

Francesc Xavier AvilÃ©s i Puigvert

List of Publications by Year in descending order

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250
papers

10,321
citations

31976

53
h-index

46799

89
g-index

255
all docs

255
docs citations

255
times ranked

9667
citing authors

#	ARTICLE	IF	CITATIONS
1	Analysis of the mast cell expressed carboxypeptidase A3 and its structural and evolutionary relationship to other vertebrate carboxypeptidases. <i>Developmental and Comparative Immunology</i> , 2022, 127, 104273.	2.3	9
2	Carboxypeptidase inhibition by NvCI suppresses airway hyperreactivity in a mouse asthma model. <i>Allergy: European Journal of Allergy and Clinical Immunology</i> , 2021, 76, 2234-2237.	5.7	6
3	Substrate Specificity and Structural Modeling of Human Carboxypeptidase Z: A Unique Protease with a Frizzled-Like Domain. <i>International Journal of Molecular Sciences</i> , 2020, 21, 8687.	4.1	3
4	Characterization, Recombinant Production and Structure-Function Analysis of NvCI, A Picomolar Metallo-carboxypeptidase Inhibitor from the Marine Snail <i>Nerita versicolor</i> . <i>Marine Drugs</i> , 2019, 17, 511.	4.6	4
5	Synthesis and Structural/Functional Characterization of Selective M14 Metallo-carboxypeptidase Inhibitors Based on Phosphinic Pseudopeptide Scaffold: Implications on the Design of Specific Optical Probes. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 1917-1931.	6.4	8
6	Inhibitors of aldehyde dehydrogenases of the 1A subfamily as putative anticancer agents: Kinetic characterization and effect on human cancer cells. <i>Chemico-Biological Interactions</i> , 2019, 306, 123-130.	4.0	17
7	Crystal structure and mechanism of human carboxypeptidase O: Insights into its specific activity for acidic residues. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3932-E3939.	7.1	15
8	Biochemical characterization of the YBPCI miniprotein, the first carboxypeptidase inhibitor isolated from Yellow Bell Pepper (<i>Capsicum annuum</i> L). A novel contribution to the knowledge of miniproteins stability. <i>Protein Expression and Purification</i> , 2018, 144, 55-61.	1.3	8
9	Biochemical and MALDI-TOF Mass Spectrometric Characterization of a Novel Native and Recombinant Cystine Knot Miniprotein from <i>Solanum tuberosum</i> subsp. <i>andigenum</i> cv. <i>Churqueña</i> . <i>International Journal of Molecular Sciences</i> , 2018, 19, 678.	4.1	7
10	Intensity fading MALDI-TOF mass spectrometry and functional proteomics assignments to identify protease inhibitors in marine invertebrates. <i>Journal of Proteomics</i> , 2017, 165, 75-92.	2.4	8
11	Identification of Carboxypeptidase Substrates by C-Terminal COFRADIC. <i>Methods in Molecular Biology</i> , 2017, 1574, 115-133.	0.9	4
12	Discovery of Mechanism-Based Inactivators for Human Pancreatic Carboxypeptidase A from a Focused Synthetic Library. <i>ACS Medicinal Chemistry Letters</i> , 2017, 8, 1122-1127.	2.8	8
13	Plasticity in the Oxidative Folding Pathway of the High Affinity <i>Nerita versicolor</i> Carboxypeptidase Inhibitor (NvCI). <i>Scientific Reports</i> , 2017, 7, 5457.	3.3	5
14	A Bowmanâ€™s Birk protease inhibitor purified, cloned, sequenced and characterized from the seeds of <i>Maclura pomifera</i> (Raf.) Schneid. <i>Planta</i> , 2017, 245, 343-353.	3.2	7
15	Identification of Tight-Binding Plasmepsin II and Falcipain 2 Inhibitors in Aqueous Extracts of Marine Invertebrates by the Combination of Enzymatic and Interaction-Based Assays. <i>Marine Drugs</i> , 2017, 15, 123.	4.6	7
16	Substrate specificity of human metallo-carboxypeptidase D: Comparison of the two active carboxypeptidase domains. <i>PLoS ONE</i> , 2017, 12, e0187778.	2.5	6
17	Biochemical characterization of a novel carboxypeptidase inhibitor from a variety of Andean potatoes. <i>Phytochemistry</i> , 2015, 120, 36-45.	2.9	7
18	C-terminomics Screen for Natural Substrates of Cytosolic Carboxypeptidase 1 Reveals Processing of Acidic Protein C termini. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 177-190.	3.8	25

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19	Amyloid Formation by Human Carboxypeptidase D Transthyretin-like Domain under Physiological Conditions. <i>Journal of Biological Chemistry</i> , 2014, 289, 33783-33796.	3.4	18
20	The cytosolic carboxypeptidases CCP2 and CCP3 catalyze posttranslational removal of acidic amino acids. <i>Molecular Biology of the Cell</i> , 2014, 25, 3017-3027.	2.1	62
21	Use of artichoke (<i>Cynara scolymus</i>) flower extract as a substitute for bovine rennet in the manufacture of Gouda-type cheese: Characterization of aspartic proteases. <i>Food Chemistry</i> , 2014, 159, 55-63.	8.2	44
22	Synthesis, biological evaluation and SAR studies of novel bicyclic antitumor platinum(IV) complexes. <i>European Journal of Medicinal Chemistry</i> , 2014, 83, 374-388.	5.5	21
23	A Noncanonical Mechanism of Carboxypeptidase Inhibition Revealed by the Crystal Structure of the Tri-Kunitz SmCl in Complex with Human CPA4. <i>Structure</i> , 2013, 21, 1118-1126.	3.3	11
24	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 2096-2110.	3.8	40
25	Functional segregation and emerging role of cilia-related cytosolic carboxypeptidases (CCPs). <i>FASEB Journal</i> , 2013, 27, 424-431.	0.5	31
26	Carboxypeptidase B. , 2013, , 1324-1329.		4
27	Insect Gut Carboxypeptidase 3. , 2013, , 1370-1375.		0
28	Metallo-carboxypeptidases and their Inhibitors: Recent Developments in Biomedically Relevant Protein and Organic Ligands. <i>Current Medicinal Chemistry</i> , 2013, 20, 1595-1608.	2.4	16
29	Crystal Structure of Novel Metallo-carboxypeptidase Inhibitor from Marine Mollusk <i>Nerita versicolor</i> in Complex with Human Carboxypeptidase A4. <i>Journal of Biological Chemistry</i> , 2012, 287, 9250-9258.	3.4	24
30	The novel structure of a cytosolic M14 metallo-carboxypeptidase (CCP) from <i>Pseudomonas aeruginosa</i> : a model for mammalian CCPs. <i>FASEB Journal</i> , 2012, 26, 3754-3764.	0.5	15
31	Characterization of the proteolytic system present in <i>Vasconcellea quercifolia</i> latex. <i>Planta</i> , 2012, 236, 1471-1484.	3.2	13
32	Tri-domain Bifunctional Inhibitor of Metallo-carboxypeptidases A and Serine Proteases Isolated from Marine Annelid <i>Sabellastarte magnifica</i> . <i>Journal of Biological Chemistry</i> , 2012, 287, 15427-15438.	3.4	23
33	Detection and characterisation of a new metallo-carboxypeptidase inhibitor from <i>Solanum tuberosum</i> cv. Desirée using proteomic techniques. <i>Food Chemistry</i> , 2012, 133, 1163-1168.	8.2	12
34	Linking amyloid protein aggregation and yeast survival. <i>Molecular BioSystems</i> , 2011, 7, 1121.	2.9	26
35	Oxidative Folding and Structural Analyses of a Kunitz-Related Inhibitor and Its Disulfide Intermediates: Functional Implications. <i>Journal of Molecular Biology</i> , 2011, 414, 427-441.	4.2	20
36	Biochemical characterization, cDNA cloning, and molecular modeling of araujiain all, a papain-like cysteine protease from <i>Araujia angustifolia</i> latex. <i>Planta</i> , 2011, 234, 293-304.	3.2	2

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37	Prediction of a new class of RNA recognition motif. <i>Journal of Molecular Modeling</i> , 2011, 17, 1863-1875.	1.8	1
38	Cloning, Sequencing, and Identification Using Proteomic Tools of a Protease from <i>Bromelia hieronymi</i> Mez. <i>Applied Biochemistry and Biotechnology</i> , 2011, 165, 583-593.	2.9	4
39	DNA interaction and cytotoxicity studies of new ruthenium(II) cyclopentadienyl derivative complexes containing heteroaromatic ligands. <i>Journal of Inorganic Biochemistry</i> , 2011, 105, 241-249.	3.5	83
40	Structural and Functional Analysis of the Complex between Citrate and the Zinc Peptidase Carboxypeptidase A. <i>Enzyme Research</i> , 2011, 2011, 1-8.	1.8	11
41	Analysis of a new crystal form of procarboxypeptidase B: Further insights into the catalytic mechanism. <i>Biopolymers</i> , 2010, 93, 178-185.	2.4	11
42	New ruthenium(II) mixed metallocene derived complexes: Synthesis, characterization by X-ray diffraction and evaluation on DNA interaction by atomic force microscopy. <i>Inorganica Chimica Acta</i> , 2010, 363, 3765-3775.	2.4	28
43	Insights into the molecular inactivation mechanism of human activated thrombin-activatable fibrinolysis inhibitor. <i>Journal of Thrombosis and Haemostasis</i> , 2010, 8, 1056-1065.	3.8	14
44	The X-ray Structure of Carboxypeptidase A Inhibited by a Thiirane Mechanism-Based Inhibitor. <i>Chemical Biology and Drug Design</i> , 2010, 75, 29-34.	3.2	10
45	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010, 7, 512-515.	19.0	106
46	Characterization of the Substrate Specificity of Human Carboxypeptidase A4 and Implications for a Role in Extracellular Peptide Processing. <i>Journal of Biological Chemistry</i> , 2010, 285, 18385-18396.	3.4	57
47	Studies of the Antiproliferative Activity of Ruthenium (II) Cyclopentadienyl-Derived Complexes with Nitrogen Coordinated Ligands. <i>Bioinorganic Chemistry and Applications</i> , 2010, 2010, 1-11.	4.1	35
48	MAPI: A Server for Improving Protein Identification from a Four Matrices Mass Spectrometry Approach. <i>Current Proteomics</i> , 2010, 7, 102-107.	0.3	0
49	Flexibility of the Thrombin-activatable Fibrinolysis Inhibitor Pro-domain Enables Productive Binding of Protein Substrates. <i>Journal of Biological Chemistry</i> , 2010, 285, 38243-38250.	3.4	8
50	Purification and Characterization of a Cysteine Endopeptidase from <i>Vasconcellea quercifolia</i> A. St.-Hil. Latex Displaying High Substrate Specificity. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 11027-11035.	5.2	19
51	Structure-Function Analysis of the Short Splicing Variant Carboxypeptidase Encoded by <i>Drosophila melanogaster</i> silver. <i>Journal of Molecular Biology</i> , 2010, 401, 465-477.	4.2	11
52	Progress in metallo-carboxypeptidases and their small molecular weight inhibitors. <i>Biochimie</i> , 2010, 92, 1484-1500.	2.6	41
53	Deciphering the Structural Basis That Guides the Oxidative Folding of Leech-derived Trypsin Inhibitor. <i>Journal of Biological Chemistry</i> , 2009, 284, 35612-35620.	3.4	15
54	Detecting and Interfering Protein Interactions: Towards the Control of Biochemical Pathways. <i>Current Medicinal Chemistry</i> , 2009, 16, 362-379.	2.4	8

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55	Mammalian metallopeptidase inhibition at the defense barrier of <i>Ascaris</i> parasite. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 1743-1747.	7.1	41
56	Protein complementation assays: Approaches for the in vivo analysis of protein interactions. FEBS Letters, 2009, 583, 1684-1691.	2.8	60
57	Sequencing and characterization of asclepain f: the first cysteine peptidase cDNA cloned and expressed from <i>Asclepias fruticosa</i> latex. Planta, 2009, 230, 319-328.	3.2	18
58	Heterogeneity of S-layer proteins from aggregating and non-aggregating <i>Lactobacillus kefir</i> strains. Antonie Van Leeuwenhoek, 2009, 95, 363-372.	1.7	62
59	A novel metalloprotease-like enzyme from the marine annelid <i>Sabellastarte f. magnifica</i> a step into the invertebrate world of proteases. FEBS Journal, 2009, 276, 4875-4890.	4.7	14
60	Aromatic Organic Compounds as Scaffolds for Metalloprotease Inhibitor Design. Chemical Biology and Drug Design, 2009, 73, 75-82.	3.2	4
61	Cytotoxicity studies of [PtCl ₂ (H ₂ bim)] (H ₂ bim=2,2'-biimidazole): Study of its interaction with a small protein PCI (potato carboxypeptidase inhibitor). Inorganica Chimica Acta, 2009, 362, 946-952.	2.4	4
62	A novel vanadyl complex with a polypyridyl DNA intercalator as ligand: A potential anti-protozoa and anti-tumor agent. Journal of Inorganic Biochemistry, 2009, 103, 1386-1394.	3.5	85
63	A new type of five-membered heterocyclic inhibitors of basic metalloproteases. European Journal of Medicinal Chemistry, 2009, 44, 3266-3271.	5.5	7
64	Cyclobutane-containing peptides: Evaluation as novel metalloprotease inhibitors and modelling of their mode of action. Bioorganic and Medicinal Chemistry, 2009, 17, 3824-3828.	3.0	42
65	Insights into the Two-Domain Architecture of the Metalloprotease Inhibitor from the <i>Ascaris</i> Parasite Inferred from the Mechanism of Its Oxidative Folding. Biochemistry, 2009, 48, 8225-8232.	2.5	5
66	Influence of Aggregation Propensity and Stability on Amyloid Fibril Formation As Studied by Fourier Transform Infrared Spectroscopy and Two-Dimensional COSY Analysis. Biochemistry, 2009, 48, 10582-10590.	2.5	28
67	Characterization of papain-like isoenzymes from latex of <i>Asclepias curassavica</i> by molecular biology validated by proteomic approach. Biochimie, 2009, 91, 1457-1464.	2.6	18
68	Designing Out Disulfide Bonds of Leech Carboxypeptidase Inhibitor: Implications for Its Folding, Stability and Function. Journal of Molecular Biology, 2009, 392, 529-546.	4.2	16
69	Molecular dynamics simulation of highly charged proteins: Comparison of the particle-particle, particle-mesh and reaction field methods for the calculation of electrostatic interactions. Protein Science, 2009, 12, 2161-2172.	7.6	42
70	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). Bioinformatics and Biology Insights, 2009, 1, 77-90.	2.0	1
71	Direct interaction between a human digestive protease and the mucoadhesive poly(acrylic acid). Acta Crystallographica Section D: Biological Crystallography, 2008, 64, 784-791.	2.5	14
72	Monitoring the interference of protein-protein interactions in vivo by bimolecular fluorescence complementation: the DnaK case. Proteomics, 2008, 8, 3433-3442.	2.2	27

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73	Synthesis, DNA interaction and cytotoxicity studies of cis-[1,2-bis(aminomethyl)cyclohexane]dihalo}platinum(II) complexes. <i>Journal of Inorganic Biochemistry</i> , 2008, 102, 973-987.	3.5	21
74	Synthesis, characterization and antiproliferative studies of the enantiomers of cis-[(1,2-camphordiamine)dichloro]platinum(II) complexes. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 1721-1737.	3.0	39
75	Thioxophosphoranyl aryl- and heteroaryloxiranes as the representants of a new class of metallocoxyypeptidase inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 4823-4828.	3.0	8
76	Study by HPLC-MS of the interaction of platinum antitumor complexes with potato carboxypeptidase inhibitor (PCI). <i>Bioorganic and Medicinal Chemistry</i> , 2008, 16, 6832-6840.	3.0	3
77	Internalization of cystatinâ€¦C in human cell lines. <i>FEBS Journal</i> , 2008, 275, 4571-4582.	4.7	48
78	Study and selection of in vivo protein interactions by coupling bimolecular fluorescence complementation and flow cytometry. <i>Nature Protocols</i> , 2008, 3, 22-33.	12.0	51
79	The molecular analysis of <i>Trypanosoma cruzi</i> metallocoxyypeptidase 1 provides insight into fold and substrate specificity. <i>Molecular Microbiology</i> , 2008, 70, 853-866.	2.5	22
80	Prediction of enzyme function by combining sequence similarity and protein interactions. <i>BMC Bioinformatics</i> , 2008, 9, 249.	2.6	27
81	Inclusion bodies: Specificity in their aggregation process and amyloid-like structure. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2008, 1783, 1815-1825.	4.1	131
82	New Palladium(II) and Platinum(II) Complexes with 9-Aminoacridine: Structures, Luminescence, Theoretical Calculations, and Antitumor Activity. <i>Inorganic Chemistry</i> , 2008, 47, 6990-7001.	4.0	89
83	Structure of Activated Thrombin-Activatable Fibrinolysis Inhibitor, a Molecular Link between Coagulation and Fibrinolysis. <i>Molecular Cell</i> , 2008, 31, 598-606.	9.7	37
84	The NMR Structure and Dynamics of the Two-Domain Tick Carboxypeptidase Inhibitor Reveal Flexibility in Its Free Form and Stiffness upon Binding to Human Carboxypeptidase B. <i>Biochemistry</i> , 2008, 47, 7066-7078.	2.5	19
85	The NMR Structures of the Major Intermediates of the Two-domain Tick Carboxypeptidase Inhibitor Reveal Symmetry in Its Folding and Unfolding Pathways. <i>Journal of Biological Chemistry</i> , 2008, 283, 27110-27120.	3.4	9
86	The Crystal Structure of Thrombin-activable Fibrinolysis Inhibitor (TAFI) Provides the Structural Basis for Its Intrinsic Activity and the Short Half-life of TAFIa. <i>Journal of Biological Chemistry</i> , 2008, 283, 29416-29423.	3.4	31
87	Scrambled Isomers as Key Intermediates in the Oxidative Folding of Ligand Binding Module 5 of the Low Density Lipoprotein Receptor. <i>Journal of Biological Chemistry</i> , 2008, 283, 13627-13637.	3.4	21
88	Oxidative Folding of Leech-Derived Tryptase Inhibitor Via Native Disulfide-Bonded Intermediates. <i>Antioxidants and Redox Signaling</i> , 2008, 10, 77-86.	5.4	11
89	Nnalâ€¦like proteins are active metallocoxyypeptidases of a new and diverse M14 subfamily. <i>FASEB Journal</i> , 2007, 21, 851-865.	0.5	95
90	Metallocoxyypeptidases: Emerging Drug Targets in Biomedicine. <i>Current Pharmaceutical Design</i> , 2007, 13, 347-364.	1.9	12

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91	Metalloproteases: Emerging Drug Targets in Biomedicine. <i>Current Pharmaceutical Design</i> , 2007, 13, 349-366.	1.9	95
92	A novel subfamily of mouse cytosolic carboxypeptidases. <i>FASEB Journal</i> , 2007, 21, 836-850.	0.5	112
93	Early Kinetics of Amyloid Fibril Formation Reveals Conformational Reorganisation of Initial Aggregates. <i>Journal of Molecular Biology</i> , 2007, 366, 1351-1363.	4.2	60
94	Caught after the Act: A Human A-Type Metalloprotease in a Product Complex with a Cleaved Hexapeptide. <i>Biochemistry</i> , 2007, 46, 6921-6930.	2.5	20
95	Ile-Phe Dipeptide Self-Assembly: Clues to Amyloid Formation. <i>Biophysical Journal</i> , 2007, 92, 1732-1741.	0.5	129
96	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). <i>Bioinformatics and Biology Insights</i> , 2007, 1, 117793220700100.	2.0	2
97	Influence of the position of substituents in the cytotoxic activity of trans platinum complexes with hydroxymethyl pyridines. <i>Bioorganic and Medicinal Chemistry</i> , 2007, 15, 969-979.	3.0	41
98	Expression, purification and characterization of porcine pancreatic Carboxypeptidase B from <i>Pichia pastoris</i> for the conversion of recombinant human insulin. <i>Enzyme and Microbial Technology</i> , 2007, 40, 476-480.	3.2	5
99	DNA interaction and antiproliferative behavior of the water soluble platinum supramolecular squares [(en)Pt(N ₃) ₄ (NO ₃) ₈] (en=ethylenediamine, N ₃ =4,4'-bipyridine or Tj ETQq1 1 0.784314 rgBT / Oælock 100f 50 4		
100	Proteomic profiling of a snake venom using high mass detection MALDI-TOF mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 600-606.	2.8	27
101	Self-assembly of human latexin into amyloid-like oligomers. <i>BMC Structural Biology</i> , 2007, 7, 75.	2.3	6
102	Structural and functional characterization of binding sites in metalloproteases based on Optimal Docking Area analysis. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 131-144.	2.6	10
103	Detection of transient protein-protein interactions by bimolecular fluorescence complementation: The Abl-SH3 case. <i>Proteomics</i> , 2007, 7, 1023-1036.	2.2	85
104	Detection of non-covalent protein interactions by 'intensity fading' MALDI-TOF mass spectrometry: applications to proteases and protease inhibitors. <i>Nature Protocols</i> , 2007, 2, 119-130.	12.0	34
105	A potato carboxypeptidase inhibitor gene provides pathogen resistance in transgenic rice. <i>Plant Biotechnology Journal</i> , 2007, 5, 537-553.	8.3	45
106	AGGRESKAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. <i>BMC Bioinformatics</i> , 2007, 8, 65.	2.6	845
107	Exploring the "intensity fading" phenomenon in the study of noncovalent interactions by MALDI-TOF mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , 2007, 18, 359-367.	2.8	20
108	Recombinant expression of disulfide-rich proteins: carboxypeptidase inhibitors as model proteins. <i>Microbial Cell Factories</i> , 2006, 5, P47.	4.0	1

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109	Palladium(II) and Platinum(II) Organometallic Complexes with the Model Nucleobase Anions of Thymine, Uracil, and Cytosine: Antitumor Activity and Interactions with DNA of the Platinum Compounds. <i>Inorganic Chemistry</i> , 2006, 45, 6347-6360.	4.0	82
110	Proteome of the Bacterium <i>Mycoplasma penetrans</i> . <i>Journal of Proteome Research</i> , 2006, 5, 688-694.	3.7	20
111	Detection of Noncovalent Complexes in Biological Samples by Intensity Fading and High-Mass Detection MALDI-TOF Mass Spectrometry. <i>Journal of Proteome Research</i> , 2006, 5, 2711-2719.	3.7	28
112	Response of the digestive system of <i>Helicoverpa zea</i> to ingestion of potato carboxypeptidase inhibitor and characterization of an uninhibited carboxypeptidase B. <i>Insect Biochemistry and Molecular Biology</i> , 2006, 36, 654-664.	2.7	34
113	Mutagenesis of the central hydrophobic cluster in A β 42 Alzheimer's peptide. Side-chain properties correlate with aggregation propensities. <i>FEBS Journal</i> , 2006, 273, 658-668.	4.7	164
114	Isolation and Characterization of Hieronymain II, Another Peptidase Isolated from Fruits of <i>Bromelia hieronymi</i> Mez (Bromeliaceae). <i>Protein Journal</i> , 2006, 25, 224-231.	1.6	25
115	Folding of small disulfide-rich proteins: clarifying the puzzle. <i>Trends in Biochemical Sciences</i> , 2006, 31, 292-301.	7.5	154
116	Characterizing the Tick Carboxypeptidase Inhibitor. <i>Journal of Biological Chemistry</i> , 2006, 281, 22906-22916.	3.4	17
117	Identification of function-associated loop motifs and application to protein function prediction. <i>Bioinformatics</i> , 2006, 22, 2237-2243.	4.1	41
118	NMR Structural Characterization and Computational Predictions of the Major Intermediate in Oxidative Folding of Leech Carboxypeptidase Inhibitor. <i>Structure</i> , 2005, 13, 1193-1202.	3.3	18
119	Synthesis, Characterization and Biological Activity of trans-Platinum(II) and trans-Platinum(IV) Complexes with 4-Hydroxymethylpyridine. <i>ChemBioChem</i> , 2005, 6, 2068-2077.	2.6	19
120	Detailed molecular comparison between the inhibition mode of A/B-type carboxypeptidases in the zymogen state and by the endogenous inhibitor latexin. <i>Cellular and Molecular Life Sciences</i> , 2005, 62, 1996-2014.	5.4	19
121	Multiple insect resistance in transgenic tomato plants over-expressing two families of plant proteinase inhibitors. <i>Plant Molecular Biology</i> , 2005, 57, 189-202.	3.9	130
122	Prediction of "hot spots" of aggregation in disease-linked polypeptides. <i>BMC Structural Biology</i> , 2005, 5, 18.	2.3	173
123	Prediction of the conformation and geometry of loops in globular proteins: Testing ArchDB, a structural classification of loops. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 60, 746-757.	2.6	21
124	Structural basis of the resistance of an insect carboxypeptidase to plant protease inhibitors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 16602-16607.	7.1	64
125	Functional Screening of Serine Protease Inhibitors in the Medical Leech <i>Hirudo medicinalis</i> Monitored by Intensity Fading MALDI-TOF MS. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1602-1613.	3.8	29
126	Structure of human carboxypeptidase A4 with its endogenous protein inhibitor, latexin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 3978-3983.	7.1	89

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127	Detecting remotely related proteins by their interactions and sequence similarity. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 7151-7156.	7.1	26
128	A Carboxypeptidase Inhibitor from the Tick Rhipicephalus bursa. Journal of Biological Chemistry, 2005, 280, 3441-3448.	3.4	70
129	The Three-Dimensional Structures of Tick Carboxypeptidase Inhibitor in Complex with A/B Carboxypeptidases Reveal a Novel Double-headed Binding Mode. Journal of Molecular Biology, 2005, 350, 489-498.	4.2	57
130	Study of a Major Intermediate in the Oxidative Folding of Leech Carboxypeptidase Inhibitor: Contribution of the Fourth Disulfide Bond. Journal of Molecular Biology, 2005, 352, 961-975.	4.2	17
131	Mechanism of action of potato carboxypeptidase inhibitor (PCI) as an EGF blocker. Cancer Letters, 2005, 226, 169-184.	7.2	30
132	New Palladium(II) and Platinum(II) Complexes with the Model Nucleobase 1-Methylcytosine: Antitumor Activity and Interactions with DNA. Inorganic Chemistry, 2005, 44, 7365-7376.	4.0	107
133	Human kallikrein 6 activity is regulated via an autoproteolytic mechanism of activation/inactivation. Biological Chemistry, 2004, 385, 517-24.	2.5	62
134	Short amino acid stretches can mediate amyloid formation in globular proteins: The Src homology 3 (SH3) case. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 7258-7263.	7.1	241
135	Role of Kinetic Intermediates in the Folding of Leech Carboxypeptidase Inhibitor. Journal of Biological Chemistry, 2004, 279, 37261-37270.	3.4	26
136	ArchDB: automated protein loop classification as a tool for structural genomics. Nucleic Acids Research, 2004, 32, 185D-188.	14.5	61
137	TrSDB: a proteome database of transcription factors. Nucleic Acids Research, 2004, 32, 171D-173.	14.5	14
138	Funastrain c II: A Cysteine Endopeptidase Purified from the Latex of Funastrum clausum. Protein Journal, 2004, 23, 205-215.	1.6	30
139	Purification and Biochemical Characterization of Asclepain c I from the Latex of Asclepias curassavica L.. Protein Journal, 2004, 23, 403-411.	1.6	32
140	Classification of common functional loops of kinase super-families. Proteins: Structure, Function and Bioinformatics, 2004, 56, 539-555.	2.6	23
141	Water-soluble platinum(II) complexes of diamine chelating ligands bearing amino-acid type substituents: the effect of the linked amino acid and the diamine chelate ring size on antitumor activity, and interactions with 5'-GMP and DNA. Journal of Inorganic Biochemistry, 2004, 98, 1933-1946.	3.5	39
142	Secondary Binding Site of the Potato Carboxypeptidase Inhibitor. Contribution to Its Structure, Folding, and Biological Properties. Biochemistry, 2004, 43, 7973-7982.	2.5	18
143	Analysis of Phenetic Trees Based on Metabolic Capabilities Across the Three Domains of Life. Journal of Molecular Biology, 2004, 340, 491-512.	4.2	35
144	Amyloid Fibril Formation by a Partially Structured Intermediate State of β -Chymotrypsin. Journal of Molecular Biology, 2004, 342, 321-331.	4.2	206

#	ARTICLE	IF	CITATIONS
145	Intensity-fading MALDI-TOF-MS: novel screening for ligand binding and drug discovery. Drug Discovery Today: TARGETS, 2004, 3, 23-30.	0.5	9
146	Carboxypeptidase B. , 2004, , 831-833.		1
147	Analysis of Protein-Protein Interactions in Complex Biological Samples by MALDI TOF MS. Feasibility and Use of the Intensity-Fading (IF-) Approach. Principles and Practice, 2004, , 183-202.	0.3	0
148	Platinum complexes of diamino-carboxylic acids and their ethyl ester derivatives: the effect of the chelate ring size on antitumor activity and interactions with GMP and DNA. Journal of Inorganic Biochemistry, 2003, 96, 493-502.	3.5	45
149	Procarboxypeptidase A from the insect pest <i>Helicoverpa armigera</i> and its derived enzyme. FEBS Journal, 2003, 270, 3026-3035.	0.2	27
150	Analysis of the effect of potato carboxypeptidase inhibitor pro-sequence on the folding of the mature protein. FEBS Journal, 2003, 270, 3641-3650.	0.2	10
151	Structure and dynamics of the potato carboxypeptidase inhibitor by 1H and 15N NMR. Proteins: Structure, Function and Bioinformatics, 2003, 50, 410-422.	2.6	19
152	NMR solution structure of the activation domain of human procarboxypeptidase A2. Protein Science, 2003, 12, 296-305.	7.6	9
153	Major Kinetic Traps for the Oxidative Folding of Leech Carboxypeptidase Inhibitor. Biochemistry, 2003, 42, 6754-6761.	2.5	26
154	Ligand Screening by Exoproteolysis and Mass Spectrometry in Combination With Computer Modelling. Journal of Molecular Biology, 2003, 330, 1039-1048.	4.2	10
155	Identification of Protein Ligands in Complex Biological Samples Using Intensity-Fading MALDI-TOF Mass Spectrometry. Analytical Chemistry, 2003, 75, 3385-3395.	6.5	30
156	SNOW: Standard Nomenclature Wizard to help searching for (bio) chemical standardized names. Bioinformatics, 2003, 19, 2492-2493.	4.1	1
157	Monitoring disappearance of monomers and generation of resistance to proteolysis during the formation of the activation domain of human procarboxypeptidase A2 (ADA2h) amyloid fibrils by matrix-assisted laser-desorption ionization-time-of-flight-MS. Biochemical Journal, 2003, 374, 489-495.	3.7	8
158	The Structure of Human Prokallikrein 6 Reveals a Novel Activation Mechanism for the Kallikrein Family. Journal of Biological Chemistry, 2002, 277, 27273-27281.	3.4	74
159	The Unfolding Pathway of Leech Carboxypeptidase Inhibitor. Journal of Biological Chemistry, 2002, 277, 17538-17543.	3.4	19
160	TranScout: prediction of gene expression regulatory proteins from their sequences. Bioinformatics, 2002, 18, 597-607.	4.1	9
161	Identification and Characterization of Three Members of the Human Metallo-carboxypeptidase Gene Family. Journal of Biological Chemistry, 2002, 277, 14954-14964.	3.4	69
162	Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). Journal of Molecular Biology, 2002, 321, 537-547.	4.2	66

#	ARTICLE	IF	CITATIONS
163	Protein secondary structure and stability determined by combining exoproteolysis and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. <i>Journal of Mass Spectrometry</i> , 2002, 37, 974-984.	1.6	16
164	Human betacellulin structure modeled from other members of EGF family. <i>Journal of Molecular Modeling</i> , 2002, 8, 131-144.	1.8	4
165	Structural similarity to link sequence space: New potential superfamilies and implications for structural genomics. <i>Protein Science</i> , 2002, 11, 1101-1116.	7.6	20
166	Automated structure-based prediction of functional sites in proteins: applications to assessing the validity of inheriting protein function from homology in genome annotation and to protein docking. <i>Journal of Molecular Biology</i> , 2001, 311, 395-408.	4.2	230
167	Crystal structure of a novel Mid-gut procarboxypeptidase from the cotton pest <i>Helicoverpa armigera</i> . <i>Journal of Molecular Biology</i> , 2001, 313, 629-638.	4.2	42
168	Monitoring the expression and purification of recombinant proteins by MALDI-TOF mass spectrometry. <i>Enzyme and Microbial Technology</i> , 2001, 29, 99-103.	3.2	13
169	Classification of protein disulphide-bridge topologies. <i>Journal of Computer-Aided Molecular Design</i> , 2001, 15, 477-487.	2.9	16
170	The Crystal Structure of the Inhibitor-complexed Carboxypeptidase D Domain II and the Modeling of Regulatory Carboxypeptidases. <i>Journal of Biological Chemistry</i> , 2001, 276, 16177-16184.	3.4	71
171	Mutations in the N- and C-terminal Tails of Potato Carboxypeptidase Inhibitor Influence Its Oxidative Refolding Process at the Reshuffling Stage. <i>Journal of Biological Chemistry</i> , 2001, 276, 11683-11690.	3.4	19
172	Structures of scrambled disulfide forms of the potato carboxypeptidase inhibitor predicted by molecular dynamics simulations with constraints. <i>Proteins: Structure, Function and Bioinformatics</i> , 2000, 40, 482-493.	2.6	7
173	Contribution of C-tail residues of potato carboxypeptidase inhibitor to the binding to carboxypeptidase A. <i>FEBS Journal</i> , 2000, 267, 1502-1509.	0.2	18
174	Thermodynamic analysis of helix-engineered forms of the activation domain of human procarboxypeptidase A2. <i>FEBS Journal</i> , 2000, 267, 5891-5899.	0.2	13
175	Structure of a novel leech carboxypeptidase inhibitor determined free in solution and in complex with human carboxypeptidase A2. <i>Nature Structural Biology</i> , 2000, 7, 322-328.	9.7	71
176	Metalloproteases and their protein inhibitors. <i>BBA - Proteins and Proteomics</i> , 2000, 1477, 284-298.	2.1	129
177	Refinement of modelled structures by knowledge-based energy profiles and secondary structure prediction: application to the human procarboxypeptidase A2. <i>Journal of Computer-Aided Molecular Design</i> , 2000, 14, 83-92.	2.9	8
178	Protein engineering as a strategy to avoid formation of amyloid fibrils. <i>Protein Science</i> , 2000, 9, 1700-1708.	7.6	109
179	A generalized Langevin dynamics approach to model solvent dynamics effects on proteins via a solvent-accessible surface. The carboxypeptidase A inhibitor protein as a model. <i>Theoretical Chemistry Accounts</i> , 2000, 105, 101-109.	1.4	10
180	The Unfolding Pathway and Conformational Stability of Potato Carboxypeptidase Inhibitor. <i>Journal of Biological Chemistry</i> , 2000, 275, 14205-14211.	3.4	29

#	ARTICLE	IF	CITATIONS
181	Hydrogen exchange monitored by MALDI-TOF mass spectrometry for rapid characterization of the stability and conformation of proteins. <i>FEBS Letters</i> , 2000, 472, 27-33.	2.8	25
182	Purification of Balansain I, an Endopeptidase from Unripe Fruits of <i>Bromelia balansae</i> Mez (Bromeliaceae). <i>Journal of Agricultural and Food Chemistry</i> , 2000, 48, 3795-3800.	5.2	38
183	The identification of nuclear proteins that bind the homopyrimidine strand of d(GATC) _n DNA sequences, but not the homopurine strand. <i>Nucleic Acids Research</i> , 1999, 27, 3267-3275.	14.5	12
184	Mapping the Pro-region of Carboxypeptidase B by Protein Engineering. <i>Journal of Biological Chemistry</i> , 1999, 274, 19925-19933.	3.4	45
185	Application of matrix-assisted laser desorption/ionization time-of-flight mass spectrometry to the structure determination of medium and large macrocycles formed by palladium(0)-catalyzed allylation of arenesulfonamides, sulfamide, and cyanamide. , 1999, 13, 2359-2365.		3
186	Crystal structure of avian carboxypeptidase D domain II: a prototype for the regulatory metallocarboxypeptidase subfamily. <i>EMBO Journal</i> , 1999, 18, 5817-5826.	7.8	71
187	Detection of Molecular Interactions by Using a New Peptide-Displaying Bacteriophage Biosensor. <i>Biochemical and Biophysical Research Communications</i> , 1999, 262, 801-805.	2.1	6
188	Carboxypeptidases. , 1999, , 13-34.		8
189	Cloning, sequencing and functional expression of a cDNA encoding porcine pancreatic preprocarboxypeptidase A1. <i>FEBS Journal</i> , 1999, 259, 719-726.	0.2	8
190	Cutting at the right place. The importance of selective limited proteolysis in the activation of proproteinase E. <i>FEBS Journal</i> , 1998, 251, 839-844.	0.2	7
191	Modelling repressor proteins docking to DNA. , 1998, 33, 535-549.		48
192	Statistical Analysis of the Loop-Geometry on a Non-Redundant Database of Proteins. <i>Journal of Molecular Modeling</i> , 1998, 4, 347-354.	1.8	4
193	Characterization of the wound-induced metallocarboxypeptidase inhibitor from potato1. <i>FEBS Letters</i> , 1998, 440, 175-182.	2.8	42
194	Automated classification of antibody complementarity determining region 3 of the heavy chain (H3) loops into canonical forms and its application to protein structure prediction. <i>Journal of Molecular Biology</i> , 1998, 279, 1193-1210.	4.2	80
195	Refolding of potato carboxypeptidase inhibitor by molecular dynamics simulations with disulfide bond constraints aEdited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1998, 284, 145-172.	4.2	25
196	Conformational flexibility in a highly mobile protein loop of foot-and-mouth disease virus: distinct structural requirements for integrin and antibody binding 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1998, 283, 331-338.	4.2	20
197	Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. <i>Journal of Molecular Biology</i> , 1998, 283, 1027-1036.	4.2	165
198	Protein similarities beyond disulphide bridge topology. <i>Journal of Molecular Biology</i> , 1998, 284, 541-548.	4.2	34

#	ARTICLE	IF	CITATIONS
199	Comparative Analysis of the Sequences and Three-Dimensional Models of Human Procarboxypeptidases A1, A2 and B. <i>Biological Chemistry</i> , 1998, 379, 149-156.	2.5	13
200	A Carboxypeptidase Inhibitor from the Medical Leech <i>Hirudo medicinalis</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 32927-32933.	3.4	78
201	Potato Carboxypeptidase Inhibitor, a T-knot Protein, Is an Epidermal Growth Factor Antagonist That Inhibits Tumor Cell Growth. <i>Journal of Biological Chemistry</i> , 1998, 273, 12370-12377.	3.4	78
202	Overexpression of Human Procarboxypeptidase A2 in <i>Pichia pastoris</i> and Detailed Characterization of Its Activation Pathway. <i>Journal of Biological Chemistry</i> , 1998, 273, 3535-3541.	3.4	52
203	An automated classification of the structure of protein loops. <i>Journal of Molecular Biology</i> , 1997, 266, 814-830.	4.2	189
204	Crystal structure of an oligomer of proteolytic zymogens: detailed conformational analysis of the bovine ternary complex and implications for their activation 1 Edited by I. A. Wilson. <i>Journal of Molecular Biology</i> , 1997, 269, 861-880.	4.2	28
205	Inhibition of carboxypeptidase A by excess zinc: analysis of the structural determinants by X-ray crystallography. <i>FEBS Letters</i> , 1997, 400, 336-340.	2.8	81
206	Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2. <i>FEBS Letters</i> , 1997, 420, 7-10.	2.8	19
207	Favourable native-like helical local interactions can accelerate protein folding. <i>Folding & Design</i> , 1997, 2, 23-33.	4.5	92
208	The three-dimensional structure of human procarboxypeptidase A2. Deciphering the basis of the inhibition, activation and intrinsic activity of the zymogen. <i>EMBO Journal</i> , 1997, 16, 6906-6913.	7.8	92
209	Free Energies of Transfer of Trp Analogs from Chloroform to Water: A Comparison of Theory and Experiment and the Importance of Adequate Treatment of Electrostatic and Internal Interactions. <i>Journal of the American Chemical Society</i> , 1996, 118, 6285-6294.	13.7	52
210	On the sensitivity of MD trajectories to changes in water-protein interaction parameters: The potato carboxypeptidase inhibitor in water as a test case for the GROMOS force field. , 1996, 25, 89-103.		37
211	Determination of hemihedral twinning and initial structural analysis of crystals of the procarboxypeptidase A ternary complex. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1995, 51, 819-823.	2.5	2
212	Structure and atomic fluctuation patterns of potato carboxypeptidase a inhibitor protein. <i>European Biophysics Journal</i> , 1995, 24, 1-11.	2.2	7
213	The activation pathway of procarboxypeptidase B from porcine pancreas: Participation of the active enzyme in the proteolytic processing. <i>Protein Science</i> , 1995, 4, 1792-1800.	7.6	27
214	The Sequence and Conformation of Human Pancreatic Procarboxypeptidase A2. <i>Journal of Biological Chemistry</i> , 1995, 270, 6651-6657.	3.4	31
215	Crystallization and preliminary X-ray analysis of the ternary complex of procarboxypeptidase A from bovine pancreas. <i>FEBS Letters</i> , 1995, 367, 211-213.	2.8	1
216	Procarboxypeptidase in rat pancreas Overall characterization and comparison of the activation processes. <i>FEBS Journal</i> , 1994, 222, 55-64.	0.2	22

#	ARTICLE	IF	CITATIONS
217	Overproduction of a recombinant carboxypeptidase inhibitor by optimization of fermentation conditions. <i>Applied Microbiology and Biotechnology</i> , 1994, 41, 632-637.	3.6	13
218	On the water-promoted mechanism of peptide cleavage by carboxypeptidase A. A theoretical study. <i>Canadian Journal of Chemistry</i> , 1994, 72, 2077-2083.	1.1	18
219	Advances in metallo-procarboxypeptidases. , 1994, , 19-27.		0
220	Advances in metallo-procarboxypeptidases. Emerging details on the inhibition mechanism and on the activation process. <i>FEBS Journal</i> , 1993, 211, 381-389.	0.2	77
221	Pancreatic Procarboxypeptidases: Their Activation Processes Related to the Structural Features of the Zymogens and Activation Segments. <i>Biological Chemistry Hoppe-Seyler</i> , 1992, 373, 387-392.	1.4	12
222	Expression of a synthetic gene encoding potato carboxypeptidase inhibitor using a bacterial secretion vector. <i>Gene</i> , 1992, 116, 129-138.	2.2	42
223	Three-dimensional structure of porcine pancreatic procarboxypeptidase A. <i>Journal of Molecular Biology</i> , 1992, 224, 141-157.	4.2	117
224	Comparison of the NMR solution structure with the X-ray crystal structure of the activation domain from procarboxypeptidase B. <i>Journal of Biomolecular NMR</i> , 1992, 2, 1-10.	2.8	20
225	Stability and fluctuations of the potato carboxypeptidase a protein inhibitor fold: A molecular dynamics study. <i>Biochemical and Biophysical Research Communications</i> , 1991, 176, 616-621.	2.1	23
226	A molecular dynamics study of a model built Pro-36-Gly mutant derived from the potato carboxypeptidase a inhibitor protein. <i>Biochemical and Biophysical Research Communications</i> , 1991, 176, 627-632.	2.1	7
227	Analysis of the activation process of porcine procarboxypeptidase B and determination of the sequence of its activation segment. <i>Biochemistry</i> , 1991, 30, 4082-4089.	2.5	50
228	Differential scanning calorimetric study of carboxypeptidase B, procarboxypeptidase B and its globular activation domain. <i>FEBS Journal</i> , 1991, 200, 663-670.	0.2	46
229	Autolysis of proproteinase E in bovine procarboxypeptidase A ternary complex gives rise to subunit III. <i>FEBS Letters</i> , 1990, 277, 37-41.	2.8	19
230	Purification and properties of five different forms of human procarboxypeptidases. <i>FEBS Journal</i> , 1989, 179, 609-616.	0.2	62
231	Improvements in the application of the 4,4-N,N-Dimethylaminoazobenzene-4- α -isothiocyanate micromethod to the sequence analysis of proteins. <i>Analytical Biochemistry</i> , 1989, 180, 374-379.	2.4	3
232	Kinetic analysis of the carboxypeptidase a hydrolysis of oligopeptides by reversed-phase high-performance liquid chromatography. <i>Journal of Chromatography A</i> , 1989, 479, 27-37.	3.7	3
233	The separation of pancreatic procarboxypeptidases by high-performance liquid chromatography and chromatofocusing. <i>Journal of Chromatography A</i> , 1989, 481, 233-243.	3.7	7
234	Computerized sequence-based predictive methods: their use in the conformational characterization of proteins and in the analysis of their homologies a practical case employing lysozyme and β -lactalbumin. <i>Biochemical Education</i> , 1989, 17, 36-41.	0.1	1

#	ARTICLE	IF	CITATIONS
235	Generation of a subunit III-like protein by autolysis of human and porcine proproteinase E in a binary complex with procarboxypeptidase A. <i>Biochemical and Biophysical Research Communications</i> , 1989, 163, 1191-1196.	2.1	9
236	Enzymatic and chemical fragmentation of proteins: A simple laboratory visualization of differences in yield, specificity and applicability. <i>Biochemical Education</i> , 1988, 16, 174-176.	0.1	2
237	Primary structure of the activation segment of procarboxypeptidase a from porcine pancreas. <i>Biochemical and Biophysical Research Communications</i> , 1986, 141, 517-523.	2.1	26
238	Regeneration of reversed-phase high-performance liquid chromatographic columns by flow reversal. <i>Journal of Chromatography A</i> , 1986, 356, 420-422.	3.7	5
239	Complete amino acid analysis of proteins by dabsyl derivatization and reversed-phase liquid chromatography. <i>Journal of Chromatography A</i> , 1986, 358, 401-413.	3.7	88
240	A scanning microcalorimetric study of procarboxypeptidase A and its tryptic pieces carboxypeptidase A and activation segment. <i>Biochemical Society Transactions</i> , 1985, 13, 343-344.	3.4	2
241	Nuclear magnetic resonance studies on the isolated activation segment from porcine pancreatic procarboxypeptidase A. <i>Biochemical Society Transactions</i> , 1985, 13, 344-345.	3.4	0
242	Sequential homologies between procarboxypeptidases A and B from porcine pancreas. <i>Biochemical and Biophysical Research Communications</i> , 1985, 130, 97-103.	2.1	15
243	Urea-gradient gel electrophoresis studies on the association of procarboxypeptidases A and B, proproteinase E, and their tryptic activation products. <i>FEBS Letters</i> , 1985, 191, 273-277.	2.8	26
244	Isolation and re-association of the subunits from the pro-(carboxypeptidase A)â€“pro-(proteinase E) binary complex from pig pancreas. <i>Biochemical Journal</i> , 1982, 205, 449-452.	3.7	17
245	The activation segment of procarboxypeptidase A from porcine pancreas constitutes a folded structural domain. <i>FEBS Letters</i> , 1982, 149, 257-260.	2.8	19
246	The severed activation segment of porcine pancreatic procarboxypeptidase a is a powerful inhibitor of the active enzyme Isolation and characterisation of the activation peptide. <i>BBA - Proteins and Proteomics</i> , 1982, 707, 74-80.	2.1	61
247	The Central Tryptic Fragment of Histones H1 and H5 Is a Fully Compacted Domain and Is the Only Folded Region in the Polypeptide Chain. A Thermodynamic Study. <i>FEBS Journal</i> , 1982, 122, 327-331.	0.2	31
248	Specific interaction of histone H1 with eukaryotic DNA. <i>Nucleic Acids Research</i> , 1981, 9, 1383-1394.	14.5	13
249	The structure of histone H1 and its location in chromatin. <i>Nature</i> , 1980, 288, 675-679.	27.8	710
250	On the interaction of histone H1 and H1 peptides with DNA. <i>Biochimie</i> , 1978, 60, 445-451.	2.6	9