Maria Miller

List of Publications by Year
in descending order

42 papers	5,089 citations	279798 23 h-index	302126 39 g-index
42 all docs	42 docs citations	42 times ranked	3387 citing authors

#	Article	IF	Citations
1	Elucidation of the structure of retroviral proteases: aÂreminiscence. FEBS Journal, 2015, 282, 4059-4066.	4.7	8
2	Structural insights into interactions of C/EBP transcriptional activators with the Taz2 domain of p300. Acta Crystallographica Section D: Biological Crystallography, 2014, 70, 1914-1921.	2.5	21
3	Crystal structures of the reverse transcriptase-associated ribonuclease H domain of xenotropic murine leukemia-virus related virus. Journal of Structural Biology, 2012, 177, 638-645.	2.8	16
4	The early years of retroviral protease crystal structures. Biopolymers, 2010, 94, 521-529.	2.4	12
5	RSK-Mediated Phosphorylation in the C/EBPÎ² Leucine Zipper Regulates DNA Binding, Dimerization, and Growth Arrest Activity. Molecular and Cellular Biology, 2010, 30, 2621-2635.	2.3	63
6	CCAAT/Enhancer-binding Protein Î² DNA Binding Is Auto-inhibited by Multiple Elements That Also Mediate Association with p300/CREB-binding Protein (CBP). Journal of Biological Chemistry, 2010, 285, 21399-21410.	3.4	39
7	Structural Basis for p300 Taz2-p53 TAD1 Binding and Modulation by Phosphorylation. Structure, 2009, 17, 202-210.	3.3	126
8	Structure of the Taz2 domain of p300: insights into ligand binding. Acta Crystallographica Section D: Biological Crystallography, 2009, 65, 1301-1308.	2.5	13
9	Two Distinct Motifs within the p53 Transactivation Domain Bind to the Taz2 Domain of p300 and Are Differentially Affected by Phosphorylation. Biochemistry, 2009, 48, 1244-1255.	2.5	63
10	The Importance of Being Flexible: The Case of Basic Region Leucine Zipper Transcriptional Regulators. Current Protein and Peptide Science, 2009, 10, 244-269.	1.4	91
11	Phospho-dependent Protein Recognition Motifs Contained in C/EBP Family of Transcription Factors: in Silico Studies. Cell Cycle, 2006, 5, 2501-2508.	2.6	9
12	Structural Basis for DNA Recognition by the Basic Region Leucine Zipper Transcription Factor CCAAT/Enhancer-binding Protein Î±. Journal of Biological Chemistry, 2003, 278, 15178-15184.	3.4	119
13	Structural basis of oncogenic activation caused by point mutations in the kinase domain of the MET proto-oncogene: Modeling studies. Proteins: Structure, Function and Bioinformatics, 2001, 44, 32-43.	2.6	60
14	Interaction of Macrophage-stimulating Protein with Its Receptor. Journal of Biological Chemistry, 1999, 274, 29937-29943.	3.4	35
15	Novel mutations of the MET proto-oncogene in papillary renal carcinomas. Oncogene, 1999, 18, 2343-2350.	5.9	487
16	Probing the structural basis of the catalytic activity of HIV-1 PR through total chemical protein synthesis. Computational and Theoretical Chemistry, 1998, 423, 137-152.	1.5	9
17	Mode of receptor binding and activation by plasminogen-related growth factors1. FEBS Letters, 1998, 429, 1-3.	2.8	16
18	Structure of Monellin Refined to 2.3 Ã... Resolution in the Orthorhombic Crystal Form. Acta Crystallographica Section D: Biological Crystallography, 1997, 53, 713-719.	2.5	12

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19	Analysis of the structure of chemically synthesized HIV-1 protease complexed with a hexapeptide inhibitor. Part I: Crystallographic refinement of 2 Ã... data. , 1997, 27, 184-195.		15
20	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
21	The oligomerization domain of p53: Crystal structure of the trigonal form. FEBS Letters, 1996, 399, 166-170.	2.8	37
22	A comparison of the crystal structures of bacterial l-asparaginases. Techniques in Protein Chemistry, 1996, 7, 373-IN1.	0.3	1
23	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
24	A left-handed crossover involved in amidohydrolase catalysis. FEBS Letters, 1993, 328, 275-279.	2.8	76
25	X-ray crystallographic structure of a complex between a synthetic protease of human immunodeficiency virus 1 and a substrate-based hydroxyethylamine inhibitor.. Proceedings of the National Academy of Sciences of the United States of America, 1990, 87, 8805-8809.	7.1	295
26	Crystal structure of two covalent nucleoside derivatives of ribonuclease A. Biochemistry, 1990, 29, 928-937.	2.5	60
27	Structure of the aspartic protease from Rous sarcoma retrovirus refined at 2-.ANG. resolution. Biochemistry, 1990, 29, 5889-5898.	2.5	100
28	X-Ray Analysis of HIV-1 Protease and Its Complexes with Inhibitors. , 1990, , 93-106.		1
29	Conserved folding in retroviral proteases: crystal structure of a synthetic HIV-1 protease. Science, 1989, 245, 616-621.	12.6	1,201
30	Crystal structure of a retroviral protease proves relationship to aspartic protease family. Nature, 1989, 337, 576-579.	27.8	378
31	Molecular modeling of the HIV-1 protease and its substrate binding site. Science, 1989, 243, 928-931.	12.6	179
32	Structure of complex of synthetic HIV-1 protease with a substrate-based inhibitor at 2.3 A resolution. Science, 1989, 246, 1149-1152.	12.6	735
33	Crystal structure of 15-mer DNA duplex containing unpaired bases. Nature, 1988, 334, 85-86.	27.8	77
34	Preliminary crystallographic study of a retroviral protease. Journal of Molecular Biology, 1988, 204, 211-212.	4.2	7
35	Conformational transitions of synthetic DNA sequences with inserted bases, related to the dodecamer d(CGCGAATTCGCG). Nucleic Acids Research, 1987, 15, 3877-3890.	14.5	16
36	Crystallization of a DNA duplex 15-mer containing unpaired bases: d(CGCGAAATTTACGCG). Journal of Molecular Biology, 1987, 195, 967-968.	4.2	7

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37	Mechanism of oligonucleotide loop formation in solution. Biochemistry, 1986, 25, 7417-7423.	2.5	48
38	Crystal structure analysis and refinement at 2Â·5 Ã... of hexameric C-phycocyanin from the cyanobacterium Agmenellum quadruplicatum. Journal of Molecular Biology, 1986, 188, 651-676.	4.2	269
39	Nuclear magnetic resonance and neutron diffraction studies of the complex of ribonuclease A with uridine vanadate, a transition-state analog. Biochemistry, 1985, 24, 2058-2067.	2.5	163
40	Active site of RNase: neutron diffraction study of a complex with uridine vanadate, a transition-state analog.. Proceedings of the National Academy of Sciences of the United States of America, 1983, 80, 3628-3631.	7.1	186
41	Red-ox transformations of NAD+ model compounds. Bioelectrochemistry, 1982, 9, 287-298.	1.0	15
42	The effects of tetraalkylammonium salts on helix-coil transition parameters in natural and synthetic ribo- and deoxyribo-polynucleotides. Chemico-Biological Interactions, 1980, 30, 209-222.	4.0	8