

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	AGGRESKAN: a server for the prediction and evaluation of "hot spots" of aggregation in polypeptides. BMC Bioinformatics, 2007, 8, 65.	2.6	845
2	The structure of histone H1 and its location in chromatin. Nature, 1980, 288, 675-679.	27.8	710
3	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
4	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. Journal of Molecular Biology, 2001, 311, 395-408.	4.2	230
5	Amyloid Fibril Formation by a Partially Structured Intermediate State of Î±-Chymotrypsin. Journal of Molecular Biology, 2004, 342, 321-331.	4.2	206
6	An automated classification of the structure of protein loops. Journal of Molecular Biology, 1997, 266, 814-830.	4.2	189
7	Prediction of "hot spots" of aggregation in disease-linked polypeptides. BMC Structural Biology, 2005, 5, 18.	2.3	173
8	Structure of the transition state in the folding process of human procarboxypeptidase A2 activation domain. Journal of Molecular Biology, 1998, 283, 1027-1036.	4.2	165
9	Mutagenesis of the central hydrophobic cluster in Aβ42 Alzheimer's peptide. Side-chain properties correlate with aggregation propensities. FEBS Journal, 2006, 273, 658-668.	4.7	164
10	Folding of small disulfide-rich proteins: clarifying the puzzle. Trends in Biochemical Sciences, 2006, 31, 292-301.	7.5	154
11	Inclusion bodies: Specificity in their aggregation process and amyloid-like structure. Biochimica Et Biophysica Acta - Molecular Cell Research, 2008, 1783, 1815-1825.	4.1	131
12	Multiple insect resistance in transgenic tomato plants over-expressing two families of plant proteinase inhibitors. Plant Molecular Biology, 2005, 57, 189-202.	3.9	130
13	Metalloproteases and their protein inhibitors. BBA - Proteins and Proteomics, 2000, 1477, 284-298.	2.1	129
14	Ile-Phe Dipeptide Self-Assembly: Clues to Amyloid Formation. Biophysical Journal, 2007, 92, 1732-1741.	0.5	129
15	Three-dimensional structure of porcine pancreatic procarboxypeptidase A. Journal of Molecular Biology, 1992, 224, 141-157.	4.2	117
16	A novel subfamily of mouse cytosolic carboxypeptidases. FASEB Journal, 2007, 21, 836-850.	0.5	112
17	Protein engineering as a strategy to avoid formation of amyloid fibrils. Protein Science, 2000, 9, 1700-1708.	7.6	109
18	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

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19	Complementary positional proteomics for screening substrates of endo- and exoproteases. <i>Nature Methods</i> , 2010, 7, 512-515.	19.0	106
20	Nnalá€like proteins are active metallo-carboxypeptidases of a new and diverse M14 subfamily. <i>FASEB Journal</i> , 2007, 21, 851-865.	0.5	95
21	Metallo-carboxypeptidases: Emerging Drug Targets in Biomedicine. <i>Current Pharmaceutical Design</i> , 2007, 13, 349-366.	1.9	95
22	Favourable native-like helical local interactions can accelerate protein folding. <i>Folding & Design</i> , 1997, 2, 23-33.	4.5	92
23	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
24	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
25	New Palladium(II) and Platinum(II) Complexes with 9-Aminoacridine: Structures, Luminiscence, Theoretical Calculations, and Antitumor Activity. <i>Inorganic Chemistry</i> , 2008, 47, 6990-7001.	4.0	89
26	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
27	Detection of transient proteinâ€protein interactions by bimolecular fluorescence complementation: The Abl-SH3 case. <i>Proteomics</i> , 2007, 7, 1023-1036.	2.2	85
28	A novel vanadyl complex with a polypyridyl DNA intercalator as ligand: A potential anti-protozoa and anti-tumor agent. <i>Journal of Inorganic Biochemistry</i> , 2009, 103, 1386-1394.	3.5	85
29	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
30	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 Compoundsâ€€. <i>Inorganic Chemistry</i> , 2006, 45, 6347-6360.	4.0	82
31	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
32	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
33	A Carboxypeptidase Inhibitor from the Medical Leech <i>Hirudo medicinalis</i> . <i>Journal of Biological Chemistry</i> , 1998, 273, 32927-32933.	3.4	78
34	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
35	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
36	The Structure of Human Prokallikrein 6 Reveals a Novel Activation Mechanism for the Kallikrein Family. <i>Journal of Biological Chemistry</i> , 2002, 277, 27273-27281.	3.4	74

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37	Crystal structure of avian carboxypeptidase D domain II: a prototype for the regulatory metallo-carboxypeptidase subfamily. <i>EMBO Journal</i> , 1999, 18, 5817-5826.	7.8	71
38	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
39	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
40	A Carboxypeptidase Inhibitor from the Tick <i>Rhipicephalus bursa</i> . <i>Journal of Biological Chemistry</i> , 2005, 280, 3441-3448.	3.4	70
41	Identification and Characterization of Three Members of the Human Metallo-carboxypeptidase Gene Family. <i>Journal of Biological Chemistry</i> , 2002, 277, 14954-14964.	3.4	69
42	Human Procarboxypeptidase B: Three-dimensional Structure and Implications for Thrombin-activatable Fibrinolysis Inhibitor (TAFI). <i>Journal of Molecular Biology</i> , 2002, 321, 537-547.	4.2	66
43	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
44	Purification and properties of five different forms of human procarboxypeptidases. <i>FEBS Journal</i> , 1989, 179, 609-616.	0.2	62
45	Human kallikrein 6 activity is regulated via an autoproteolytic mechanism of activation/inactivation. <i>Biological Chemistry</i> , 2004, 385, 517-24.	2.5	62
46	Heterogeneity of S-layer proteins from aggregating and non-aggregating <i>Lactobacillus kefir</i> strains. <i>Antonie Van Leeuwenhoek</i> , 2009, 95, 363-372.	1.7	62
47	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
48	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
49	ArchDB: automated protein loop classification as a tool for structural genomics. <i>Nucleic Acids Research</i> , 2004, 32, 185D-188.	14.5	61
50	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
51	Protein complementation assays: Approaches for the in vivo analysis of protein interactions. <i>FEBS Letters</i> , 2009, 583, 1684-1691.	2.8	60
52	The Three-Dimensional Structures of Tick Carboxypeptidase Inhibitor in Complex with A/B Carboxypeptidases Reveal a Novel Double-headed Binding Mode. <i>Journal of Molecular Biology</i> , 2005, 350, 489-498.	4.2	57
53	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
54	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

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55	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
56	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
57	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
58	DNA interaction and antiproliferative behavior of the water soluble platinum supramolecular squares [(en)Pt(Nâ€“N)] ₄ (NO ₃) ₈ (en=ethylenediamine, Nâ€“N=4,4â€“bipyridine or Tj ETQqO O O rgBT /Overlock 10 Tf 50 6â€“7 Td (1,4-	10.5	50
59	Modelling repressor proteins docking to DNA. , 1998, 33, 535-549.		48
60	Internalization of cystatinâ€“fC in human cell lines. <i>FEBS Journal</i> , 2008, 275, 4571-4582.	4.7	48
61	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
62	Mapping the Pro-region of Carboxypeptidase B by Protein Engineering. <i>Journal of Biological Chemistry</i> , 1999, 274, 19925-19933.	3.4	45
63	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. <i>Journal of Inorganic Biochemistry</i> , 2003, 96, 493-502.	3.5	45
64	A potato carboxypeptidase inhibitor gene provides pathogen resistance in transgenic rice. <i>Plant Biotechnology Journal</i> , 2007, 5, 537-553.	8.3	45
65	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
66	Expression of a synthetic gene encoding potato carboxypeptidase inhibitor using a bacterial secretion vector. <i>Gene</i> , 1992, 116, 129-138.	2.2	42
67	Characterization of the wound-induced metallo-carboxypeptidase inhibitor from potato1. <i>FEBS Letters</i> , 1998, 440, 175-182.	2.8	42
68	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
69	Cyclobutane-containing peptides: Evaluation as novel metallo-carboxypeptidase inhibitors and modelling of their mode of action. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 3824-3828.	3.0	42
70	Molecular dynamics simulation of highly charged proteins: Comparison of the particle-particle particle-mesh and reaction field methods for the calculation of electrostatic interactions. <i>Protein Science</i> , 2009, 12, 2161-2172.	7.6	42
71	Identification of function-associated loop motifs and application to protein function prediction. <i>Bioinformatics</i> , 2006, 22, 2237-2243.	4.1	41
72	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

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73	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
74	Progress in metallo-carboxypeptidases and their small molecular weight inhibitors. Biochimie, 2010, 92, 1484-1500.	2.6	41
75	Proteome-derived Peptide Libraries to Study the Substrate Specificity Profiles of Carboxypeptidases. Molecular and Cellular Proteomics, 2013, 12, 2096-2110.	3.8	40
76	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
77	Synthesis, characterization and antiproliferative studies of the enantiomers of <i>cis</i> -[(1,2-camphordiamine)dichloro]platinum(II) complexes. Bioorganic and Medicinal Chemistry, 2008, 16, 1721-1737.	3.0	39
78	Purification of Balansain I, an Endopeptidase from Unripe Fruits of <i>Bromelia balansae</i> Mez (Bromeliaceae). Journal of Agricultural and Food Chemistry, 2000, 48, 3795-3800.	5.2	38
79	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
80	Structure of Activated Thrombin-Activatable Fibrinolysis Inhibitor, a Molecular Link between Coagulation and Fibrinolysis. Molecular Cell, 2008, 31, 598-606.	9.7	37
81	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
82	Studies of the Antiproliferative Activity of Ruthenium (II) Cyclopentadienyl-Derived Complexes with Nitrogen Coordinated Ligands. Bioinorganic Chemistry and Applications, 2010, 2010, 1-11.	4.1	35
83	Protein similarities beyond disulphide bridge topology. Journal of Molecular Biology, 1998, 284, 541-548.	4.2	34
84	Response of the digestive system of <i>Helicoverpa zea</i> to ingestion of potato carboxypeptidase inhibitor and characterization of an uninhibited carboxypeptidase B. Insect Biochemistry and Molecular Biology, 2006, 36, 654-664.	2.7	34
85	Detection of non-covalent protein interactions by 'intensity fading' MALDI-TOF mass spectrometry: applications to proteases and protease inhibitors. Nature Protocols, 2007, 2, 119-130.	12.0	34
86	Purification and Biochemical Characterization of Asclepain c I from the Latex of <i>Asclepias curassavica</i> L.. Protein Journal, 2004, 23, 403-411.	1.6	32
87	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. FEBS Journal, 1982, 122, 327-331.	0.2	31
88	The Sequence and Conformation of Human Pancreatic Procarboxypeptidase A2. Journal of Biological Chemistry, 1995, 270, 6651-6657.	3.4	31
89	The Crystal Structure of Thrombin-activable Fibrinolysis Inhibitor (TAFI) Provides the Structural Basis for Its Intrinsic Activity and the Short Half-life of TAFIa. Journal of Biological Chemistry, 2008, 283, 29416-29423.	3.4	31
90	Functional segregation and emerging role of cilia-related cytosolic carboxypeptidases (CCPs). FASEB Journal, 2013, 27, 424-431.	0.5	31

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91	Identification of Protein Ligands in Complex Biological Samples Using Intensity-Fading MALDI-TOF Mass Spectrometry. <i>Analytical Chemistry</i> , 2003, 75, 3385-3395.	6.5	30
92	Funastrain c II: A Cysteine Endopeptidase Purified from the Latex of <i>Funastrum clausum</i> . <i>Protein Journal</i> , 2004, 23, 205-215.	1.6	30
93	Mechanism of action of potato carboxypeptidase inhibitor (PCI) as an EGF blocker. <i>Cancer Letters</i> , 2005, 226, 169-184.	7.2	30
94	The Unfolding Pathway and Conformational Stability of Potato Carboxypeptidase Inhibitor. <i>Journal of Biological Chemistry</i> , 2000, 275, 14205-14211.	3.4	29
95	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
96	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
97	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
98	Influence of Aggregation Propensity and Stability on Amyloid Fibril Formation As Studied by Fourier Transform Infrared Spectroscopy and Two-Dimensional COS Analysis. <i>Biochemistry</i> , 2009, 48, 10582-10590.	2.5	28
99	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
100	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
101	Procarboxypeptidase A from the insect pest <i>Helicoverpa armigera</i> and its derived enzyme. <i>FEBS Journal</i> , 2003, 270, 3026-3035.	0.2	27
102	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
103	Monitoring the interference of protein-protein interactions <i>in vivo</i> by bimolecular fluorescence complementation: the DnaK case. <i>Proteomics</i> , 2008, 8, 3433-3442.	2.2	27
104	Prediction of enzyme function by combining sequence similarity and protein interactions. <i>BMC Bioinformatics</i> , 2008, 9, 249.	2.6	27
105	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
106	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
107	Major Kinetic Traps for the Oxidative Folding of Leech Carboxypeptidase Inhibitor. <i>Biochemistry</i> , 2003, 42, 6754-6761.	2.5	26
108	Role of Kinetic Intermediates in the Folding of Leech Carboxypeptidase Inhibitor. <i>Journal of Biological Chemistry</i> , 2004, 279, 37261-37270.	3.4	26

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109	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
110	Linking amyloid protein aggregation and yeast survival. Molecular BioSystems, 2011, 7, 1121.	2.9	26
111	Refolding of potato carboxypeptidase inhibitor by molecular dynamics simulations with disulfide bond constraints a Edited by A. R. Fersht. Journal of Molecular Biology, 1998, 284, 145-172.	4.2	25
112	Hydrogen exchange monitored by MALDI-TOF mass spectrometry for rapid characterization of the stability and conformation of proteins. FEBS Letters, 2000, 472, 27-33.	2.8	25
113	Isolation and Characterization of Hieronymain II, Another Peptidase Isolated from Fruits of Bromelia hieronymi Mez (Bromeliaceae). Protein Journal, 2006, 25, 224-231.	1.6	25
114	C-terminomics Screen for Natural Substrates of Cytosolic Carboxypeptidase 1 Reveals Processing of Acidic Protein C termini. Molecular and Cellular Proteomics, 2015, 14, 177-190.	3.8	25
115	Crystal Structure of Novel Metallo-carboxypeptidase Inhibitor from Marine Mollusk Nerita versicolor in Complex with Human Carboxypeptidase A4. Journal of Biological Chemistry, 2012, 287, 9250-9258.	3.4	24
116	Stability and fluctuations of the potato carboxypeptidase a protein inhibitor fold: A molecular dynamics study. Biochemical and Biophysical Research Communications, 1991, 176, 616-621.	2.1	23
117	Classification of common functional loops of kinase super-families. Proteins: Structure, Function and Bioinformatics, 2004, 56, 539-555.	2.6	23
118	Tri-domain Bifunctional Inhibitor of Metallo-carboxypeptidases A and Serine Proteases Isolated from Marine Annelid Sabellastarte magnifica. Journal of Biological Chemistry, 2012, 287, 15427-15438.	3.4	23
119	Procarboxypeptidase in rat pancreas Overall characterization and comparison of the activation processes. FEBS Journal, 1994, 222, 55-64.	0.2	22
120	The molecular analysis of <i>Trypanosoma cruzi</i> metallo-carboxypeptidase 1 provides insight into fold and substrate specificity. Molecular Microbiology, 2008, 70, 853-866.	2.5	22
121	Prediction of the conformation and geometry of loops in globular proteins: Testing ArchDB, a structural classification of loops. Proteins: Structure, Function and Bioinformatics, 2005, 60, 746-757.	2.6	21
122	Synthesis, DNA interaction and cytotoxicity studies of cis-[1, 2-bis(aminomethyl)cyclohexane]dihalo}platinum(II) complexes. Journal of Inorganic Biochemistry, 2008, 102, 973-987.	3.5	21
123	Scrambled Isomers as Key Intermediates in the Oxidative Folding of Ligand Binding Module 5 of the Low Density Lipoprotein Receptor. Journal of Biological Chemistry, 2008, 283, 13627-13637.	3.4	21
124	Synthesis, biological evaluation and SAR studies of novel bicyclic antitumor platinum(IV) complexes. European Journal of Medicinal Chemistry, 2014, 83, 374-388.	5.5	21
125	Comparison of the NMR solution structure with the X-ray crystal structure of the activation domain from procarboxypeptidase B. Journal of Biomolecular NMR, 1992, 2, 1-10.	2.8	20
126	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. Journal of Molecular Biology, 1998, 283, 331-338.	4.2	20

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127	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
128	Proteome of the Bacterium <i>Mycoplasmagenitrix</i> . <i>Journal of Proteome Research</i> , 2006, 5, 688-694.	3.7	20
129	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
130	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
131	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
132	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
133	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
134	Characterisation and preliminary X-ray diffraction analysis of human pancreatic procarboxypeptidase A2. <i>FEBS Letters</i> , 1997, 420, 7-10.	2.8	19
135	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
136	The Unfolding Pathway of Leech Carboxypeptidase Inhibitor. <i>Journal of Biological Chemistry</i> , 2002, 277, 17538-17543.	3.4	19
137	Structure and dynamics of the potato carboxypeptidase inhibitor by ¹ H and ¹⁵ N NMR. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 50, 410-422.	2.6	19
138	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
139	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
140	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
141	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
142	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
143	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
144	Secondary Binding Site of the Potato Carboxypeptidase Inhibitor. Contribution to Its Structure, Folding, and Biological Properties. <i>Biochemistry</i> , 2004, 43, 7973-7982.	2.5	18

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145	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
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