

Maria Miller

List of Publications by Year in descending order

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42
papers

5,089
citations

279798

23
h-index

302126

39
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42
all docs

42
docs citations

42
times ranked

3387
citing authors

#	ARTICLE	IF	CITATIONS
1	Conserved folding in retroviral proteases: crystal structure of a synthetic HIV-1 protease. <i>Science</i> , 1989, 245, 616-621.	12.6	1,201
2	Structure of complex of synthetic HIV-1 protease with a substrate-based inhibitor at 2.3 Å resolution. <i>Science</i> , 1989, 246, 1149-1152.	12.6	735
3	Novel mutations of the MET proto-oncogene in papillary renal carcinomas. <i>Oncogene</i> , 1999, 18, 2343-2350.	5.9	487
4	Crystal structure of a retroviral protease proves relationship to aspartic protease family. <i>Nature</i> , 1989, 337, 576-579.	27.8	378
5	X-ray crystallographic structure of a complex between a synthetic protease of human immunodeficiency virus 1 and a substrate-based hydroxyethylamine inhibitor.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 8805-8809.	7.1	295
6	Crystal structure analysis and refinement at 2.5 Å of hexameric C-phycocyanin from the cyanobacterium <i>Agmenellum quadruplicatum</i> . <i>Journal of Molecular Biology</i> , 1986, 188, 651-676.	4.2	269
7	Active site of RNase: neutron diffraction study of a complex with uridine vanadate, a transition-state analog.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1983, 80, 3628-3631.	7.1	186
8	Molecular modeling of the HIV-1 protease and its substrate binding site. <i>Science</i> , 1989, 243, 928-931.	12.6	179
9	Nuclear magnetic resonance and neutron diffraction studies of the complex of ribonuclease A with uridine vanadate, a transition-state analog. <i>Biochemistry</i> , 1985, 24, 2058-2067.	2.5	163
10	Structural Basis for p300 Taz2-p53 TAD1 Binding and Modulation by Phosphorylation. <i>Structure</i> , 2009, 17, 202-210.	3.3	126
11	Structural Basis for DNA Recognition by the Basic Region Leucine Zipper Transcription Factor CCAAT/Enhancer-binding Protein 1±. <i>Journal of Biological Chemistry</i> , 2003, 278, 15178-15184.	3.4	119
12	Structure of the aspartic protease from Rous sarcoma retrovirus refined at 2-Å resolution. <i>Biochemistry</i> , 1990, 29, 5889-5898.	2.5	100
13	The Importance of Being Flexible: The Case of Basic Region Leucine Zipper Transcriptional Regulators. <i>Current Protein and Peptide Science</i> , 2009, 10, 244-269.	1.4	91
14	Crystal structure of 15-mer DNA duplex containing unpaired bases. <i>Nature</i> , 1988, 334, 85-86.	27.8	77
15	A left-handed crossover involved in amidohydrolase catalysis. <i>FEBS Letters</i> , 1993, 328, 275-279.	2.8	76
16	Two Distinct Motifs within the p53 Transactivation Domain Bind to the Taz2 Domain of p300 and Are Differentially Affected by Phosphorylation. <i>Biochemistry</i> , 2009, 48, 1244-1255.	2.5	63
17	RSK-Mediated Phosphorylation in the C/EBPβ Leucine Zipper Regulates DNA Binding, Dimerization, and Growth Arrest Activity. <i>Molecular and Cellular Biology</i> , 2010, 30, 2621-2635.	2.3	63
18	Crystal structure of two covalent nucleoside derivatives of ribonuclease A. <i>Biochemistry</i> , 1990, 29, 928-937.	2.5	60

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19	Structural basis of oncogenic activation caused by point mutations in the kinase domain of the MET proto-oncogene: Modeling studies. <i>Proteins: Structure, Function and Bioinformatics</i> , 2001, 44, 32-43.	2.6	60
20	Mechanism of oligonucleotide loop formation in solution. <i>Biochemistry</i> , 1986, 25, 7417-7423.	2.5	48
21	CCAAT/Enhancer-binding Protein \hat{I}^2 DNA Binding Is Auto-inhibited by Multiple Elements That Also Mediate Association with p300/CREB-binding Protein (CBP). <i>Journal of Biological Chemistry</i> , 2010, 285, 21399-21410.	3.4	39
22	The oligomerization domain of p53: Crystal structure of the trigonal form. <i>FEBS Letters</i> , 1996, 399, 166-170.	2.8	37
23	Interaction of Macrophage-stimulating Protein with Its Receptor. <i>Journal of Biological Chemistry</i> , 1999, 274, 29937-29943.	3.4	35
24	Structural insights into interactions of C/EBP transcriptional activators with the Taz2 domain of p300. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 1914-1921.	2.5	21
25	Conformational transitions of synthetic DNA sequences with inserted bases, related to the dodecamer d(CGCGAATTCGCG). <i>Nucleic Acids Research</i> , 1987, 15, 3877-3890.	14.5	16
26	Mode of receptor binding and activation by plasminogen-related growth factors1. <i>FEBS Letters</i> , 1998, 429, 1-3.	2.8	16
27	Crystal structures of the reverse transcriptase-associated ribonuclease H domain of xenotropic murine leukemia-virus related virus. <i>Journal of Structural Biology</i> , 2012, 177, 638-645.	2.8	16
28	Red-ox transformations of NAD ⁺ model compounds. <i>Bioelectrochemistry</i> , 1982, 9, 287-298.	1.0	15
29	Analysis of the structure of chemically synthesized HIV-1 protease complexed with a hexapeptide inhibitor. Part I: Crystallographic refinement of 2 Å... data. , 1997, 27, 184-195.		15
30	Analysis of the structure of HIV-1 protease complexed with a hexapeptide inhibitor. Part II: Molecular dynamic studies of the active site region. , 1997, 27, 195-203.		13
31	Structure of the Taz2 domain of p300: insights into ligand binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2009, 65, 1301-1308.	2.5	13
32	Structure of Monellin Refined to 2.3 Å... Resolution in the Orthorhombic Crystal Form. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 1997, 53, 713-719.	2.5	12
33	The early years of retroviral protease crystal structures. <i>Biopolymers</i> , 2010, 94, 521-529.	2.4	12
34	Probing the structural basis of the catalytic activity of HIV-1 PR through total chemical protein synthesis. <i>Computational and Theoretical Chemistry</i> , 1998, 423, 137-152.	1.5	9
35	Phospho-dependent Protein Recognition Motifs Contained in C/EBP Family of Transcription Factors: in Silico Studies. <i>Cell Cycle</i> , 2006, 5, 2501-2508.	2.6	9
36	The effects of tetraalkylammonium salts on helix-coil transition parameters in natural and synthetic ribo- and deoxyribo-polynucleotides. <i>Chemico-Biological Interactions</i> , 1980, 30, 209-222.	4.0	8

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37	Elucidation of the structure of retroviral proteases: aÂreminiscence. FEBS Journal, 2015, 282, 4059-4066.	4.7	8
38	Crystallization of a DNA duplex 15-mer containing unpaired bases: d(CGCGAAATTTACGCG). Journal of Molecular Biology, 1987, 195, 967-968.	4.2	7
39	Preliminary crystallographic study of a retroviral protease. Journal of Molecular Biology, 1988, 204, 211-212.	4.2	7
40	Breaking the Shackles of the Genetic Code: Engineering Retroviral Proteases Through Total Chemical Synthesis. Advances in Experimental Medicine and Biology, 1995, 362, 425-438.	1.6	3
41	A comparison of the crystal structures of bacterial l-asparaginases. Techniques in Protein Chemistry, 1996, 7, 373-IN1.	0.3	1
42	X-Ray Analysis of HIV-1 Protease and Its Complexes with Inhibitors. , 1990, , 93-106.		1