Walter De Azevedo

List of Publications by Year
in descending order

193	7,191	61687	87275
papers	citations	45 h-index	74 g-index

193	193	193	7282
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Bioinformatics Approach on Bioisosterism Softwares to be Used in Drug Discovery and Development. Current Bioinformatics, 2022, 17, 19-30.	0.7	2
2	The Impact of CrystallographicData for the Development of Machine Learning Models to Predict Protein-Ligand Binding Affinity. Current Medicinal Chemistry, 2021, 28, 7006-7022.	1.2	8
3	Protein-Ligand Docking Simulations with AutoDock4 Focused on the Main Protease of SARS-CoV-2. Current Medicinal Chemistry, 2021, 28, 7614-7633.	1.2	6
4	Overview of PCTK3/CDK18: A Cyclin-Dependent Kinase Involved in Specific Functions in Post-Mitotic Cells. Current Medicinal Chemistry, 2021, 28, 6846-6865.	1.2	7
5	Machine Learning-Based Scoring Functions, Development and Applications with SAnDReS. Current Medicinal Chemistry, 2021, 28, 1746-1756.	1.2	11
6	Computational Prediction of Binding Affinity for CDK2-ligand Complexes. A Protein Target for Cancer Drug Discovery. Current Medicinal Chemistry, 2021, 28, .	1.2	4
7	Electrostatic Potential Energy in Protein-Drug Complexes. Current Medicinal Chemistry, 2021, 28, 4954-4971.	1.2	14
8	Application of Machine Learning Techniques for Drug Discovery. Current Medicinal Chemistry, 2021, 28, 7805-7807.	1.2	8
9	Protein-ligand interactions. High-resolution structures of CDK2.. Current Drug Targets, 2021, 22, .	1.0	0
10	Taba: A Tool to Analyze the Binding Affinity. Journal of Computational Chemistry, 2020, 41, 69-73.	1.5	27
11	Structural Basis for Inhibition of Enoyl-[Acyl Carrier Protein] Reductase (InhA) from Mycobacterium tuberculosis. Current Medicinal Chemistry, 2020, 27, 745-759.	1.2	20
12	Computational Analysis of Dipyrone Metabolite 4-Aminoantipyrine As A Cannabinoid Receptor 1 Agonist. Current Medicinal Chemistry, 2020, 27, 4741-4749.	1.2	5
13	Application of Machine Learning Techniques to Predict Binding Affinity for Drug Targets: A Study of Cyclin-Dependent Kinase 2. Current Medicinal Chemistry, 2020, 28, 253-265.	1.2	21
14	Meet Our Section Editor. Combinatorial Chemistry and High Throughput Screening, 2020, 23, 1-1.	0.6	10
15	Molecular Dynamics Simulations with NAMD2. Methods in Molecular Biology, 2019, 2053, 109-124.	0.4	4
16	SAnDReS: A Computational Tool for Docking. Methods in Molecular Biology, 2019, 2053, 51-65.	0.4	7
17	Van der Waals Potential in Protein Complexes. Methods in Molecular Biology, 2019, 2053, 79-91.	0.4	14
18	Docking with AutoDock4. Methods in Molecular Biology, 2019, 2053, 125-148.	0.4	56

#	Article	IF	Citations
19	Docking Screens for Drug Discovery. Methods in Molecular Biology, 2019, , .	0.4	11
20	Molegro Virtual Docker for Docking. Methods in Molecular Biology, 2019, 2053, 149-167.	0.4	108
21	Docking with SwissDock. Methods in Molecular Biology, 2019, 2053, 189-202.	0.4	55
22	Molecular Docking Simulations with ArgusLab. Methods in Molecular Biology, 2019, 2053, 203-220.	0.4	20
23	Homology Modeling of Protein Targets with MODELLER. Methods in Molecular Biology, 2019, 2053, 231-249.	0.4	26
24	Machine Learning to Predict Binding Affinity. Methods in Molecular Biology, 2019, 2053, 251-273.	0.4	26
25	Exploring the Scoring Function Space. Methods in Molecular Biology, 2019, 2053, 275-281.	0.4	5
26	Electrostatic Energy in Proteinâ€“Ligand Complexes. Methods in Molecular Biology, 2019, 2053, 67-77.	0.4	10
27	Hydrogen Bonds in Protein-Ligand Complexes. Methods in Molecular Biology, 2019, 2053, 93-107.	0.4	23
28	Advances in the Understanding of the Cannabinoid Receptor 1 â€“ Focusing on the Inverse Agonists Interactions. Current Medicinal Chemistry, 2019, 26, 1908-1919.	1.2	18
29	Cyclin-Dependent Kinase 2 in Cellular Senescence and Cancer. A Structural and Functional Review. Current Drug Targets, 2019, 20, 716-726.	1.0	42
30	How Docking Programs Work. Methods in Molecular Biology, 2019, 2053, 35-50.	0.4	6
31	Docking with GemDock. Methods in Molecular Biology, 2019, 2053, 169-188.	0.4	3
32	Development of machine learning models to predict inhibition of 3â€dehydroquinate dehydratase. Chemical Biology and Drug Design, 2018, 92, 1468-1474.	1.5	23
33	Development of CDK-targeted scoring functions for prediction of binding affinity. Biophysical Chemistry, 2018, 235, 1-8.	1.5	41
34	Pre-clinical effects of metformin and aspirin on the cell lines of different breast cancer subtypes. Investigational New Drugs, 2018, 36, 782-796.	1.2	48
35	Development of a machine-learning model to predict Gibbs free energy of binding for protein-ligand complexes. Biophysical Chemistry, 2018, 240, 63-69.	1.5	48
36	Optimized Virtual Screening Workflow: Towards Target-Based Polynomial Scoring Functions for HIV-1 Protease. Combinatorial Chemistry and High Throughput Screening, 2018, 20, 820-827.	0.6	24

#	Article	IF	Citations
37	Computational Approach to the Discovery of Phytochemical Molecules with Therapeutic Potential Targets to the PKCZ protein. Letters in Drug Design and Discovery, 2018, 15, 488-499.	0.4	19
38	Supervised machine learning techniques to predict binding affinity. AÂstudy for cyclin-dependent kinase 2. Biochemical and Biophysical Research Communications, 2017, 494, 305-310.	1.0	55
39	Supervised Machine Learning Methods Applied to Predict Ligand- Binding Affinity. Current Medicinal Chemistry, 2017, 24, 2459-2470.	1.2	64
40	Understanding the Structural Basis for Inhibition of Cyclin-Dependent Kinases. New Pieces in the Molecular Puzzle. Current Drug Targets, 2017, 18, 1104-1111.	1.0	48
41	SAnDReS a Computational Tool for Statistical Analysis of Docking Results and Development of Scoring Functions. Combinatorial Chemistry and High Throughput Screening, 2016, 19, 801-812.	0.6	74
42	Opinion Paper: Targeting Multiple Cyclin-Dependent Kinases (CDKs): A New Strategy for Molecular Docking Studies. Current Drug Targets, 2015, 17, 2-2.	1.0	32
43	Meet the Editorial Board. Current Bioinformatics, 2015, 10, 1-1.	0.7	0
44	A lupane-triterpene isolated from Combretum leprosum Mart. fruit extracts that interferes with the intracellular development of Leishmania (L.) amazonensis in vitro. BMC Complementary and Alternative Medicine, 2015, 15, 165.	3.7	33
45	Shikimate Kinase, a Protein Target for Drug Design. Current Medicinal Chemistry, 2014, 21, 592-604.	1.2	39
46	Data Mining of Docking Results. Application to 3-Dehydroquinate Dehydratase. Current Bioinformatics, 2014, 9, 361-379.	0.7	10
47	Recent Progress of Molecular Docking Simulations Applied to Development of Drugs. Current Bioinformatics, 2012, 7, 352-365.	0.7	50
48	Targeting imidazoline site on monoamine oxidase B through molecular docking simulations. Journal of Molecular Modeling, 2012, 18, 3877-3886.	0.8	15
49	Anti-Trypanosoma cruzi activity of nicotinamide. Acta Tropica, 2012, 122, 224-229.	0.9	49
50	Crystal structure and molecular dynamics studies of purine nucleoside phosphorylase from Mycobacterium tuberculosis associated with acyclovir. Biochimie, 2012, 94, 155-165.	1.3	15
51	Role of Serine140 in the mode of action of Mycobacterium tuberculosis Î²-ketoacyl-ACP Reductase (MabA). BMC Research Notes, 2012, 5, 526.	0.6	9
52	Combining molecular dynamics and docking simulations of the cytidine deaminase from Mycobacterium tuberculosis H37Rv. Journal of Molecular Modeling, 2012, 18, 467-479.	0.8	7
53	Identification of new potential Mycobacterium tuberculosis shikimate kinase inhibitors through molecular docking simulations. Journal of Molecular Modeling, 2012, 18, 755-764.	0.8	50
54	Antimalarial Activity of Physalins B, D, F, and G. Journal of Natural Products, 2011, 74, 2269-2272.	1.5	78

#	Article	IF	Citations
55	Crystal structure determination and dynamic studies of Mycobacterium tuberculosis Cytidine deaminase in complex with products. Archives of Biochemistry and Biophysics, 2011, 509, 108-115.	1.4	6
56	Structural basis for both pro- and anti-inflammatory response induced by mannose-specific legume lectin from Cymbosema roseum. Biochimie, 2011, 93, 806-816.	1.3	39
57	Editorial [Hot Topic:Protein targets for development of drugs against Mycobacterium tuberculosis (Guest Editor: Walter Filgueira de Azevedo)]. Current Medicinal Chemistry, 2011, 18, 1255-1257.	1.2	12
58	Bio-Inspired Algorithms Applied to Molecular Docking Simulations. Current Medicinal Chemistry, 2011, 18, 1339-1352.	1.2	68
59	Molecular Dynamics Simulations of Protein Targets Identified in Mycobacterium tuberculosis. Current Medicinal Chemistry, 2011, 18, 1353-1366.	1.2	58
60	Editorial [Hot topic: Structure-Based Virtual Screening (Guest Editor: Walter Filgueira De Azevedo) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.0	26
61	Molecular dynamics studies of a hexameric purine nucleoside phosphorylase. Journal of Molecular Modeling, 2010, 16, 543-550.	0.8	5
62	SKPDB: a structural database of shikimate pathway enzymes. BMC Bioinformatics, 2010, 11, 12.	1.2	37
63	Crystallographic and docking studies of purine nucleoside phosphorylase from Mycobacterium tuberculosis. Bioorganic and Medicinal Chemistry, 2010, 18, 4769-4774.	1.4	26
64	MolDock Applied to Structure-Based Virtual Screening. Current Drug Targets, 2010, 11, 327-334.	1.0	89
65	Halogen Atoms in the Modern Medicinal Chemistry: Hints for the Drug Design. Current Drug Targets, 2010, 11, 303-314.	1.0	528
66	Crystal structure and molecular dynamics studies of human purine nucleoside phosphorylase complexed with 7-deazaguanine. Journal of Structural Biology, 2010, 169, 379-388.	1.3	7
67	Structural and functional analyses of Mycobacterium tuberculosis Rv3315c-encoded metal-dependent homotetrameric cytidine deaminase. Journal of Structural Biology, 2010, 169, 413-423.	1.3	15
68	Bioinformatics Tools for Screening of Antiparasitic Drugs. Current Drug Targets, 2009, 10, 232-239.	1.0	12
69	Structural studies of shikimate dehydrogenase from Bacillus anthracis complexed with cofactor NADP. Journal of Molecular Modeling, 2009, 15, 147-55.	0.8	8
70	Molecular modeling and dynamics studies of purine nucleoside phosphorylase from Bacteroides fragilis. Journal of Molecular Modeling, 2009, 15, 913-922.	0.8	4
71	Purification, Characterization, and Preliminary X-Ray Diffraction Analysis of a Lactose-Specific Lectin from Cymbosema roseum Seeds. Applied Biochemistry and Biotechnology, 2009, 152, 383-393.	1.4	16
72	Molecular modeling and dynamics simulation of human cyclin-dependent kinase 3 complexed with inhibitors. Computers in Biology and Medicine, 2009, 39, 130-140.	3.9	19

#	Article	IF	Citations
73	Molecular modeling, dynamics and docking studies of Purine Nucleoside Phosphorylase from Streptococcus pyogenes. Biophysical Chemistry, 2009, 142, 7-16.	1.5	10
74	Structural studies of PNP from Toxoplasma gondii. International Journal of Bioinformatics Research and Applications, 2009, 5, 154.	0.1	0
75	Protein-Drug Interaction Studies for Development of Drugs Against Plasmodium falciparum. Current Drug Targets, 2009, 10, 271-278.	1.0	21
76	Selection of Targets for Drug Development Against Protozoan Parasites. Current Drug Targets, 2009, 10, 193-201.	1.0	24
77	Genomic Databases and the Search of Protein Targets for Protozoan Parasites. Current Drug Targets, 2009, 10, 240-245.	1.0	11
78	Molecular modeling and dynamics studies of cytidylate kinase from Mycobacterium tuberculosis H37Rv. Journal of Molecular Modeling, 2008, 14, 427-434.	0.8	16
79	Structural studies of shikimate 5â€dehydrogenase from Mycobacterium tuberculosis. Proteins: Structure, Function and Bioinformatics, 2008, 72, 720-730.	1.5	21
80	Structural studies of prephenate dehydratase from Mycobacterium tuberculosis H37Rv by SAXS, ultracentrifugation, and computational analysis. Proteins: Structure, Function and Bioinformatics, 2008, 72, 1352-1362.	1.5	8
81	Molecular modeling and dynamics simulations of PNP from Streptococcus agalactiae. Bioorganic and Medicinal Chemistry, 2008, 16, 4984-4993.	1.4	33
82	Molecular modeling and dynamics studies of Shikimate Kinase from Bacillus anthracis. Bioorganic and Medicinal Chemistry, 2008, 16, 8098-8108.	1.4	19
83	Evaluation of ligand-binding affinity using polynomial empirical scoring functions. Bioorganic and Medicinal Chemistry, 2008, 16, 9378-9382.	1.4	32
84	Identification of a new quaternary association for legume lectins. Journal of Structural Biology, 2008, 161, 133-143.	1.3	33
85	Crystal structure of Dioclea rostrata lectin: Insights into understanding the pH-dependent dimer-tetramer equilibrium and the structural basis for carbohydrate recognition in Diocleinae lectins. Journal of Structural Biology, 2008, 164, 177-182.	1.3	26
86	Structural studies of human purine nucleoside phosphorylase: Towards a new specific empirical scoring function. Archives of Biochemistry and Biophysics, 2008, 479, 28-38.	1.4	36
87	Expression and purification of human respiratory syncytial virus recombinant fusion protein. Protein Expression and Purification, 2008, 62, 146-152.	0.6	5
88	Dynamics of Glyphosate-Induced Conformational Changes of Mycobacterium tuberculosis 5-Enolpyruvylshikimate-3-phosphate Synthase (EC 2.5.1.19) Determined by Hydrogenâ"Deuterium Exchange and Electrospray Mass Spectrometry. Biochemistry, 2008, 47, 7509-7522.	1.2	29
89	In Silico and In Vitro: Identifying New Drugs. Current Drug Targets, 2008, 9, 1054-1061.	1.0	24
90	Virtual Screening of Drugs: Score Functions, Docking, and Drug Design. Current Computer-Aided Drug Design, 2008, 4, 265-272.	0.8	36

#	Article	IF	Citations
91	Molecular Modeling as a Tool for Drug Discovery. Current Drug Targets, 2008, 9, 1084-1091.	1.0	20
92	Molecular Docking Algorithms. Current Drug Targets, 2008, 9, 1040-1047.	1.0	180
93	Editorial [Hot Topic:Protein-Drug Interactions(Guest Editor: Walter Filgueira de Azevedo Jr.)]. Current Drug Targets, 2008, 9, 1030-1030.	1.0	14
94	Structural Bioinformatics Study of PNP from Listeria monocytogenes. Protein and Peptide Letters, 2008, 15, 843-849.	0.4	7
95	Drug-Binding Databases. Current Drug Targets, 2008, 9, 1092-1099.	1.0	30
96	Computational Methods for Calculation of Ligand-Binding Affinity. Current Drug Targets, 2008, 9, 1031-1039.	1.0	64
97	Molecular Recognition Models: A Challenge to Overcome. Current Drug Targets, 2008, 9, 1077-1083.	1.0	16
98	Experimental Approaches to Evaluate the Thermodynamics of Protein- Drug Interactions. Current Drug Targets, 2008, 9, 1071-1076.	1.0	53
99	Protein Crystallography in Drug Discovery. Current Drug Targets, 2008, 9, 1048-1053.	1.0	45
100	Evaluation of Molecular Docking Using Polynomial Empirical Scoring Functions. Current Drug Targets, 2008, 9, 1062-1070.	1.0	39
101	CDK9 a Potential Target for Drug Development. Medicinal Chemistry, 2008, 4, 210-218.	0.7	53
102	Chorismate Synthase: An Attractive Target For Drug Development Against Orphan Diseases. Current Drug Targets, 2007, 8, 437-444.	1.0	49
103	Protein Kinases as Targets for Antiparasitic Chemotherapy Drugs. Current Drug Targets, 2007, 8, 389-398.	1.0	58
104	Molecular Dynamics and Structural Studies of the Ets Domain-DNA Complexes. Current Bioinformatics, 2007, 2, 222-228.	0.7	1
105	The Inhibition of 5-enolpyruvylshikimate-3-phosphate Synthase as a Model for Development of Novel Antimicrobials. Current Drug Targets, 2007, 8, 445-457.	1.0	48
106	Molecular Modeling Databases: A New Way in the Search of Protein Targets for Drug Development. Current Bioinformatics, 2007, 2, 1-10.	0.7	11
107	Shikimate Kinase: A Potential Target for Development of Novel Antitubercular Agents. Current Drug Targets, 2007, 8, 459-468.	1.0	44
108	Crystallographic studies on the binding of isonicotinyl-NAD adduct to wild-type and isoniazid resistant 2-trans-enoyl-ACP (CoA) reductase from Mycobacterium tuberculosis. Journal of Structural Biology, 2007, 159, 369-380.	1.3	52

#	Article	IF	Citations
109	Structural analysis of Canavalia maritima and Canavalia gladiata lectins complexed with different dimannosides: New insights into the understanding of the structureâ€“biological activity relationship in legume lectins. Journal of Structural Biology, 2007, 160, 168-176.	1.3	39
110	Effects of the magnesium and chloride ions and shikimate on the structure of shikimate kinase fromMycobacterium tuberculosis. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 1-6.	0.7	31
111	Structure of a lectin from Canavalia gladiata seeds: new structural insights for old molecules. BMC Structural Biology, 2007, 7, 52.	2.3	54
112	4-Arylazo-3,5-diamino-1H-pyrazole CDK Inhibitors:â€‰ SAR Study, Crystal Structure in Complex with CDK2, Selectivity, and Cellular Effects. Journal of Medicinal Chemistry, 2006, 49, 6500-6509.	2.9	166
113	Phosphate closes the solution structure of the 5-enolpyruvylshikimate-3-phosphate synthase (EPSPS) from Mycobacterium tuberculosis. Archives of Biochemistry and Biophysics, 2006, 452, 156-164.	1.4	22
114	Crystallographic and Pre-steady-state Kinetics Studies on Binding of NADH to Wild-type and Isoniazid-resistant Enoyl-ACP(CoA) Reductase Enzymes from Mycobacterium tuberculosis. Journal of Molecular Biology, 2006, 359, 646-666.	2.0	67
115	Structure of chorismate synthase from Mycobacterium tuberculosis. Journal of Structural Biology, 2006, 154, 130-143.	1.3	41
116	Crystal structure of a lectin from Canavalia maritima (ConM) in complex with trehalose and maltose reveals relevant mutation in ConA-like lectins. Journal of Structural Biology, 2006, 154, 280-286.	1.3	34
117	Expression, purification, and circular dichroism analysis of human CDK9. Protein Expression and Purification, 2006, 47, 614-620.	0.6	9
118	Purification, partial characterization and preliminary X-ray diffraction analysis of a mannose-specific lectin fromCymbosema roseumseeds. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 235-237.	0.7	5
119	Crystallization and preliminary X-ray diffraction analysis of prephenate dehydratase fromMycobacterium tuberculosisH37Rv. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 357-360.	0.7	3
120	Crystallization and preliminary X-ray diffraction analysis of an anti-H(O) lectin fromLotus tetragonolobusseeds. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 680-683.	0.7	2
121	New crystal forms of Diocleinae lectins in the presence of different dimannosides. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 1100-1103.	0.7	2
122	cDNA cloning and 1.75â€ƒÃ… crystal structure determination of PPL2, an endochitinase and N-acetylglucosamine-binding hemagglutinin from Parkia platycephala seeds. FEBS Journal, 2006, 273, 3962-3974.	2.2	25
123	DBMODELING: A Database Applied to the Study of Protein Targets From Genome Projects. Cell Biochemistry and Biophysics, 2006, 44, 366-374.	0.9	11
124	Molecular Models of Tryptophan Synthase From Mycobacterium tuberculosis Complexed With Inhibitors. Cell Biochemistry and Biophysics, 2006, 44, 375-384.	0.9	14
125	Determining the Structural Basis for Specificity of Ligands Using Crystallographic Screening. Cell Biochemistry and Biophysics, 2006, 44, 405-411.	0.9	10
126	Crotacetin, a Novel Snake Venom C-Type Lectin Homolog of Convulxin, Exhibits an Unpredictable Antimicrobial Activity. Cell Biochemistry and Biophysics, 2006, 44, 412-423.	0.9	31

#	Article	IF	Citations
127	Rattlesnake Hemoglobins: Functional Properties and Tetrameric Stability. Protein and Peptide Letters, 2006, 13, 517-523.	0.4	1
128	The use of biodiversity as source of new chemical entities against defined molecular targets for treatment of malaria, tuberculosis, and T-cell mediated diseases: a review. Memorias Do Instituto Oswaldo Cruz, 2005, 100, 475-506.	0.8	73
129	Molecular models of protein kinase 6 from Plasmodium falciparum. Journal of Molecular Modeling, 2005, 12, 42-48.	0.8	27
130	Molecular models of protein targets from Mycobacterium tuberculosis. Journal of Molecular Modeling, 2005, 11, 160-166.	0.8	21
131	Structure of human PNP complexed with ligands. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 856-862.	2.5	33
132	Crystallization and preliminary X-ray diffraction analysis of a lectin fromCanavalia maritimaseeds. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 87-89.	0.7	3
133	Crystallization and preliminary X-ray diffraction analysis of a new chitin-binding protein fromParkia platycephalaseeds. Acta Crystallographica Section F: Structural Biology Communications, 2005, 61, 841-843.	0.7	5
134	Molecular models of NS3 protease variants of the Hepatitis C virus. BMC Structural Biology, 2005, 5, 1.	2.3	27
135	Crotacetin, a novel snake venom C-type lectin, is homolog of convulxin. Journal of Venomous Animals and Toxins Including Tropical Diseases, 2005, 11, 557.	0.8	1
136	Structural Basis for Interaction of Inhibitors with Cyclin-Dependent Kinase 2. Current Computer-Aided Drug Design, 2005, 1, 53-64.	0.8	25
137	Native crystal structure of a nitric oxide-releasing lectin from the seeds of Canavalia maritima. Journal of Structural Biology, 2005, 152, 185-194.	1.3	45
138	Crystal structure of human PNP complexed with hypoxanthine and sulfate ion. Biochemical and Biophysical Research Communications, 2005, 326, 335-338.	1.0	33
139	New catalytic mechanism for human purine nucleoside phosphorylase. Biochemical and Biophysical Research Communications, 2005, 327, 646-649.	1.0	44
140	Automated NMR structure determination and disulfide bond identification of the myotoxin crotamine from Crotalus durissus terrificus. Toxicon, 2005, 46, 759-767.	0.8	84
141	Kinetics and crystal structure of human purine nucleoside phosphorylase in complex with 7-methyl-6-thio-guanosine. Archives of Biochemistry and Biophysics, 2005, 442, 49-58.	1.4	37
142	Conformation and lytic activity of eumenine mastoparan: a new antimicrobial peptide from wasp venom. Chemical Biology and Drug Design, 2004, 64, 95-103.	1.2	55
143	Allosteric water and phosphate effects in Hoplosternum littorale hemoglobins. FEBS Journal, 2004, 271, 4270-4274.	0.2	3
144	Crystallization and preliminary X-ray diffraction analysis of the lectin fromCanavalia gladiataseeds. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 1493-1495.	2.5	13

#	Article	IF	Citations
145	Crystallization and preliminary X-ray crystallographic analysis of chorismate synthase fromMycobacterium tuberculosis. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2003-2005.	2.5	8
146	Structure of shikimate kinase fromMycobacterium tuberculosisreveals the binding of shikimic acid. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2310-2319.	2.5	48
147	How C-Terminal Carboxyamidation Alters the Biological Activity of Peptides from the Venom of the Eumenine Solitary Wasp. Biochemistry, 2004, 43, 5608-5617.	1.2	90
148	Structures of human purine nucleoside phosphorylase complexed with inosine and ddI. Biochemical and Biophysical Research Communications, 2004, 313, 907-914.	1.0	55
149	Molecular models for shikimate pathway enzymes of Xylella fastidiosa. Biochemical and Biophysical Research Communications, 2004, 320, 979-991.	1.0	30
150	Structural bioinformatics study of PNP from Schistosoma mansoni. Biochemical and Biophysical Research Communications, 2004, 322, 100-104.	1.0	29
151	Molecular models of cyclin-dependent kinase 1 complexed with inhibitors. Biochemical and Biophysical Research Communications, 2004, 324, 661-666.	1.0	44
152	Crystallographic structure of PNP from Mycobacterium tuberculosis at 1.9Ã... resolution. Biochemical and Biophysical Research Communications, 2004, 324, 789-794.	1.0	25
153	Molecular modeling and small angle X-ray scattering studies of Hoplosternum littorale cathodic haemoglobin. Biochemical and Biophysical Research Communications, 2004, 325, 487-493.	1.0	3
154	Parmodel: a web server for automated comparative modeling of proteins. Biochemical and Biophysical Research Communications, 2004, 325, 1481-1486.	1.0	58
155	Structural and functional characterization of N-terminally blocked peptides isolated from the venom of the social wasp Polybia paulista. Peptides, 2004, 25, 2069-2078.	1.2	20
156	Mutational analysis of the GAP-related domain of the neurofibromatosis type 1 gene in Brazilian NF1 patients. Genetics and Molecular Biology, 2004, 27, 326-330.	0.6	4
157	Crystallization, preliminary X-ray analysis and molecular-replacement solution of haemoglobin-II from the fish matrinxÃ£ (Brycon cephalus). Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 752-754.	2.5	2
158	Docking and small angle X-ray scattering studies of purine nucleoside phosphorylase. Biochemical and Biophysical Research Communications, 2003, 309, 923-928.	1.0	45
159	Structural basis for inhibition of human PNP by immucillin-H. Biochemical and Biophysical Research Communications, 2003, 309, 917-922.	1.0	47
160	Structural bioinformatics study of EPSP synthase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2003, 312, 608-614.	1.0	51
161	Crystal structure of human PNP complexed with guanine. Biochemical and Biophysical Research Communications, 2003, 312, 767-772.	1.0	39
162	Crystal structure of human purine nucleoside phosphorylase at 2.3Ã... resolution. Biochemical and Biophysical Research Communications, 2003, 308, 545-552.	1.0	54

#	Article	IF	Citations
163	Crystal structure of human purine nucleoside phosphorylase complexed with acyclovir. Biochemical and Biophysical Research Communications, 2003, 308, 553-559.	1.0	58
164	Structural bioinformatics study of cyclin-dependent kinases complexed with inhibitors. Ecletica Quimica, 2003, 28, 45-53.	0.2	5
165	Crystal Structure of Hemoglobin from the Maned Wolf (Chrysocyon Brachyurus) Using Synchrotron Radiation. Protein and Peptide Letters, 2003, 10, 551-559.	0.4	1
166	Structural basis for inhibition of cyclin-dependent kinase 9 by flavopiridol. Biochemical and Biophysical Research Communications, 2002, 293, 566-571.	1.0	128
167	Molecular model of shikimate kinase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2002, 295, 142-148.	1.0	50
168	Molecular model of cyclin-dependent kinase 5 complexed with roscovitine. Biochemical and Biophysical Research Communications, 2002, 297, 1154-1158.	1.0	66
169	Title is missing!. Transition Metal Chemistry, 2002, 27, 433-436.	0.7	3
170	Molecular Model for the Binary Complex of Uropepsin and Pepstatin. Biochemical and Biophysical Research Communications, 2001, 287, 277-281.	1.0	44
171	A influÃªncia do fator de vibraÃ§Ã£o tÃ©rmica na densidade eletrÃ´nica de cristais bidimensionais. Revista Brasileira De Ensino De Fisica, 2001, 23, 211-214.	0.2	0
172	Simulation of electron density maps for two-dimensional crystal structures usingMathematica. Journal of Applied Crystallography, 2001, 34, 658-660.	1.9	5
173	Purification, crystallization and Patterson search of haemoglobin IV from the armoured catfishLiposarcus anisitsi. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1329-1331.	2.5	3
174	Structure of human uropepsin at 2.45â€…Ã… resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1560-1570.	2.5	32
175	Preliminary cryocrystallography analysis of an eumenine mastoparan toxin isolated from the venom of the wasp Anterhynchium flavomarginatum micado. BBA - Proteins and Proteomics, 2001, 1545, 372-376.	2.1	8
176	Anoplin, a novel antimicrobial peptide from the venom of the solitary wasp Anoplius samariensis. BBA - Proteins and Proteomics, 2001, 1550, 70-80.	2.1	139
177	Purification, crystallization and preliminary X-ray diffraction analysis of carboxyhaemoglobin-II from the fishPiaractus mesopotamicus(pacu). Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 366-367.	2.5	2
178	Purification, crystallization and preliminary X-ray analysis of haemoglobin I from the armoured catfishLiposarcus anisitsi. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 495-497.	2.5	3
179	Crystallization and preliminary X-ray diffraction analysis of a eumenine mastoparan toxin: a new class of mast-cell degranulating peptide in the wasp venom. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1434-1436.	2.5	4
180	Crystallization, preliminary X-ray analysis and molecular-replacement solution of the carboxy form of haemoglobin I from the fishBrycon cephalus. Acta Crystallographica Section D: Biological Crystallography, 2000, 56, 1685-1687.	2.5	2

#	Article	IF	Citations
181	Crystallographic studies of fish hemoglobins. Ecletica Quimica, 2000, 25, 147-159.	0.2	2
182	Crystallization, preliminary X-ray diffraction analysis and Patterson search of oxyhaemoglobin I from the wolf (Chrysocyon brachiurus). Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1618-1619.	2.5	2
183	Crystallization and X-ray diffraction data analysis of human deoxyhaemoglobin A0 fully stripped of any anions. Acta Crystallographica Section D: Biological Crystallography, 1999, 55, 1914-1916.	2.5	15
184	Structure of a Lys49-Phospholipase A2 homologue isolated from the venom of Bothrops nummifer (jumping viper). Toxicon, 1999, 37, 371-384.	0.8	40
185	Purification and partial characterization of cathepsin D from porcine (Sus scrofa) liver using affinity chromatography. IUBMB Life, 1998, 45, 797-803.	1.5	6
186	Crystallization, preliminary xâ€ray analysis and patterson search of a new aspartic protease isolated from human urine. IUBMB Life, 1998, 46, 355-363.	1.5	0
187	Crystallographic and spectroscopic characterization of a molecular hinge: Conformational changes in bothropstoxin I, a dimeric Lys49-phospholipase A2 homologue. , 1998, 30, 442-454.		91
188	Crystal structure of piratoxin-I: A calcium-independent, myotoxic phospholipase A2-homologue from Bothrops pirajai venom. Toxicon, 1998, 36, 1395-1406.	0.8	37
189	At the interface: Crystal structures of phospholipases A2. Toxicon, 1998, 36, 1623-1633.	0.8	47
190	Inhibition of Cyclin-Dependent Kinases by Purine Analogues. Crystal Structure of Human cdk2 Complexed with Roscovitine. FEBS Journal, 1997, 243, 518-526.	0.2	590
191	Structural basis for specificity and potency of a flavonoid inhibitor of human CDK2, a cell cycle kinase.. Proceedings of the National Academy of Sciences of the United States of America, 1996, 93, 2735-2740.	3.3	459
192	Structural basis for chemical inhibition of CDK2. , 1996, 2, 137-145.		42
193	cis-[1,2-Bis(propylsulfinyl)ethane-S,S']dichloroplatinum(II). Acta Crystallographica Section C: Crystal Structure Communications, 1995, 51, 619-621.	0.4	8