Fernanda Canduri

List of Publications by Year
in descending order

47 papers	1,489 citations	236912 25 h-index	315719 38 g-index
48 all docs	48 docs citations	48 times ranked	1223 citing authors

#	Article	IF	Citations
1	Overview of PCTK3/CDK18: A Cyclin-Dependent Kinase Involved in Specific Functions in Post-Mitotic Cells. Current Medicinal Chemistry, 2021, 28, 6846-6865.	2.4	7
2	Influence of pH, temperature, and sisal pulp on the production of cellulases from Aspergillus sp. CBMAI 1198 and hydrolysis of cellulosic materials with different hemicelluloses content, crystallinity, and average molar mass. Biomass Conversion and Biorefinery, 2020, 10, 483-494.	4.6	8
3	New inhibitors of homoserine dehydrogenase from Paracoccidioides brasiliensis presenting antifungal activity. Journal of Molecular Modeling, 2019, 25, 325.	1.8	13
4	New 4-methoxy-naphthalene derivatives as promisor antifungal agents for paracoccidioidomycosis treatment. Future Microbiology, 2019, 14, 235-245.	2.0	8
5	Heterologous expression of Homo sapiens alpha-folate receptors in E. coli by fusion with a trigger factor for enhanced solubilization. Protein Expression and Purification, 2018, 142, 75-80.	1.3	3
6	The Emerging Picture of CDK11: Genetic, Functional and Medicinal Aspects. Current Medicinal Chemistry, 2018, 25, 880-888.	2.4	22
7	The emerging picture of CDK9/P-TEFb: more than 20 years of advances since PITALRE. Molecular BioSystems, 2017, 13, 246-276.	2.9	51
8	Structural studies of the Trypanosoma cruzi Old Yellow Enzyme: Insights into enzyme dynamics and specificity. Biophysical Chemistry, 2013, 184, 44-53.	2.8	18
9	Expression, purification and molecular analysis of the human ZNF706 protein. Biological Procedures Online, 2013, 15, 10.	2.9	7
10	Molecular modeling and dynamics simulation of human cyclin-dependent kinase 3 complexed with inhibitors. Computers in Biology and Medicine, 2009, 39, 130-140.	7.0	19
11	Protein Crystallography in Drug Discovery. Current Drug Targets, 2008, 9, 1048-1053.	2.1	45
12	Protein Kinases as Targets for Antiparasitic Chemotherapy Drugs. Current Drug Targets, 2007, 8, 389-398.	2.1	58
13	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.	4.2	67
14	Expression, purification, and circular dichroism analysis of human CDK9. Protein Expression and Purification, 2006, 47, 614-620.	1.3	9
15	DBMODELING: A Database Applied to the Study of Protein Targets From Genome Projects. Cell Biochemistry and Biophysics, 2006, 44, 366-374.	1.8	11
16	Molecular Models of Tryptophan Synthase From Mycobacterium tuberculosis Complexed With Inhibitors. Cell Biochemistry and Biophysics, 2006, 44, 375-384.	1.8	14
17	Determining the Structural Basis for Specificity of Ligands Using Crystallographic Screening. Cell Biochemistry and Biophysics, 2006, 44, 405-411.	1.8	10
18	Molecular models of protein kinase 6 from Plasmodium falciparum. Journal of Molecular Modeling, 2005, 12, 42-48.	1.8	27

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19	Molecular models of protein targets from Mycobacterium tuberculosis. Journal of Molecular Modeling, 2005, 11, 160-166.	1.8	21
20	Structure of human PNP complexed with ligands. Acta Crystallographica Section D: Biological Crystallography, 2005, 61, 856-862.	2.5	33
21	Structural Basis for Interaction of Inhibitors with Cyclin-Dependent Kinase 2. Current Computer-Aided Drug Design, 2005, 1, 53-64.	1.2	25
22	Crystal structure of human PNP complexed with hypoxanthine and sulfate ion. Biochemical and Biophysical Research Communications, 2005, 326, 335-338.	2.1	33
23	New catalytic mechanism for human purine nucleoside phosphorylase. Biochemical and Biophysical Research Communications, 2005, 327, 646-649.	2.1	44
24	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.	3.0	37
25	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
26	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
27	Structure of shikimate kinase fromMycobacterium tuberculosisreveals the binding of shikimic acid. Acta Crystallographica Section D: Biological Crystallography, 2004, 60, 2310-2319.	2.5	48
28	Structures of human purine nucleoside phosphorylase complexed with inosine and ddI. Biochemical and Biophysical Research Communications, 2004, 313, 907-914.	2.1	55
29	Molecular models for shikimate pathway enzymes of Xylella fastidiosa. Biochemical and Biophysical Research Communications, 2004, 320, 979-991.	2.1	30
30	Structural bioinformatics study of PNP from Schistosoma mansoni. Biochemical and Biophysical Research Communications, 2004, 322, 100-104.	2.1	29
31	Molecular models of cyclin-dependent kinase 1 complexed with inhibitors. Biochemical and Biophysical Research Communications, 2004, 324, 661-666.	2.1	44
32	Crystallographic structure of PNP from Mycobacterium tuberculosis at 1.9Ã... resolution. Biochemical and Biophysical Research Communications, 2004, 324, 789-794.	2.1	25
33	Parmodel: a web server for automated comparative modeling of proteins. Biochemical and Biophysical Research Communications, 2004, 325, 1481-1486.	2.1	58
34	Structural basis for inhibition of human PNP by immucillin-H. Biochemical and Biophysical Research Communications, 2003, 309, 917-922.	2.1	47
35	Structural bioinformatics study of EPSP synthase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2003, 312, 608-614.	2.1	51
36	Crystal structure of human PNP complexed with guanine. Biochemical and Biophysical Research Communications, 2003, 312, 767-772.	2.1	39

#	Article	IF	Citations
37	Crystal structure of human purine nucleoside phosphorylase at 2.3Ã... resolution. Biochemical and Biophysical Research Communications, 2003, 308, 545-552.	2.1	54
38	Crystal structure of human purine nucleoside phosphorylase complexed with acyclovir. Biochemical and Biophysical Research Communications, 2003, 308, 553-559.	2.1	58
39	Crystal Structure of Hemoglobin from the Maned Wolf (Chrysocyon Brachyurus) Using Synchrotron Radiation. Protein and Peptide Letters, 2003, 10, 551-559.	0.9	1
40	Docking and small angle X-ray scattering studies of purine nucleoside phosphorylase. Biochemical and Biophysical Research Communications, 2003, 309, 923-8.	2.1	5
41	Structural basis for inhibition of cyclin-dependent kinase 9 by flavopiridol. Biochemical and Biophysical Research Communications, 2002, 293, 566-571.	2.1	128
42	Molecular model of shikimate kinase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2002, 295, 142-148.	2.1	50
43	Molecular model of cyclin-dependent kinase 5 complexed with roscovitine. Biochemical and Biophysical Research Communications, 2002, 297, 1154-1158.	2.1	66
44	Molecular Model for the Binary Complex of Uropepsin and Pepstatin. Biochemical and Biophysical Research Communications, 2001, 287, 277-281.	2.1	44
45	Structure of human uropepsin at 2.45â€...Ã... resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1560-1570.	2.5	32
46	Crystallographic studies of fish hemoglobins. Ecletica Quimica, 2000, 25, 147-159.	0.5	2
47	Crystallization of piratoxin I, a myotoxic Lys49-phospholipase A2 homologue isolated from the venom of Bothrops pirajai. Toxicon, 1998, 36, 547-551.	1.6	7