

Petr Man

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3106495/publications.pdf>

Version: 2024-02-01

127
papers

3,496
citations

159358

30
h-index

197535

49
g-index

135
all docs

135
docs citations

135
times ranked

5368
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for long-chain isoprenoid synthesis by <i>cis</i> -prenyltransferases. <i>Science Advances</i> , 2022, 8, eabn1171.	4.7	3
2	Allosteric Communication in the Multifunctional and Redox NQO1 Protein Studied by Cavity-Making Mutations. <i>Antioxidants</i> , 2022, 11, 1110.	2.2	12
3	Motif orientation matters: Structural characterization of TEAD1 recognition of genomic DNA. <i>Structure</i> , 2021, 29, 345-356.e8.	1.6	2
4	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
5	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
6	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
7	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
8	Chimeric Cellobiose Dehydrogenases Reveal the Function of Cytochrome Domain Mobility for the Electron Transfer to Lytic Polysaccharide Monooxygenase. <i>ACS Catalysis</i> , 2021, 11, 517-532.	5.5	19
9	Studying Protein-DNA Interactions by Hydrogen/Deuterium Exchange Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2021, 2247, 193-219.	0.4	6
10	A single evolutionarily divergent mutation determines the different FAD-binding affinities of human and rat NQO1 due to site-specific phosphorylation. <i>FEBS Letters</i> , 2021, 596, 29.	1.3	2
11	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
12	Bacteriocin ASM1 is an O/S diglycosylated, plasmid-encoded homologue of glycocin F. <i>FEBS Letters</i> , 2020, 594, 1196-1206.	1.3	10
13	Conserved cysteine dioxidation enhances membrane interaction of human Cl ^{sup>”} intracellular channel 5. <i>FASEB Journal</i> , 2020, 34, 9925-9940.	0.2	4
14	Structural basis of heterotetrameric assembly and disease mutations in the human <i>cis</i> -prenyltransferase complex. <i>Nature Communications</i> , 2020, 11, 5273.	5.8	23
15	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
16	The H ₂ O ₂ -dependent activity of a fungal lytic polysaccharide monooxygenase investigated with a turbidimetric assay. <i>Biotechnology for Biofuels</i> , 2020, 13, 37.	6.2	50
17	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
18	Structural Dynamics of Lytic Polysaccharide Monooxygenase during Catalysis. <i>Biomolecules</i> , 2020, 10, 242.	1.8	12

#	ARTICLE	IF	CITATIONS
19	Different Reaction Specificities of F ₄₂₀ H ₂ -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
20	14-3-3 protein binding blocks the dimerization interface of caspase-2. <i>FEBS Journal</i> , 2020, 287, 3494-3510.	2.2	14
21	Molecular Basis of 14-3-3 Protein Dependent Regulation of Caspase-2. <i>FASEB Journal</i> , 2020, 34, 1-1.	0.2	0
22	Ergochromes: Heretofore Neglected Side of Ergot Toxicity. <i>Toxins</i> , 2019, 11, 439.	1.5	11
23	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
24	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
25	MS-Based Approaches Enable the Structural Characterization of Transcription Factor/DNA Response Element Complex. <i>Biomolecules</i> , 2019, 9, 535.	1.8	9
26	A three-pronged "Pitchfork" 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
27	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
28	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
29	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
30	Impact of Chemical Cross-Linking on Protein Structure and Function. <i>Analytical Chemistry</i> , 2018, 90, 1104-1113.	3.2	44
31	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
32	<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
33	Structural Basis for the 14-3-3 Protein-Dependent Inhibition of Phosducin Function. <i>Biophysical Journal</i> , 2017, 112, 1339-1349.	0.2	8
34	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
35	Dynamic distinctions in the Na ⁺ /Ca ²⁺ exchanger adopting the inward- and outward-facing conformational states. <i>Journal of Biological Chemistry</i> , 2017, 292, 12311-12323.	1.6	27
36	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

#	ARTICLE	IF	CITATIONS
37	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
38	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
39	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
40	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
41	Architecture of TAF11/TAF13/TBP complex suggests novel regulation properties of general transcription factor TFIID. <i>ELife</i> , 2017, 6, .	2.8	29
42	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
43	Structural characterization of the heme-based oxygen sensor, <i>AfGcHK</i> , 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
44	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
45	Cysteine residues mediate high-affinity binding of thioredoxin to <i>ASK1</i> . <i>FEBS Journal</i> , 2016, 283, 3821-3838.	2.2	27
46	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
47	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
48	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
49	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
50	Addressing proteolytic efficiency in enzymatic degradation therapy for celiac disease. <i>Scientific Reports</i> , 2016, 6, 30980.	1.6	54
51	Asymmetric Preorganization of Inverted Pair Residues in the Sodium-Calcium Exchanger. <i>Scientific Reports</i> , 2016, 6, 20753.	1.6	32
52	Oligomeric interface modulation causes misregulation of purine 5'-nucleotidase in relapsed leukemia. <i>BMC Biology</i> , 2016, 14, 91.	1.7	9
53	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
54	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

#	ARTICLE	IF	CITATIONS
55	Biologically Active Metabolites Produced by the Basidiomycete <i>Quambalaria cyanescens</i> . PLoS ONE, 2015, 10, e0118913.	1.1	20
56	Structural insight into the calcium ion modulated interdomain electron transfer in cellobiose dehydrogenase. FEBS Letters, 2015, 589, 1194-1199.	1.3	22
57	Structural Characterization of Phosducin and Its Complex with the 14-3-3 Protein. Journal of Biological Chemistry, 2015, 290, 16246-16260.	1.6	20
58	Catalytic enhancement of the heme-based oxygen-sensing phosphodiesterase EcDOS by hydrogen sulfide is caused by changes in heme coordination structure. BioMetals, 2015, 28, 637-652.	1.8	8
59	A highly diverse spectrum of naphthoquinone derivatives produced by the endophytic fungus <i>Biatriospora</i> sp. CCF 4378. Folia Microbiologica, 2015, 60, 259-267.	1.1	18
60	Mapping the Binding Site of a Cross-Reactive <i>Plasmodium falciparum</i> PfEMP1 Monoclonal Antibody Inhibitory of ICAM-1 Binding. Journal of Immunology, 2015, 195, 3273-3283.	0.4	25
61	Recombinant Nepenthesin II for Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2015, 87, 6681-6687.	3.2	54
62	Mechanistic Insight into the 14-3-3 Protein-Dependent Activation of Yeast Neutral Trehalase Nth1. FASEB Journal, 2015, 29, 572.2.	0.2	0
63	The Assembly and Intermolecular Properties of the Hsp70-Tomm34-Hsp90 Molecular Chaperone Complex. Journal of Biological Chemistry, 2014, 289, 9887-9901.	1.6	42
64	Expression and characterization of plant aspartic protease nepenthesin-1 from <i>Nepenthes gracilis</i> . Protein Expression and Purification, 2014, 95, 121-128.	0.6	33
65	Role of the EF-hand-like Motif in the 14-3-3 Protein-mediated Activation of Yeast Neutral Trehalase Nth1. Journal of Biological Chemistry, 2014, 289, 13948-13961.	1.6	23
66	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. Journal of Inorganic Biochemistry, 2014, 140, 29-38.	1.5	11
67	Aspartic Protease Nepenthesin-1 as a Tool for Digestion in Hydrogen/Deuterium Exchange Mass Spectrometry. Analytical Chemistry, 2014, 86, 4287-4294.	3.2	63
68	Cloning of the first human anti-JCPyV/VP1 neutralizing monoclonal antibody: Epitope definition and implications in risk stratification of patients under natalizumab therapy. Antiviral Research, 2014, 108, 94-103.	1.9	13
69	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). BioMetals, 2013, 26, 839-852.	1.8	10
70	Identification of a second Nutlin-3 responsive interaction site in the N-terminal domain of MDM2 using hydrogen/deuterium exchange mass spectrometry. Proteomics, 2013, 13, 2512-2525.	1.3	28
71	Structural basis of the 14-3-3 protein-dependent activation of yeast neutral trehalase Nth1. Biochimica Et Biophysica Acta - General Subjects, 2013, 1830, 4491-4499.	1.1	34
72	Structural Model of Lymphocyte Receptor NKR-P1C Revealed by Mass Spectrometry and Molecular Modeling. Analytical Chemistry, 2013, 85, 1597-1604.	3.2	19

#	ARTICLE	IF	CITATIONS
73	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
74	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
75	Facile production of <i>Aspergillus niger</i> α -N-acetylgalactosaminidase in yeast. <i>Protein Expression and Purification</i> , 2012, 81, 106-114.	0.6	5
76	The combination of hydrogen/deuterium exchange or chemical cross-linking techniques with mass spectrometry: Mapping of human 14-3-3 η homodimer interface. <i>Journal of Structural Biology</i> , 2012, 179, 10-17.	1.3	19
77	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
78	Interaction of Late Apoptotic and Necrotic Cells with Vitronectin. <i>PLoS ONE</i> , 2011, 6, e19243.	1.1	22
79	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
80	Cysteine γ -glycosylation, a new post-translational modification found in glycopeptide bacteriocins. <i>FEBS Letters</i> , 2011, 585, 645-650.	1.3	132
81	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
82	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
83	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
84	Isolation and characterization of novel pI 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
85	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
86	p47 Molecular Activation for Assembly of the Neutrophil NADPH Oxidase Complex. <i>Journal of Biological Chemistry</i> , 2010, 285, 28980-28990.	1.6	41
87	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
88	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
89	Conformational changes in p47 ^{phox} 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
90	Utilization of high-accuracy FTICR-MS data in protein quantitation experiments. <i>Journal of Mass Spectrometry</i> , 2009, 44, 1565-1570.	0.7	4

#	ARTICLE	IF	CITATIONS
91	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
92	Hydroxylated anthraquinones produced by <i>Geosmithia</i> species. <i>Folia Microbiologica</i> , 2009, 54, 179-187.	1.1	23
93	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
94	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
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	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
97	153-P: Analysis of HLA-B27 peptides from healthy individuals and ankylosing spondylitis patients. <i>Human Immunology</i> , 2008, 69, S84.	1.2	0
98	Deciphering Dorin M Glycosylation by Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2008, 14, 345-354.	0.5	9
99	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
100	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
101	Large Propeptides of Fungal β -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
102	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
103	Structure of the dimeric N-glycosylated form of fungal β -N-acetylhexosaminidase revealed by computer modeling, vibrational spectroscopy, and biochemical studies. <i>BMC Structural Biology</i> , 2007, 7, 32.	2.3	24
104	Native proteomic analysis of protein complexes in murine intestinal brush border membranes. <i>Proteomics</i> , 2007, 7, 121-129.	1.3	33
105	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
106	Proteomic analysis of erythroid differentiation induced by hexamethylene bisacetamide in murine erythroleukemia cells. <i>Experimental Hematology</i> , 2007, 35, 193-202.	0.2	7
107	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
108	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

#	ARTICLE	IF	CITATIONS
109	Separation of nuclear protein complexes by blue native polyacrylamide gel electrophoresis. Electrophoresis, 2006, 27, 1277-1287.	1.3	28
110	Proteomic analysis of iron overload in human hepatoma cells. American Journal of Physiology - Renal Physiology, 2006, 290, G1059-G1066.	1.6	25
111	Proteomic analysis of hepatic iron overload. FASEB Journal, 2006, 20, LB118.	0.2	0
112	Mass spectrometric analysis of the glycosphingolipid-enriched microdomains of rat natural killer cells. Proteomics, 2005, 5, 113-122.	1.3	31
113	Identification of heme binding protein complexes in murine erythroleukemic cells: Study by a novel two-dimensional native separation - liquid chromatography and electrophoresis. Proteomics, 2005, 5, 340-350.	1.3	30
114	Protein Patterns of Pig Oocytes During In Vitro Maturation1. Biology of Reproduction, 2004, 71, 1533-1539.	1.2	89
115	Fluorescent Labelled Thiourea-Bridged Glycodendrons. ChemBioChem, 2004, 5, 445-452.	1.3	27
116	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. Immunology Letters, 2004, 94, 261-265.	1.1	3
117	Identification of the N-glycosylation sites on glutamate carboxypeptidase II necessary for proteolytic activity. Protein Science, 2004, 13, 1627-1635.	3.1	93
118	N-glycosylated catalytic unit meets O-glycosylated propeptide: complex protein architecture in a fungal hexosaminidase. Biochemical Society Transactions, 2004, 32, 764-765.	1.6	19
119	The Isoforms of Rat Natural Killer Cell Receptor NKR-P1 Display a Distinct Binding of Complex Saccharide Ligands - RETRACTED. Collection of Czechoslovak Chemical Communications, 2004, 69, 631-644.	1.0	7
120	Molecular Characterization of Binding of Calcium and Carbohydrates by an Early Activation Antigen of Lymphocytes CD69. Biochemistry, 2003, 42, 9295-9306.	1.2	33
121	Purification and characterization of a saccharide-binding protein from penetration glands of Diplostomum pseudospathaceum a bifunctional molecule with cysteine protease activity. Parasitology, 2003, 127, 69-77.	0.7	29
122	Application of Proteomics in the Search for Novel Proteins Associated with the Anti-cancer Effect of the Synthetic Cyclin-dependent Kinases Inhibitor, Bohemine. Technology in Cancer Research and Treatment, 2002, 1, 247-256.	0.8	7
123	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. Journal of Mass Spectrometry, 2002, 37, 507-511.	0.7	11
124	Characterization of the lectin from females of Phlebotomus duboscqi sand flies. FEBS Journal, 2002, 269, 6294-6301.	0.2	39
125	Activation of macrophages by gliadin fragments: isolation and characterization of active peptide. Journal of Leukocyte Biology, 2002, 71, 625-31.	1.5	56
126	Characterization of the rplB Gene from Streptomyces collinus and Its Protein Product by Mass Spectrometry. Biochemical and Biophysical Research Communications, 2001, 285, 1344-1349.	1.0	5

#	ARTICLE	IF	CITATIONS
127	Identification of HL60 Proteins Affected by 5-Aminolevulinic Acid-Based Photodynamic Therapy Using Mass Spectrometric Approach. Collection of Czechoslovak Chemical Communications, 2001, 66, 1720-1728.	1.0	10