

# Fabio Polticelli

## List of Publications by Year in descending order

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196  
papers

4,950  
citations

81900

39  
h-index

144013

57  
g-index

200  
all docs

200  
docs citations

200  
times ranked

6204  
citing authors

#	ARTICLE	IF	CITATIONS
1	Insulin-Degrading Enzyme Is a Non Proteasomal Target of Carfilzomib and Affects the 20S Proteasome Inhibition by the Drug. <i>Biomolecules</i> , 2022, 12, 315.	4.0	3
2	FGDB: a comprehensive graph database of ligand fragments from the Protein Data Bank. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	3.0	2
3	Molecular Characterization of Kunitz-Type Protease Inhibitors from Blister Beetles (Coleoptera,) Tj ETQq1 1 0.784314 rgBT /Overlock 10	4.0	1
4	Binding of direct oral anticoagulants to the FA1 site of human serum albumin. <i>Journal of Molecular Recognition</i> , 2021, 34, e2877.	2.1	6
5	In Silico Analysis of Huntingtin Homologs in Lower Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3214.	4.1	1
6	Inhibition by Thyroid Hormones of Cell Migration Activated by IGF-1 and MCP-1 in THP-1 Monocytes: Focus on Signal Transduction Events Proximal to Integrin $\alpha 5 \beta 3$ . <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 651492.	3.7	3
7	Computational studies of the mitochondrial carrier family SLC25. Present status and future perspectives. <i>Bio-Algorithms and Med-Systems</i> , 2021, 17, 65-78.	2.4	2
8	Structural determinants of ligands recognition by the human mitochondrial basic amino acids transporter SLC25A29. Insights from molecular dynamics simulations of the c-state. <i>Computational and Structural Biotechnology Journal</i> , 2021, 19, 5600-5612.	4.1	6
9	Modelling of the Citrus CCD4 Family Members: In Silico Analysis of Membrane Binding and Substrate Preference. <i>International Journal of Molecular Sciences</i> , 2021, 22, 13616.	4.1	2
10	Neonicotinoid trapping by the FA1 site of human serum albumin. <i>IUBMB Life</i> , 2020, 72, 716-723.	3.4	7
11	Uncovering the structure and function of <i>Pseudomonas aeruginosa</i> periplasmic proteins by an in silico approach. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, 38, 4508-4520.	3.5	1
12	Contaminations in (meta)genome data: An open issue for the scientific community. <i>IUBMB Life</i> , 2020, 72, 698-705.	3.4	13
13	Haptoglobin and the related haptoglobin protein: the N-terminus makes the difference. <i>Journal of Biomolecular Structure and Dynamics</i> , 2020, , 1-10.	3.5	2
14	Dynamical Behavior of the Human Ferroportin Homologue from <i>Bdellovibrio bacteriovorus</i> : Insight into the Ligand Recognition Mechanism. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6785.	4.1	4
15	DockingApp RF: A State-of-the-Art Novel Scoring Function for Molecular Docking in a User-Friendly Interface to AutoDock Vina. <i>International Journal of Molecular Sciences</i> , 2020, 21, 9548.	4.1	21
16	Computational Methods for the Identification of Molecular Targets of Toxic Food Additives. Butylated Hydroxytoluene as a Case Study. <i>Molecules</i> , 2020, 25, 2229.	3.8	11
17	Mycobacterial and Human Nitrobindins: Structure and Function. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 229-246.	5.4	17
18	Structural Basis of Drug Recognition by Human Serum Albumin. <i>Current Medicinal Chemistry</i> , 2020, 27, 4907-4931.	2.4	40

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19	Computational methods and tools for binding site recognition between proteins and small molecules: from classical geometrical approaches to modern machine learning strategies. <i>Journal of Computer-Aided Molecular Design</i> , 2019, 33, 887-903.	2.9	18
20	In silico Selection and Experimental Validation of FDA-Approved Drugs as Anti-quorum Sensing Agents. <i>Frontiers in Microbiology</i> , 2019, 10, 2355.	3.5	38
21	Ruxolitinib binding to human serum albumin: bioinformatics, biochemical and functional characterization in JAK2V617F+ cell models. <i>Scientific Reports</i> , 2019, 9, 16379.	3.3	6
22	Fragment-Based Ligand-Protein Contact Statistics: Application to Docking Simulations. <i>International Journal of Molecular Sciences</i> , 2019, 20, 2499.	4.1	7
23	The Four FAD-Dependent Histone Demethylases of Arabidopsis Are Differently Involved in the Control of Flowering Time. <i>Frontiers in Plant Science</i> , 2019, 10, 669.	3.6	21
24	Cytochrome c: An extreme multifunctional protein with a key role in cell fate. <i>International Journal of Biological Macromolecules</i> , 2019, 136, 1237-1246.	7.5	134
25	Oxygen dissociation from ferrous oxygenated human hemoglobin:haptoglobin complexes confirms that in the R-state $\hat{1}\pm$ and $\hat{1}^2$ chains are functionally heterogeneous. <i>Scientific Reports</i> , 2019, 9, 6780.	3.3	8
26	Exploring the activity of polyamine analogues on polyamine and spermine oxidase: methoctramine, a potent and selective inhibitor of polyamine oxidase. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2019, 34, 740-752.	5.2	12
27	Identification of lipid A deacylase as a novel, highly conserved and protective antigen against enterohemorrhagic Escherichia coli. <i>Scientific Reports</i> , 2019, 9, 17014.	3.3	4
28	NBS1 interacts with HP1 to ensure genome integrity. <i>Cell Death and Disease</i> , 2019, 10, 951.	6.3	15
29	Bioinformatics analysis of Ras homologue enriched in the striatum, a potential target for Huntington's disease therapy. <i>International Journal of Molecular Medicine</i> , 2019, 44, 2223-2233.	4.0	9
30	Fipronil recognition by the FA1 site of human serum albumin. <i>Journal of Molecular Recognition</i> , 2018, 31, e2713.	2.1	9
31	The ferroportin-ceruloplasmin system and the mammalian iron homeostasis machine: regulatory pathways and the role of lactoferrin. <i>BioMetals</i> , 2018, 31, 399-414.	4.1	47
32	LIBRA-WA: a web application for ligand binding site detection and protein function recognition. <i>Bioinformatics</i> , 2018, 34, 878-880.	4.1	22
33	Reductive nitrosylation of ferric human hemoglobin bound to human haptoglobin 1-1 and 2-2. <i>Journal of Biological Inorganic Chemistry</i> , 2018, 23, 437-445.	2.6	13
34	A comprehensive <i>in silico</i> analysis of huntingtin and its interactome. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 3155-3171.	3.5	6
35	Characterization of three novel pathogenic SLC40A1 mutations and genotype/phenotype correlations in 7 Italian families with type 4 hereditary hemochromatosis. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2018, 1864, 464-470.	3.8	6
36	No Lanthanide-based Catalysis in Eukaryotes. <i>IUBMB Life</i> , 2018, 71, 398-399.	3.4	4

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37	Human nitrobindin: the first example of an all- $\alpha$ -barrel ferric heme-protein that catalyzes peroxynitrite detoxification. <i>FEBS Open Bio</i> , 2018, 8, 2002-2010.	2.3	17
38	Lanthanide-based catalysis in eukaryotes. <i>IUBMB Life</i> , 2018, 70, 1067-1075.	3.4	5
39	Identification of FDA-Approved Drugs as Antivirulence Agents Targeting the <i>qpqs</i> Quorum-Sensing System of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	82
40	Human Serum Albumin Is an Essential Component of the Host Defense Mechanism Against <i>Clostridium difficile</i> Intoxication. <i>Journal of Infectious Diseases</i> , 2018, 218, 1424-1435.	4.0	45
41	Protein-ligand binding site detection as an alternative route to molecular docking and drug repurposing. <i>Bio-Algorithms and Med-Systems</i> , 2018, 14, .	2.4	1
42	The plastoquinol-plastoquinone exchange mechanism in photosystem II: insight from molecular dynamics simulations. <i>Photosynthesis Research</i> , 2017, 131, 15-30.	2.9	18
43	DockingApp: a user friendly interface for facilitated docking simulations with AutoDock Vina. <i>Journal of Computer-Aided Molecular Design</i> , 2017, 31, 213-218.	2.9	85
44	Structural evidence of quercetin multi-target bioactivity: A reverse virtual screening strategy. <i>European Journal of Pharmaceutical Sciences</i> , 2017, 106, 393-403.	4.0	33
45	Multiple functions of insulin-degrading enzyme: a metabolic crosslight?. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2017, 52, 554-582.	5.2	73
46	Nitrophorins and nitrobindins: structure and function. <i>Biomolecular Concepts</i> , 2017, 8, 105-118.	2.2	19
47	Cantharidin inhibits competitively heme-F(III) binding to the FA1 site of human serum albumin. <i>Journal of Molecular Recognition</i> , 2017, 30, e2641.	2.1	10
48	Human serum albumin: A modulator of cannabinoid drugs. <i>IUBMB Life</i> , 2017, 69, 834-840.	3.4	17
49	<i>In silico</i> study of the structure and function of <i>Streptococcus mutans</i> plasmidic proteins. <i>Bio-Algorithms and Med-Systems</i> , 2017, 13, 51-61.	2.4	0
50	Neuroglobin and friends. <i>Journal of Molecular Recognition</i> , 2017, 30, e2654.	2.1	20
51	Spectroscopic and calorimetric characterization of spermine oxidase and its association forms. <i>Biochemical Journal</i> , 2017, 474, 4253-4268.	3.7	3
52	The key role played by charge in the interaction of cytochrome c with cardiolipin. <i>Journal of Biological Inorganic Chemistry</i> , 2017, 22, 19-29.	2.6	40
53	An improved structural model of the human iron exporter ferroportin. Insight into the role of pathogenic mutations in hereditary hemochromatosis type 4. <i>Bio-Algorithms and Med-Systems</i> , 2017, 13, 215-222.	2.4	6
54	Small and Random Peptides: An Unexplored Reservoir of Potentially Functional Primitive Organocatalysts. The Case of Seryl-Histidine. <i>Life</i> , 2017, 7, 19.	2.4	38

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55	Staphylococcus aureus Esx Factors Control Human Dendritic Cell Functions Conditioning Th1/Th17 Response. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 330.	3.9	21
56	Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a $\beta$ -Helical Passenger. <i>Frontiers in Microbiology</i> , 2017, 8, 2607.	3.5	17
57	Selective binding of estrogen receptor $\beta$ to ubiquitin chains. <i>IUBMB Life</i> , 2016, 68, 569-577.	3.4	10
58	Molecular Evolution of Alternative Oxidase Proteins: A Phylogenetic and Structure Modeling Approach. <i>Journal of Molecular Evolution</i> , 2016, 82, 207-218.	1.8	27
59	Multiple allosteric sites are involved in the modulation of insulin-degrading enzyme activity by somatostatin. <i>FEBS Journal</i> , 2016, 283, 3755-3770.	4.7	18
60	Peptidomimetic Targeting of $Ca^{v2}$ Overcomes Dysregulation of the L-Type Calcium Channel Density and Recovers Cardiac Function. <i>Circulation</i> , 2016, 134, 534-546.	1.6	42
61	Molecular models of human visual pigments: insight into the atomic bases of spectral tuning. <i>Bio-Algorithms and Med-Systems</i> , 2016, 12, 141-146.	2.4	0
62	Nitrobindin: An Ubiquitous Family of All $\beta$ -Barrel Heme-proteins. <i>IUBMB Life</i> , 2016, 68, 423-428.	3.4	20
63	Stability of spermine oxidase to thermal and chemical denaturation: comparison with bovine serum amine oxidase. <i>Amino Acids</i> , 2016, 48, 2283-2291.	2.7	11
64	The human iron exporter ferroportin. Insight into the transport mechanism by molecular modeling. <i>Bio-Algorithms and Med-Systems</i> , 2016, 12, 1-7.	2.4	3
65	Resveratrol and its methoxy-derivatives as modulators of DNA damage induced by ionising radiation. <i>Mutagenesis</i> , 2016, 31, 433-441.	2.6	19
66	All- trans -retinoic acid and retinol binding to the FA1 site of human serum albumin competitively inhibits heme-Fe(III) association. <i>Archives of Biochemistry and Biophysics</i> , 2016, 590, 56-63.	3.0	13
67	Different disulfide bridge connectivity drives alternative folds in highly homologous <i>Brassicaceae</i> trypsin inhibitors. <i>IUBMB Life</i> , 2015, 67, 966-970.	3.4	0
68	Functional and Spectroscopic Characterization of <i>Chlamydomonas reinhardtii</i> Truncated Hemoglobins. <i>PLoS ONE</i> , 2015, 10, e0125005.	2.5	13
69	A bacterial homologue of the human iron exporter ferroportin. <i>FEBS Letters</i> , 2015, 589, 3829-3835.	2.8	12
70	Pacific oyster polyamine oxidase: a protein missing link in invertebrate evolution. <i>Amino Acids</i> , 2015, 47, 949-961.	2.7	2
71	Enhanced heme accessibility in horse heart mini-myoglobin: Insights from molecular modelling and reactivity studies. <i>Archives of Biochemistry and Biophysics</i> , 2015, 585, 1-9.	3.0	3
72	Cardiolipin-cytochrome <i>c</i> complex: Switching cytochrome <i>c</i> from an electron-transfer shuttle to a myoglobin- and a peroxidase-like heme-protein. <i>IUBMB Life</i> , 2015, 67, 98-109.	3.4	45

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73	LIBRA: Ligand Binding site Recognition Application. <i>Bioinformatics</i> , 2015, 31, 4020-4022.	4.1	21
74	Structure/Function/Dynamics of Photosystem II Plastoquinone Binding Sites. <i>Current Protein and Peptide Science</i> , 2014, 15, 285-295.	1.4	56
75	The Glu216/Ser218 pocket is a major determinant of spermine oxidase substrate specificity. <i>Biochemical Journal</i> , 2014, 461, 453-459.	3.7	11
76	Role of Intermediate States in Protein Folding and Misfolding. , 2014, , 433-455.		0
77	Imatinib binding to human serum albumin modulates heme association and reactivity. <i>Archives of Biochemistry and Biophysics</i> , 2014, 560, 100-112.	3.0	25
78	ASSIST: a fast versatile local structural comparison tool. <i>Bioinformatics</i> , 2014, 30, 1022-1024.	4.1	13
79	A structural model of human ferroportin and of its iron binding site. <i>FEBS Journal</i> , 2014, 281, 2851-2860.	4.7	35
80	Cardiolipin modulates allosterically the nitrite reductase activity of horse heart cytochrome c. <i>Journal of Biological Inorganic Chemistry</i> , 2014, 19, 1195-1201.	2.6	18
81	Polar Localization of PhoN2, a Periplasmic Virulence-Associated Factor of <i>Shigella flexneri</i> , Is Required for Proper IcsA Exposition at the Old Bacterial Pole. <i>PLoS ONE</i> , 2014, 9, e90230.	2.5	27
82	Role of Cardiolipin in Mitochondrial Diseases and Apoptosis. <i>Current Medicinal Chemistry</i> , 2014, 21, 2702-2714.	2.4	28
83	Ceruloplasmin-ferroportin system of iron traffic in vertebrates. <i>World Journal of Biological Chemistry</i> , 2014, 5, 204-15.	4.3	63
84	Structure-Function Relationships in the Evolutionary Framework of Spermine Oxidase. <i>Journal of Molecular Evolution</i> , 2013, 76, 365-370.	1.8	21
85	Inhibition of acetylpolyamine and spermine oxidases by the polyamine analogue chlorhexidine. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2013, 28, 463-467.	5.2	13
86	Design and biophysical characterization of atrazine-sensing peptides mimicking the <i>Chlamydomonas reinhardtii</i> plastoquinone binding niche. <i>Physical Chemistry Chemical Physics</i> , 2013, 15, 13108.	2.8	12
87	Reactivity of the human hemoglobin "Dark side". <i>IUBMB Life</i> , 2013, 65, 121-126.	3.4	5
88	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2013, 1834, 1750-1756.	2.3	27
89	Role of Lysines in Cytochrome c-Cardiolipin Interaction. <i>Biochemistry</i> , 2013, 52, 4578-4588.	2.5	83
90	Automatic Protein Abbreviations Discovery and Resolution from Full-Text Scientific Papers: The PRAISED Framework. <i>Bio-Algorithms and Med-Systems</i> , 2012, 8, 13.	2.4	13

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91	A Knowledge Discovery Methodology for Semantic Categorization of Unstructured Textual Sources. , 2012, , .		3
92	GA/GB Fold switching may modulate fatty acid transfer from human serum albumin to bacteria. IUBMB Life, 2012, 64, 885-888.	3.4	10
93	Recombinant expression and insecticidal properties of a <i>Conus ventricosus</i> conotoxin-GST fusion protein. Toxicon, 2012, 60, 744-751.	1.6	15
94	Conversion of cytochrome c into a peroxidase: Inhibitory mechanisms and implication for neurodegenerative diseases. Archives of Biochemistry and Biophysics, 2012, 522, 62-69.	3.0	36
95	Molecular evolution of the polyamine oxidase gene family in Metazoa. BMC Evolutionary Biology, 2012, 12, 90.	3.2	38
96	Cyanide binding to human plasma hemeâ€œhemopexin: A comparative study. Biochemical and Biophysical Research Communications, 2012, 428, 239-244.	2.1	2
97	Cupricyclins, Novel Redox-Active Metallopeptides Based on Conotoxins Scaffold. PLoS ONE, 2012, 7, e30739.	2.5	6
98	Resveratrol acts as a topoisomerase II poison in human glioma cells. International Journal of Cancer, 2012, 131, E173-8.	5.1	36
99	Spermine oxidase: ten years after. Amino Acids, 2012, 42, 441-450.	2.7	71
100	Do Natural Proteins Differ from Random Sequences Polypeptides? Natural vs. Random Proteins Classification Using an Evolutionary Neural Network. PLoS ONE, 2012, 7, e36634.	2.5	25
101	A framework for semi-automatic identification, disambiguation and storage of protein-related abbreviations in scientific literature. , 2011, , .		7
102	PS1-045. The conserved acidic cluster domain of HIV-1 Nef is required to induces a proinflammatory state in primary macrophages: involvement of TNF alpha Receptor Associated Factor 2. Cytokine, 2011, 56, 28.	3.2	0
103	Computational Biology, Protein Engineering, and Biosensor Technology: a Close Cooperation for Herbicides Monitoring. , 2011, , .		6
104	The structure of maize polyamine oxidase K300M mutant in complex with the natural substrates provides a snapshot of the catalytic mechanism of polyamine oxidation. FEBS Journal, 2011, 278, 809-821.	4.7	14
105	The effects of ATP and sodium chloride on the cytochrome câ€œcardiolipin interaction: The contrasting behavior of the horse heart and yeast proteins. Journal of Inorganic Biochemistry, 2011, 105, 1365-1372.	3.5	27
106	Probing mammalian spermine oxidase enzymeâ€œsubstrate complex through molecular modeling, site-directed mutagenesis and biochemical characterization. Amino Acids, 2011, 40, 1115-1126.	2.7	35
107	Cardiolipin drives cytochrome c proapoptotic and antiapoptotic actions. IUBMB Life, 2011, 63, 160-165.	3.4	33
108	Experimentation of an automatic resolution method for protein abbreviations in full-text papers. , 2011, , .		4

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109	Xenosensors CAR and PXR at Work: Impact on Statin Metabolism. <i>Current Drug Metabolism</i> , 2011, 12, 300-311.	1.2	10
110	An Automatic Identification and Resolution System for Protein-Related Abbreviations in Scientific Papers. <i>Lecture Notes in Computer Science</i> , 2011, , 171-176.	1.3	10
111	Directed Evolution and In Silico Analysis of Reaction Centre Proteins Reveal Molecular Signatures of Photosynthesis Adaptation to Radiation Pressure. <i>PLoS ONE</i> , 2011, 6, e16216.	2.5	21
112	HIV-1 Nef Induces Proinflammatory State in Macrophages through Its Acidic Cluster Domain: Involvement of TNF Alpha Receptor Associated Factor 2. <i>PLoS ONE</i> , 2011, 6, e22982.	2.5	36
113	Cytochromes: Reactivity of the "dark side" of the heme. <i>Biophysical Chemistry</i> , 2010, 152, 21-27.	2.8	19
114	Extended cardiolipin anchorage to cytochrome c: a model for protein "mitochondrial membrane binding. <i>Journal of Biological Inorganic Chemistry</i> , 2010, 15, 689-700.	2.6	105
115	Spermine oxidase (SMO) activity in breast tumor tissues and biochemical analysis of the anticancer spermine analogues BENSpm and CPENSpm. <i>BMC Cancer</i> , 2010, 10, 555.	2.6	39
116	Role of External Loops of Human Ceruloplasmin in Copper Loading by ATP7B and Ccc2p. <i>Journal of Biological Chemistry</i> , 2010, 285, 20507-20513.	3.4	11
117	Dominant Mutants of Ceruloplasmin Impair the Copper Loading Machinery in Aceruloplasminemia. <i>Journal of Biological Chemistry</i> , 2009, 284, 4545-4554.	3.4	39
118	Massive non-natural proteins structure prediction using grid technologies. <i>BMC Bioinformatics</i> , 2009, 10, S22.	2.6	13
119	<i>In silico</i> Structural Study of Random Amino Acid Sequence Proteins Not Present in Nature. <i>Chemistry and Biodiversity</i> , 2009, 6, 2311-2336.	2.1	10
120	Structure-based design of novel <i>Chlamydomonas reinhardtii</i> D1-2 photosynthetic proteins for herbicide monitoring. <i>Protein Science</i> , 2009, 18, 2139-2151.	7.6	57
121	Cupryphans, metal-binding, redox active, redesigned conopeptides. <i>Protein Science</i> , 2009, 18, NA-NA.	7.6	5
122	ATP Acts as a Regulatory Effector in Modulating Structural Transitions of Cytochrome <i>c</i> : Implications for Apoptotic Activity. <i>Biochemistry</i> , 2009, 48, 3279-3287.	2.5	55
123	Spermine Metabolism and Anticancer Therapy. <i>Current Cancer Drug Targets</i> , 2009, 9, 118-130.	1.6	48
124	Human haptoglobin structure and function " a molecular modelling study. <i>FEBS Journal</i> , 2008, 275, 5648-5656.	4.7	78
125	S-Glutathionylation of metallothioneins by nitrosative/oxidative stress. <i>Experimental Gerontology</i> , 2008, 43, 415-422.	2.8	15
126	The R215W mutation in NBS1 impairs Î³-H2AX binding and affects DNA repair: molecular bases for the severe phenotype of 657del5/R215W Nijmegen breakage syndrome patients. <i>Biochemical and Biophysical Research Communications</i> , 2008, 369, 835-840.	2.1	23



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127	<i>Conus ventricosus</i> venom peptides profiling by HPLC-MS: A new insight in the intraspecific variation. <i>Journal of Separation Science</i> , 2008, 31, 488-498.	2.5	40
128	Characterization of a Lysine-Specific Histone Demethylase from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2008, 47, 4936-4947.	2.5	36
129	Never born proteins as a test case for ab initio protein structures prediction. <i>Bioinformatics</i> , 2008, 3, 177-179.	0.5	6
130	Probing the Effect of Mutations on Cytochrome c Stability. <i>Protein and Peptide Letters</i> , 2007, 14, 335-339.	0.9	4
131	The <i>Pseudomonas</i> Quorum-Sensing Regulator RsaL Belongs to the Tetrahelical Superclass of H-T-H Proteins. <i>Journal of Bacteriology</i> , 2007, 189, 1922-1930.	2.2	45
132	Nanosopic and Redox Characterization of Engineered Horse Cytochrome c Chemisorbed on a Bare Gold Electrode. <i>Protein Journal</i> , 2007, 26, 271-279.	1.6	4
133	Inhibition of polyamine and spermine oxidases by polyamine analogues. <i>FEBS Journal</i> , 2006, 273, 1115-1123.	4.7	60
134	Nitrosative/oxidative modifications and ageing. <i>Mechanisms of Ageing and Development</i> , 2006, 127, 544-551.	4.6	13
135	Investigation of de novo Totally Random Biosequences, Part II. <i>Chemistry and Biodiversity</i> , 2006, 3, 840-859.	2.1	56
136	The Production of de novo Folded Proteins by a Stepwise Chain Elongation: A Model for Prebiotic Chemical Evolution of Macromolecular Sequences. <i>Chemistry and Biodiversity</i> , 2006, 3, 1202-1210.	2.1	20
137	Heterologous Expression and Biochemical Characterization of a Polyamine Oxidase from <i>Arabidopsis</i> Involved in Polyamine Back Conversion. <i>Plant Physiology</i> , 2006, 141, 1519-1532.	4.8	144
138	The Quorum-Sensing Negative Regulator RsaL of <i>Pseudomonas aeruginosa</i> Binds to the <i>lasI</i> Promoter. <i>Journal of Bacteriology</i> , 2006, 188, 815-819.	2.2	97
139	Two short protein domains are responsible for the nuclear localization of the mouse spermine oxidase $\mu$ isoform. <i>FEBS Journal</i> , 2005, 272, 3052-3059.	4.7	20
140	Allosteric modulation of monomeric proteins. <i>Biochemistry and Molecular Biology Education</i> , 2005, 33, 169-176.	1.2	32
141	Lys300 Plays a Major Role in the Catalytic Mechanism of Maize Polyamine Oxidase. <i>Biochemistry</i> , 2005, 44, 16108-16120.	2.5	48
142	Probing the Cruzain S2 Recognition Subsite: A Kinetic and Binding Energy Calculation Study. <i>Biochemistry</i> , 2005, 44, 2781-2789.	2.5	15
143	Mitochondrial type I nitric oxide synthase physically interacts with cytochrome c oxidase. <i>Neuroscience Letters</i> , 2005, 384, 254-259.	2.1	81
144	ATP specifically drives refolding of non-native conformations of cytochrome c. <i>Protein Science</i> , 2005, 14, 1049-1058.	7.6	47

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145	Structural Consensus Rules for Cysteine Protease Inhibition by NO(-Donors). <i>Current Enzyme Inhibition</i> , 2005, 1, 231-238.	0.4	2
146	Mouse spermine oxidase gene splice variants. <i>FEBS Journal</i> , 2004, 271, 760-770.	0.2	60
147	Proteolytic activity of bovine lactoferrin. <i>BioMetals</i> , 2004, 17, 249-255.	4.1	23
148	<sup>1</sup> H NMR relaxometric characterization of bovine lactoferrin. <i>Journal of Inorganic Biochemistry</i> , 2004, 98, 1421-1426.	3.5	5
149	Proteolytic activity of bovine lactoferrin. <i>BioMetals</i> , 2004, 17, 745-745.	4.1	0
150	Solution structure of the cyclic peptide contryphan-Vn, a Ca <sup>2+</sup> -dependent K <sup>+</sup> -channel modulator. <i>Biopolymers</i> , 2004, 74, 189-198.	2.4	22
151	Molecular Basis for the Binding of Competitive Inhibitors of Maize Polyamine Oxidase. <i>Biochemistry</i> , 2004, 43, 3426-3435.	2.5	46
152	Interleukin-1 $\beta$ up-regulates iron efflux in rat C6 glioma cells through modulation of ceruloplasmin and ferroportin-1 synthesis. <i>Neuroscience Letters</i> , 2004, 363, 182-186.	2.1	37
153	The <i>Rhodococcus</i> sp. Cocaine Esterase: A Bacterial Candidate for Novel Pharmacokinetic-based Therapies for Cocaine Abuse. <i>IUBMB Life</i> , 2003, 55, 397-402.	3.4	3
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