	0
125	Proteomic analysis of hepatic iron overload. <i>FASEB Journal</i> , 2006, 20, LB118.	0.2	0
126	Mechanistic Insight into the 14â€“Proteinâ€“Dependent Activation of Yeast Neutral Trehalase Nth1. <i>FASEB Journal</i> , 2015, 29, 572.2.	0.2	0



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127	Molecular Basis of 14-3-3 Protein Dependent Regulation of Caspase-2. FASEB Journal, 2020, 34, 1-1.	0.2	0