

Fernanda Canduri

List of Publications by Year in descending order

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47
papers

1,489
citations

270111

25
h-index

355658

38
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48
all docs

48
docs citations

48
times ranked

1352
citing authors

#	ARTICLE	IF	CITATIONS
1	Overview of PCK3/CDK18: A Cyclin-Dependent Kinase Involved in Specific Functions in Post-Mitotic Cells. <i>Current Medicinal Chemistry</i> , 2021, 28, 6846-6865.	1.2	7
2	Influence of pH, temperature, and sisal pulp on the production of cellulases from <i>Aspergillus</i> sp. CBMAI 1198 and hydrolysis of cellulosic materials with different hemicelluloses content, crystallinity, and average molar mass. <i>Biomass Conversion and Biorefinery</i> , 2020, 10, 483-494.	2.9	8
3	New inhibitors of homoserine dehydrogenase from <i>Paracoccidioides brasiliensis</i> presenting antifungal activity. <i>Journal of Molecular Modeling</i> , 2019, 25, 325.	0.8	13
4	New 4-methoxy-naphthalene derivatives as promisor antifungal agents for paracoccidioidomycosis treatment. <i>Future Microbiology</i> , 2019, 14, 235-245.	1.0	8
5	Heterologous expression of Homo sapiens alpha-folate receptors in E. coli by fusion with a trigger factor for enhanced solubilization. <i>Protein Expression and Purification</i> , 2018, 142, 75-80.	0.6	3
6	The Emerging Picture of CDK11: Genetic, Functional and Medicinal Aspects. <i>Current Medicinal Chemistry</i> , 2018, 25, 880-888.	1.2	22
7	The emerging picture of CDK9/P-TEFb: more than 20 years of advances since PITALRE. <i>Molecular BioSystems</i> , 2017, 13, 246-276.	2.9	51
8	Structural studies of the Trypanosoma cruzi Old Yellow Enzyme: Insights into enzyme dynamics and specificity. <i>Biophysical Chemistry</i> , 2013, 184, 44-53.	1.5	18
9	Expression, purification and molecular analysis of the human ZNF706 protein. <i>Biological Procedures Online</i> , 2013, 15, 10.	1.4	7
10	Molecular modeling and dynamics simulation of human cyclin-dependent kinase 3 complexed with inhibitors. <i>Computers in Biology and Medicine</i> , 2009, 39, 130-140.	3.9	19
11	Protein Crystallography in Drug Discovery. <i>Current Drug Targets</i> , 2008, 9, 1048-1053.	1.0	45
12	Protein Kinases as Targets for Antiparasitic Chemotherapy Drugs. <i>Current Drug Targets</i> , 2007, 8, 389-398.	1.0	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. <i>Journal of Molecular Biology</i> , 2006, 359, 646-666.	2.0	67
14	Expression, purification, and circular dichroism analysis of human CDK9. <i>Protein Expression and Purification</i> , 2006, 47, 614-620.	0.6	9
15	DBMODELING: A Database Applied to the Study of Protein Targets From Genome Projects. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 366-374.	0.9	11
16	Molecular Models of Tryptophan Synthase From Mycobacterium tuberculosis Complexed With Inhibitors. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 375-384.	0.9	14
17	Determining the Structural Basis for Specificity of Ligands Using Crystallographic Screening. <i>Cell Biochemistry and Biophysics</i> , 2006, 44, 405-411.	0.9	10
18	Molecular models of protein kinase 6 from Plasmodium falciparum. <i>Journal of Molecular Modeling</i> , 2005, 12, 42-48.	0.8	27

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19	Molecular models of protein targets from <i>Mycobacterium tuberculosis</i> . <i>Journal of Molecular Modeling</i> , 2005, 11, 160-166.	0.8	21
20	Structure of human PNP complexed with ligands. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 856-862.	2.5	33
21	Structural Basis for Interaction of Inhibitors with Cyclin-Dependent Kinase 2. <i>Current Computer-Aided Drug Design</i> , 2005, 1, 53-64.	0.8	25
22	Crystal structure of human PNP complexed with hypoxanthine and sulfate ion. <i>Biochemical and Biophysical Research Communications</i> , 2005, 326, 335-338.	1.0	33
23	New catalytic mechanism for human purine nucleoside phosphorylase. <i>Biochemical and Biophysical Research Communications</i> , 2005, 327, 646-649.	1.0	44
24	Kinetics and crystal structure of human purine nucleoside phosphorylase in complex with 7-methyl-6-thio-guanosine. <i>Archives of Biochemistry and Biophysics</i> , 2005, 442, 49-58.	1.4	37
25	Crystallization and preliminary X-ray diffraction analysis of the lectin from <i>Canavalia gladiata</i> seeds. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1493-1495.	2.5	13
26	Crystallization and preliminary X-ray crystallographic analysis of chorismate synthase from <i>Mycobacterium tuberculosis</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2003-2005.	2.5	8
27	Structure of shikimate kinase from <i>Mycobacterium tuberculosis</i> reveals the binding of shikimic acid. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 2310-2319.	2.5	48
28	Structures of human purine nucleoside phosphorylase complexed with inosine and ddi. <i>Biochemical and Biophysical Research Communications</i> , 2004, 313, 907-914.	1.0	55
29	Molecular models for shikimate pathway enzymes of <i>Xylella fastidiosa</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 320, 979-991.	1.0	30
30	Structural bioinformatics study of PNP from <i>Schistosoma mansoni</i> . <i>Biochemical and Biophysical Research Communications</i> , 2004, 322, 100-104.	1.0	29
31	Molecular models of cyclin-dependent kinase 1 complexed with inhibitors. <i>Biochemical and Biophysical Research Communications</i> , 2004, 324, 661-666.	1.0	44
32	Crystallographic structure of PNP from <i>Mycobacterium tuberculosis</i> at 1.9Å... resolution. <i>Biochemical and Biophysical Research Communications</i> , 2004, 324, 789-794.	1.0	25
33	Parmodel: a web server for automated comparative modeling of proteins. <i>Biochemical and Biophysical Research Communications</i> , 2004, 325, 1481-1486.	1.0	58
34	Structural basis for inhibition of human PNP by immucillin-H. <i>Biochemical and Biophysical Research Communications</i> , 2003, 309, 917-922.	1.0	47
35	Structural bioinformatics study of EPSP synthase from <i>Mycobacterium tuberculosis</i> . <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 608-614.	1.0	51
36	Crystal structure of human PNP complexed with guanine. <i>Biochemical and Biophysical Research Communications</i> , 2003, 312, 767-772.	1.0	39

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37	Crystal structure of human purine nucleoside phosphorylase at 2.3Å... resolution. Biochemical and Biophysical Research Communications, 2003, 308, 545-552.	1.0	54
38	Crystal structure of human purine nucleoside phosphorylase complexed with acyclovir. Biochemical and Biophysical Research Communications, 2003, 308, 553-559.	1.0	58
39	Crystal Structure of Hemoglobin from the Maned Wolf (<i>Chrysocyon Brachyurus</i>) Using Synchrotron Radiation. Protein and Peptide Letters, 2003, 10, 551-559.	0.4	1
40	Docking and small angle X-ray scattering studies of purine nucleoside phosphorylase. Biochemical and Biophysical Research Communications, 2003, 309, 923-8.	1.0	5
41	Structural basis for inhibition of cyclin-dependent kinase 9 by flavopiridol. Biochemical and Biophysical Research Communications, 2002, 293, 566-571.	1.0	128
42	Molecular model of shikimate kinase from Mycobacterium tuberculosis. Biochemical and Biophysical Research Communications, 2002, 295, 142-148.	1.0	50
43	Molecular model of cyclin-dependent kinase 5 complexed with roscovitine. Biochemical and Biophysical Research Communications, 2002, 297, 1154-1158.	1.0	66
44	Molecular Model for the Binary Complex of Uropepsin and Pepstatin. Biochemical and Biophysical Research Communications, 2001, 287, 277-281.	1.0	44
45	Structure of human uropepsin at 2.45Å... resolution. Acta Crystallographica Section D: Biological Crystallography, 2001, 57, 1560-1570.	2.5	32
46	Crystallographic studies of fish hemoglobins. Ectetica Quimica, 2000, 25, 147-159.	0.2	2
47	Crystallization of piratoxin I, a myotoxic Lys49-phospholipase A2 homologue isolated from the venom of <i>Bothrops pirajai</i> . Toxicon, 1998, 36, 547-551.	0.8	7