

# Fabio Polticelli

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6059957/publications.pdf>

Version: 2024-02-01

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	AtCYS1, a cystatin from <i>Arabidopsis thaliana</i> , suppresses hypersensitive cell death. <i>FEBS Journal</i> , 2003, 270, 2593-2604.	0.2	181
2	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
3	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
4	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
5	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
6	Heterologous Expression and Characterization of Mouse Spermine Oxidase. <i>Journal of Biological Chemistry</i> , 2003, 278, 5271-5276.	3.4	86
7	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
8	Role of Lysines in Cytochrome c-Cardiolipin Interaction. <i>Biochemistry</i> , 2013, 52, 4578-4588.	2.5	83
9	Identification of FDA-Approved Drugs as Antivirulence Agents Targeting the <i>pqs</i> Quorum-Sensing System of <i>Pseudomonas aeruginosa</i> . <i>Antimicrobial Agents and Chemotherapy</i> , 2018, 62, .	3.2	82
10	Evolutionary conservativeness of electric field in the Cu,Zn superoxide dismutase active site. <i>Journal of Molecular Biology</i> , 1992, 223, 337-342.	4.2	81
11	Mitochondrial type I nitric oxide synthase physically interacts with cytochrome c oxidase. <i>Neuroscience Letters</i> , 2005, 384, 254-259.	2.1	81
12	Human haptoglobin structure and function - a molecular modelling study. <i>FEBS Journal</i> , 2008, 275, 5648-5656.	4.7	78
13	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
14	Spermine oxidase: ten years after. <i>Amino Acids</i> , 2012, 42, 441-450.	2.7	71
15	Re-Evaluation of Amino Acid Sequence and Structural Consensus Rules for Cysteine-Nitric Oxide Reactivity. <i>Biological Chemistry</i> , 2000, 381, 623-627.	2.5	68
16	Inhibition of Cysteine Protease Activity by NO-donors. <i>Current Protein and Peptide Science</i> , 2001, 2, 137-153.	1.4	68
17	Ceruloplasmin-ferroportin system of iron traffic in vertebrates. <i>World Journal of Biological Chemistry</i> , 2014, 5, 204-15.	4.3	63
18	Mouse spermine oxidase gene splice variants. <i>FEBS Journal</i> , 2004, 271, 760-770.	0.2	60

#	ARTICLE	IF	CITATIONS
19	Inhibition of polyamine and spermine oxidases by polyamine analogues. FEBS Journal, 2006, 273, 1115-1123.	4.7	60
20	A barley polyamine oxidase isoform with distinct structural features and subcellular localization. FEBS Journal, 2001, 268, 3816-3830.	0.2	59
21	Structure-based design of novel <i>Chlamydomonas reinhardtii</i> D1 photosynthetic proteins for herbicide monitoring. Protein Science, 2009, 18, 2139-2151.	7.6	57
22	Investigation of de novo Totally Random Biosequences, Part II. Chemistry and Biodiversity, 2006, 3, 840-859.	2.1	56
23	Structure/Function/Dynamics of Photosystem II Plastoquinone Binding Sites. Current Protein and Peptide Science, 2014, 15, 285-295.	1.4	56
24	ATP Acts as a Regulatory Effector in Modulating Structural Transitions of Cytochrome <i>c</i> : Implications for Apoptotic Activity. Biochemistry, 2009, 48, 3279-3287.	2.5	55
25	Contryphan-Vn: A Novel Peptide from the Venom of the Mediterranean Snail <i>Conus ventricosus</i> . Biochemical and Biophysical Research Communications, 2001, 288, 908-913.	2.1	49
26	Modulation of the Catalytic Rate of Cu,Zn Superoxide Dismutase in Single and Double Mutants of Conserved Positively and Negatively Charged Residues. Biochemistry, 1995, 34, 6043-6049.	2.5	48
27	Contryphan-Vn: a modulator of Ca <sup>2+</sup> -dependent K <sup>+</sup> channels. Biochemical and Biophysical Research Communications, 2003, 303, 238-246.	2.1	48
28	Lys300 Plays a Major Role in the Catalytic Mechanism of Maize Polyamine Oxidase. Biochemistry, 2005, 44, 16108-16120.	2.5	48
29	Spermine Metabolism and Anticancer Therapy. Current Cancer Drug Targets, 2009, 9, 118-130.	1.6	48
30	ATP specifically drives refolding of non-native conformations of cytochrome c. Protein Science, 2005, 14, 1049-1058.	7.6	47
31	The ferroportin-ceruloplasmin system and the mammalian iron homeostasis machine: regulatory pathways and the role of lactoferrin. BioMetals, 2018, 31, 399-414.	4.1	47
32	Molecular Basis for the Binding of Competitive Inhibitors of Maize Polyamine Oxidase. Biochemistry, 2004, 43, 3426-3435.	2.5	46
33	Amino Acid Sequence of Chicken Cu, Zn-Containing Superoxide Dismutase and Identification of Glutathionyl Adducts at Exposed Cysteine Residues. FEBS Journal, 1996, 237, 433-439.	0.2	45
34	The Pseudomonas Quorum-Sensing Regulator RsaL Belongs to the Tetrahelical Superclass of H-T-H Proteins. Journal of Bacteriology, 2007, 189, 1922-1930.	2.2	45
35	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. IUBMB Life, 2015, 67, 98-109.	3.4	45
36	Human Serum Albumin Is an Essential Component of the Host Defense Mechanism Against <i>Clostridium difficile</i> Intoxication. Journal of Infectious Diseases, 2018, 218, 1424-1435.	4.0	45

#	ARTICLE	IF	CITATIONS
37	Peptidomimetic Targeting of Ca <sup>v</sup> 2 Overcomes Dysregulation of the L-Type Calcium Channel Density and Recovers Cardiac Function. <i>Circulation</i> , 2016, 134, 534-546.	1.6	42
38	Nitric Oxide Inhibits the HIV-1 Reverse Transcriptase Activity. <i>Biochemical and Biophysical Research Communications</i> , 1999, 258, 624-627.	2.1	41
39	<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
40	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
41	Structural Basis of Drug Recognition by Human Serum Albumin. <i>Current Medicinal Chemistry</i> , 2020, 27, 4907-4931.	2.4	40
42	Dominant Mutants of Ceruloplasmin Impair the Copper Loading Machinery in Aceruloplasminemia. <i>Journal of Biological Chemistry</i> , 2009, 284, 4545-4554.	3.4	39
43	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
44	Molecular evolution of the polyamine oxidase gene family in Metazoa. <i>BMC Evolutionary Biology</i> , 2012, 12, 90.	3.2	38
45	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
46	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
47	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
48	Characterization of a Lysine-Specific Histone Demethylase from <i>Arabidopsis thaliana</i> . <i>Biochemistry</i> , 2008, 47, 4936-4947.	2.5	36
49	Conversion of cytochrome c into a peroxidase: Inhibitory mechanisms and implication for neurodegenerative diseases. <i>Archives of Biochemistry and Biophysics</i> , 2012, 522, 62-69.	3.0	36
50	Resveratrol acts as a topoisomerase II poison in human glioma cells. <i>International Journal of Cancer</i> , 2012, 131, E173-8.	5.1	36
51	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
52	Crystal structure of the cyanide-inhibited <i>Xenopus laevis</i> Cu,Zn superoxide dismutase at 98 K. <i>FEBS Letters</i> , 1994, 349, 93-98.	2.8	35
53	Role of the electrostatic loop charged residues in Cu, Zn superoxide dismutase. <i>Protein Science</i> , 1998, 7, 2354-2358.	7.6	35
54	Probing mammalian spermine oxidase enzyme-substrate complex through molecular modeling, site-directed mutagenesis and biochemical characterization. <i>Amino Acids</i> , 2011, 40, 1115-1126.	2.7	35

#	ARTICLE	IF	CITATIONS
55	A structural model of human ferroportin and of its iron binding site. FEBS Journal, 2014, 281, 2851-2860.	4.7	35
56	Cardiolipin drives cytochrome <i>c</i> proapoptotic and antiapoptotic actions. IUBMB Life, 2011, 63, 160-165.	3.4	33
57	Structural evidence of quercetin multi-target bioactivity: A reverse virtual screening strategy. European Journal of Pharmaceutical Sciences, 2017, 106, 393-403.	4.0	33
58	Crystallographic Study of Azide-inhibited Bovine Cu,Zn Superoxide Dismutase. Journal of Molecular Biology, 1994, 240, 179-183.	4.2	32
59	Allosteric modulation of monomeric proteins. Biochemistry and Molecular Biology Education, 2005, 33, 169-176.	1.2	32
60	Simulation of superoxide-superoxide dismutase association rate for six natural variants. Comparison with the experimental catalytic rate. The Journal of Physical Chemistry, 1994, 98, 10554-10557.	2.9	28
61	Role of Cardiolipin in Mitochondrial Diseases and Apoptosis. Current Medicinal Chemistry, 2014, 21, 2702-2714.	2.4	28
62	Structural determinants of trypsin affinity and specificity for cationic inhibitors. Protein Science, 1999, 8, 2621-2629.	7.6	27
63	The effects of ATP and sodium chloride on the cytochrome <i>c</i> cardiolipin interaction: The contrasting behavior of the horse heart and yeast proteins. Journal of Inorganic Biochemistry, 2011, 105, 1365-1372.	3.5	27
64	Non-covalent and covalent modifications modulate the reactivity of monomeric mammalian globins. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1750-1756.	2.3	27
65	Molecular Evolution of Alternative Oxidase Proteins: A Phylogenetic and Structure Modeling Approach. Journal of Molecular Evolution, 2016, 82, 207-218.	1.8	27
66	Polar Localization of PhoN2, a Periplasmic Virulence-Associated Factor of Shigella flexneri, Is Required for Proper IcsA Exposition at the Old Bacterial Pole. PLoS ONE, 2014, 9, e90230.	2.5	27
67	Modulation of the catalytic activity of cruzipain, the major cysteine proteinase from Trypanosoma cruzi, by temperature and pH. FEBS Journal, 2001, 268, 3253-3258.	0.2	26
68	Imatinib binding to human serum albumin modulates heme association and reactivity. Archives of Biochemistry and Biophysics, 2014, 560, 100-112.	3.0	25
69	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
70	Mutation of Lys-120 and Lys-134 drastically reduces the catalytic rate of Cu,Zn superoxide dismutase. FEBS Letters, 1994, 352, 76-78.	2.8	23
71	Proteolytic activity of bovine lactoferrin. BioMetals, 2004, 17, 249-255.	4.1	23
72	The R215W mutation in NBS1 impairs $\gamma$ -H2AX binding and affects DNA repair: molecular bases for the severe phenotype of 657del5/R215W Nijmegen breakage syndrome patients. Biochemical and Biophysical Research Communications, 2008, 369, 835-840.	2.1	23

#	ARTICLE	IF	CITATIONS
73	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
74	LIBRA-WA: a web application for ligand binding site detection and protein function recognition. <i>Bioinformatics</i> , 2018, 34, 878-880.	4.1	22
75	Structure-Function Relationships in the Evolutionary Framework of Spermine Oxidase. <i>Journal of Molecular Evolution</i> , 2013, 76, 365-370.	1.8	21
76	LIBRA: Ligand Binding site Recognition Application. <i>Bioinformatics</i> , 2015, 31, 4020-4022.	4.1	21
77	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
78	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
79	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
80	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
81	The Cu,Zn superoxide dismutase isoenzymes of <i>Xenopus laevis</i> : Purification, identification of a heterodimer and differential heat sensitivity. <i>Biochemical and Biophysical Research Communications</i> , 1990, 173, 1186-1193.	2.1	20
82	Low-Temperature Optical Spectroscopy of Native and Azide-Reacted Bovine Cu,Zn Superoxide Dismutase. A Structural Dynamics Study. <i>Biochemistry</i> , 1994, 33, 15103-15109.	2.5	20
83	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
84	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
85	Nitrobindin: An Ubiquitous Family of All $\alpha$ -Barrel Heme-proteins. <i>IUBMB Life</i> , 2016, 68, 423-428.	3.4	20
86	Neuroglobin and friends. <i>Journal of Molecular Recognition</i> , 2017, 30, e2654.	2.1	20
87	Substitution of arginine for lysine 134 alters electrostatic parameters of the active site in shark Cu,Zn superoxide dismutase. <i>FEBS Letters</i> , 1989, 250, 49-52.	2.8	19
88	Effect of Lys <sup>134</sup> Arg mutation on the thermal stability of Cu,Zn superoxide dismutase: influence on the monomer-dimer equilibrium. <i>Protein Engineering, Design and Selection</i> , 1996, 9, 323-325.	2.1	19
89	Cytochromes: Reactivity of the "dark side" of the heme. <i>Biophysical Chemistry</i> , 2010, 152, 21-27.	2.8	19
90	Resveratrol and its methoxy-derivatives as modulators of DNA damage induced by ionising radiation. <i>Mutagenesis</i> , 2016, 31, 433-441.	2.6	19

#	ARTICLE	IF	CITATIONS
91	Nitrophorins and nitrobindins: structure and function. <i>Biomolecular Concepts</i> , 2017, 8, 105-118.	2.2	19
92	Molecular Modeling and Electrostatic Potential Calculations on Chemically Modified Cu,Zn Superoxide Dismutases from <i>Bos taurus</i> and Shark <i>Prionace glauca</i> : Role of Lys134 in Electrostatically Steering the Substrate to the Active Site. <i>Archives of Biochemistry and Biophysics</i> , 1994, 312, 22-30.	3.0	18
93	Characterization of five new low-molecular-mass trypsin inhibitors from white mustard ( <i>Sinapis Tj</i> ETQq1 1 0.784314 rgBT /Overlock 18	0.2	18
94	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
95	Multiple allosteric sites are involved in the modulation of insulinâ€˜degradingâ€˜enzyme activity by somatostatin. <i>FEBS Journal</i> , 2016, 283, 3755-3770.	4.7	18
96	The plastoquinolâ€˜plastoquinone exchange mechanism in photosystem II: insight from molecular dynamics simulations. <i>Photosynthesis Research</i> , 2017, 131, 15-30.	2.9	18
97	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
98	Human serum albumin: A modulator of cannabinoid drugs. <i>IUBMB Life</i> , 2017, 69, 834-840.	3.4	17
99	Human nitrobindin: the first example of an allâ€˜â€˜barrel ferric hemeâ€˜protein that catalyzes peroxynitrite detoxification. <i>FEBS Open Bio</i> , 2018, 8, 2002-2010.	2.3	17
100	Identification of the Autochaperone Domain in the Type Va Secretion System (T5aSS): Prevalent Feature of Autotransporters with a Î²-Helical Passenger. <i>Frontiers in Microbiology</i> , 2017, 8, 2607.	3.5	17
101	Mycobacterial and Human Nitrobindins: Structure and Function. <i>Antioxidants and Redox Signaling</i> , 2020, 33, 229-246.	5.4	17
102	Structure/Function Relationships in Ceruloplasmin. <i>Advances in Experimental Medicine and Biology</i> , 1999, 448, 175-182.	1.6	16
103	Probing the Cruzain S2Recognition Subsite: A Kinetic and Binding Energy Calculation Studyâ€˜. <i>Biochemistry</i> , 2005, 44, 2781-2789.	2.5	15
104	S-Glutathionylation of metallothioneins by nitrosative/oxidative stress. <i>Experimental Gerontology</i> , 2008, 43, 415-422.	2.8	15
105	Recombinant expression and insecticidal properties of a <i>Conus ventricosus</i> conotoxin-GST fusion protein. <i>Toxicon</i> , 2012, 60, 744-751.	1.6	15
106	NBS1 interacts with HP1 to ensure genome integrity. <i>Cell Death and Disease</i> , 2019, 10, 951.	6.3	15
107	The structure of maize polyamine oxidase K300M mutant in complex with the natural substrates provides a snapshot of the catalytic mechanism of polyamine oxidation. <i>FEBS Journal</i> , 2011, 278, 809-821.	4.7	14
108	Low-temperature optical spectroscopy of cobalt in Cu,Co superoxide dismutase: a structural dynamics study of the solvent-unaccessible metal site. <i>Biochemistry</i> , 1995, 34, 16313-16319.	2.5	13

#	ARTICLE	IF	CITATIONS
109	Nitrosative/oxidative modifications and ageing. <i>Mechanisms of Ageing and Development</i> , 2006, 127, 544-551.	4.6	13
110	Massive non-natural proteins structure prediction using grid technologies. <i>BMC Bioinformatics</i> , 2009, 10, S22.	2.6	13
111	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
112	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
113	ASSIST: a fast versatile local structural comparison tool. <i>Bioinformatics</i> , 2014, 30, 1022-1024.	4.1	13
114	Functional and Spectroscopic Characterization of <i>Chlamydomonas reinhardtii</i> Truncated Hemoglobins. <i>PLoS ONE</i> , 2015, 10, e0125005.	2.5	13
115	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
116	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
117	Contaminations in (meta)genome data: An open issue for the scientific community. <i>IUBMB Life</i> , 2020, 72, 698-705.	3.4	13
118	Identification of the Residues Responsible for the Alkaline Inhibition of the Activity of Cu,Zn Superoxide Dismutase: A Study of Native and Chemically Modified Enzymes. <i>Archives of Biochemistry and Biophysics</i> , 1995, 321, 123-126.	3.0	12
119	Effect of Val 73 → Trp Mutation on the Reaction of <i>Chlamydomonas reinhardtii</i> Superoxide Dismutase from <i>Propionibacterium shermanii</i> with Hydrogen Peroxide. <i>Archives of Biochemistry and Biophysics</i> , 1997, 345, 156-159.	3.0	12
120	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
121	A bacterial homologue of the human iron exporter ferroportin. <i>FEBS Letters</i> , 2015, 589, 3829-3835.	2.8	12
122	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
123	Identification of the residues responsible for the alkaline inhibition of Cu, Zn superoxide dismutase: A site-directed mutagenesis approach. <i>Protein Science</i> , 1996, 5, 248-253.	7.6	11
124	Characterization of Cu,Zn Superoxide Dismutase from the Bathophilic Fish, <i>Lampanyctus crocodilus</i> . <i>Comparative Biochemistry and Physiology - B Biochemistry and Molecular Biology</i> , 1997, 117, 403-407.	1.6	11
125	Modulation of the Nitric Oxide Pathway by Copper in Glial Cells. <i>Biochemical and Biophysical Research Communications</i> , 2000, 275, 776-782.	2.1	11
126	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



#	ARTICLE	IF	CITATIONS
127	The Glu216/Ser218 pocket is a major determinant of spermine oxidase substrate specificity. <i>Biochemical Journal</i> , 2014, 461, 453-459.	3.7	11
128	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
129	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
130	Crystallization and Preliminary Crystallographic Analysis of Recombinant <i>Xenopus laevis</i> Cu, Zn Superoxide Dismutase b. <i>Biochemical and Biophysical Research Communications</i> , 1993, 194, 1008-1011.	2.1	10
131	<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
132	Xenosensors CAR and PXR at Work: Impact on Statin Metabolism. <i>Current Drug Metabolism</i> , 2011, 12, 300-311.	1.2	10
133	GA/GB Fold switching may modulate fatty acid transfer from human serum albumin to bacteria. <i>IUBMB Life</i> , 2012, 64, 885-888.	3.4	10
134	Selective binding of estrogen receptor $\hat{1}\pm$ to ubiquitin chains. <i>IUBMB Life</i> , 2016, 68, 569-577.	3.4	10
135	Cantharidin inhibits competitively heme $\hat{F}$ (III) binding to the $\hat{FA}$ 1 site of human serum albumin. <i>Journal of Molecular Recognition</i> , 2017, 30, e2641.	2.1	10
136	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
137	Fipronil recognition by the FA1 site of human serum albumin. <i>Journal of Molecular Recognition</i> , 2018, 31, e2713.	2.1	9
138	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
139	Modelling the three-dimensional structure and the electrostatic potential field of two Cu,Zn superoxide dismutase variants from tomato leaves. <i>Protein Engineering, Design and Selection</i> , 1995, 8, 551-556.	2.1	8
140	The T-Knot Motif Revisited. <i>Biological Chemistry</i> , 1999, 380, 1247-1250.	2.5	8
141	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
142	A Chimeric Mini-Trypsin Inhibitor Derived from the Oil Rape Proteinase Inhibitor Type III. <i>Biochemical and Biophysical Research Communications</i> , 2000, 275, 817-820.	2.1	7
143	Structural determinants of mini-protein stability. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 16-20.	1.2	7
144	A framework for semi-automatic identification, disambiguation and storage of protein-related abbreviations in scientific literature. , 2011, , .		7

#	ARTICLE	IF	CITATIONS
145	Fragment-Based Ligand-Protein Contact Statistics: Application to Docking Simulations. International Journal of Molecular Sciences, 2019, 20, 2499.	4.1	7
146	Neonicotinoid trapping by the FA1 site of human serum albumin. IUBMB Life, 2020, 72, 716-723.	3.4	7
147	Computational Biology, Protein Engineering, and Biosensor Technology: a Close Cooperation for Herbicides Monitoring. , 2011, , .		6
148	Cupricyclins, Novel Redox-Active Metallopeptides Based on Conotoxins Scaffold. PLoS ONE, 2012, 7, e30739.	2.5	6
149	An improved structural model of the human iron exporter ferroportin. Insight into the role of pathogenic mutations in hereditary hemochromatosis type 4. Bio-Algorithms and Med-Systems, 2017, 13, 215-222.	2.4	6
150	A comprehensive <i>in silico</i> analysis of huntingtin and its interactome. Journal of Biomolecular Structure and Dynamics, 2018, 36, 3155-3171.	3.5	6
151	Characterization of three novel pathogenic SLC40A1 mutations and genotype/phenotype correlations in 7 Italian families with type 4 hereditary hemochromatosis. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2018, 1864, 464-470.	3.8	6
152	Ruxolitinib binding to human serum albumin: bioinformatics, biochemical and functional characterization in JAK2V617F+ cell models. Scientific Reports, 2019, 9, 16379.	3.3	6
153	Binding of direct oral anticoagulants to the FA1 site of human serum albumin. Journal of Molecular Recognition, 2021, 34, e2877.	2.1	6
154	Never born proteins as a test case for ab initio protein structures prediction. Bioinformation, 2008, 3, 177-179.	0.5	6
155	Structural determinants of ligands recognition by the human mitochondrial basic amino acids transporter SLC25A29. Insights from molecular dynamics simulations of the c-state. Computational and Structural Biotechnology Journal, 2021, 19, 5600-5612.	4.1	6
156	Electrostatic Recognition in Redox Copper Proteins: A 1H NMR Study of the Protonation Behavior of His 19 in Oxidized and Reduced Cu,Zn Superoxide Dismutase. Archives of Biochemistry and Biophysics, 1993, 301, 244-250.	3.0	5
157	Structural determinants of mini- $\epsilon$ protein stability. Biochemistry and Molecular Biology Education, 2001, 29, 16-20.	1.2	5
158	1H NMR relaxometric characterization of bovine lactoferrin. Journal of Inorganic Biochemistry, 2004, 98, 1421-1426.	3.5	5
159	Cupryphans, metal-binding, redox active, redesigned conopeptides. Protein Science, 2009, 18, NA-NA.	7.6	5
160	Reactivity of the human hemoglobin "Dark side". IUBMB Life, 2013, 65, 121-126.	3.4	5
161	Lanthanides-based catalysis in eukaryotes. IUBMB Life, 2018, 70, 1067-1075.	3.4	5
162	Probing the Effect of Mutations on Cytochrome c Stability. Protein and Peptide Letters, 2007, 14, 335-339.	0.9	4

#	ARTICLE	IF	CITATIONS
163	Nanoscopic 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
164	Experimentation of an automatic resolution method for protein abbreviations in full-text papers. , 2011, , .		4
165	No Lanthanidesâ€based Catalysis in Eukaryotes. <i>IUBMB Life</i> , 2018, 71, 398-399.	3.4	4
166	Identification of lipid A deacylase as a novel, highly conserved and protective antigen against enterohemorrhagic <i>Escherichia coli</i> . <i>Scientific Reports</i> , 2019, 9, 17014.	3.3	4
167	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
168	An electrostatic enzyme-substrate recognition: the case of Cu, Zn superoxide dismutase. <i>Computational and Theoretical Chemistry</i> , 1992, 256, 153-160.	1.5	3
169	Serine proteinase inhibition by the active site titrant Nâ€Š±-(N,N-dimethylcarbamoyl)-Î±-azaornithine p-nitrophenyl ester. <i>FEBS Journal</i> , 2000, 267, 1239-1246.	0.2	3
170	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
171	A Knowledge Discovery Methodology for Semantic Categorization of Unstructured Textual Sources. , 2012, , .		3
172	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
173	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
174	Spectroscopic and calorimetric characterization of spermine oxidase and its association forms. <i>Biochemical Journal</i> , 2017, 474, 4253-4268.	3.7	3
175	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 Î±vÎ²3. <i>Frontiers in Cell and Developmental Biology</i> , 2021, 9, 651492.	3.7	3
176	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
177	Involvement of the Copper in the Inhibition of Cu, Zn Superoxide Dismutase Activity at high pH. <i>Free Radical Research Communications</i> , 1991, 12, 305-312.	1.8	2
178	Inhibition of <i>Saccharomyces cerevisiae</i> Phosphomannose Isomerase by the NO-donor S-nitroso-acetyl-penicillamine. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2001, 16, 287-292.	0.5	2
179	Cyanide binding to human plasma hemeâ€hemopexin: A comparative study. <i>Biochemical and Biophysical Research Communications</i> , 2012, 428, 239-244.	2.1	2
180	Pacific oyster polyamine oxidase: a protein missing link in invertebrate evolution. <i>Amino Acids</i> , 2015, 47, 949-961.	2.7	2

#	ARTICLE	IF	CITATIONS
181	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
182	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
183	Structural Consensus Rules for Cysteine Protease Inhibition by NO(-Donors). <i>Current Enzyme Inhibition</i> , 2005, 1, 231-238.	0.4	2
184	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
185	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
186	Time-resolved X-ray crystallography: uncovering reaction intermediates in biochemical processes. <i>Biochemistry and Molecular Biology Education</i> , 2001, 29, 31-32.	1.2	1
187	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
188	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
189	In Silico Analysis of Huntingtin Homologs in Lower Eukaryotes. <i>International Journal of Molecular Sciences</i> , 2021, 22, 3214.	4.1	1
190	Molecular Characterization of Kunitz-Type Protease Inhibitors from Blister Beetles (Coleoptera,) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 38	4.0	1
191	Proteolytic activity of bovine lactoferrin. <i>BioMetals</i> , 2004, 17, 745-745.	4.1	0
192	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. <i>Cytokine</i> , 2011, 56, 28.	3.2	0
193	Role of Intermediate States in Protein Folding and Misfolding. , 2014, , 433-455.		0
194	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
195	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
196	<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